GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: December 4, 2006, 18:35:25 ; Search time 2612 Seconds
(without alignments)
11046.851 Million cell updates/sec

Title: US-10-507-132-1
Perfect score: 516
Sequence: 1 atgggttcgcaagttcaaaa.....gggagacctttggcgacaaa 516

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	512.8	99.4	619	3	BM863356	BM863356 mgcm006xO
	2	511.8	99.2	657	3	BM864194	BM864194 mgcm008xJ
	3	511.2	99.1	664	3	BM863315	BM863315 mgcm006xE
	4	509.6	98.8	649	3	BM863340	BM863340 mgcm006xK
	5	487	94.4	593	3	BM863546	BM863546 mgcm006xF
	6	468.2	90.7	599	3	BM864156	BM864156 mgcm008xD
	7	460.8	89.3	571	3	BM863710	BM863710 mgcm007xE
	8	454.4	88.1	643	3	BM864467	BM864467 mgcm010xH
	9	448	86.8	602	3	BM863558	BM863558 mgcm006xH
	10	434.8	84.3	523	3	BM863209	BM863209 mgcm005xD
	11	422.4	81.9	486	3	BM863639	BM863639 mgcm007xG
	12	406.4	78.8	600	3	BM864472	BM864472 mgcm010xJ
c	13	398.8	77.3	781	3	BM864820	BM864820 mgap007xA
	14	394.4	76.4	530	3	BM863357	BM863357 mgcm006xO
	15	392.8	76.1	510	3	BM863374	BM863374 mgcm006xC
	16	384	74.4	504	3	BM863499	BM863499 mgcm006xL
	17	372.4	72.2	515	3	BM861796	BM861796 mgcm001xI
	18	356.6	69.1	430	4	CD028671	CD028671 mgcm007xH
	19	356.4	69.1	473	3	BM864018	BM864018 mgcm008xG
	20	303.8	58.9	366	3	BM864053	BM864053 mgcm008xM
	21	301.4	58.4	398	3	BM861952	BM861952 mgcm001xL
c	22	298.6	57.9	570	4	CD034317	CD034317 mgmt015xP
c	23	292.8	56.7	541	4	CD036729	CD036729 mgsu011xC
c	24	267	51.7	491	4	CD035038	CD035038 mgmt018xH
	25	260	50.4	552	5	CD275566	CD275566 T143B0121
	26	260	50.4	588	5	CD275905	CD275905 T143B0122
c	27	257.8	50.0	489	3	BM863213	BM863213 mgcm005xD
c	28	257	49.8	486	4	CD035120	CD035120 mgmt018xL
	29	239.6	46.4	499	5	CD273332	CD273332 T143B0196
	30	237	45.9	530	5	CD275940	CD275940 T143B0156
	31	232.2	45.0	507	5	CD275678	CD275678 T143B0071
	32	230.8	44.7	573	3	BQ109916	BQ109916 VD0100E09
	33	217	42.1	429	5	CD274144	CD274144 T143B0403
	34	213.4	41.4	441	3	BM871833	BM871833 mgns015xB
	35	181.6	35.2	377	5	CD276416	CD276416 T143B0271
c	36	124.2	24.1	670	7	BE188285	BE188285 PSI61F In
	37	112.2	21.7	476	2	BG280255	BG280255 c2b06np.r
	38	107	20.7	363	3	BP100008	BP100008 BP100008
	39	105	20.3	563	5	CK906746	CK906746 rhzma0_00
	40	91.4	17.7	697	7	BE188286	BE188286 PSI61R3 I
c	41	86.8	16.8	881	9	DN476575	DN476575 altr207xo
	42	79.2	15.3	620	4	CD028659	CD028659 mgcm006xG
c	43	71.8	13.9	295	3	BM863872	BM863872 mgcm007xL
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ALIGNMENTS

RESULT 1
BM863356
LOCUS BM863356 619 bp mRNA linear EST 06-MAY-2003
DEFINITION mgcm006xO03f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm006xO03 5', mRNA sequence.
ACCESSION BM863356
VERSION BM863356.2 GI:30391591
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE 1 (bases 1 to 619)
AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.
TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe grisea
JOURNAL Unpublished (2002)
COMMENT On Mar 7, 2002 this sequence version replaced gi:19231038.
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone dehydratase >gi|1127197|pdb|1STD|. . . 367 e-101
PCR PRimers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgcm006 row: O column: 03
Seq primer: T3.
FEATURES Location/Qualifiers
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/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="Guy11"
/db_xref="taxon:148305"
/clone="mgcm006xO03"
/sex="Mat1-2 hermaphrodite"

/cell_type="mycelium"
/clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2: XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

ORIGIN

Query Match 99.4%; Score 512.8; DB 3; Length 619;
Best Local Similarity 99.6%; Pred. No. 4.3e-115;
Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         53 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 112

Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
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Db        113 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 172

Qy        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180
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Db        173 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 232

Qy        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        233 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 292

Qy        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 352

Qy        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 412

Qy        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 472

Qy        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480
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Db        473 GTCTGGAAGTTCGCCGGCCTCAAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGG 532

Qy        481 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516
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Db        533 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 568
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RESULT 2
BM864194
LOCUS BM864194 657 bp mRNA linear EST 06-MAY-2003
DEFINITION mgcm008xJ12f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm008xJ12 5', mRNA sequence.
ACCESSION BM864194
VERSION BM864194.2 GI:30390885
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE 1 (bases 1 to 657)
AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.
TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe grisea
JOURNAL Unpublished (2002)
COMMENT On Mar 7, 2002 this sequence version replaced gi:19231876.
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone dehydratase >gi|1127197|pdb|1STD|. . . 365 e-100
PCR PRimers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgcm008 row: J column: 12
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .657
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="Guy11"
/db_xref="taxon:148305"
/clone="mgcm008xJ12"
/sex="Mat1-2 hermaphrodite"
/cell_type="mycelium"
/clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2: XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

ORIGIN

Query Match 99.2%; Score 511.8; DB 3; Length 657;
Best Local Similarity 99.4%; Pred. No. 7.6e-115;
Matches 513; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 150

Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 210

Qy        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180
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Db        211 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 270

Qy        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        271 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 330

Qy        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 390

Qy        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 450

Qy        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420
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Db        451 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 510
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Qy        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480
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Db        511 GTCTGGAAGTTCGCCGGCCTCAAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGG 570

Qy        481 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516
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Db        571 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACANA 606


RESULT 3
BM863315
LOCUS       BM863315                664 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm006xE21f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm006xE21 5', mRNA sequence.
ACCESSION   BM863315
VERSION     BM863315.2  GI:30391622
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 664)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19230997.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 364 e-100
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm006  row: E  column: 21
            Seq primer: T3.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm006xE21"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

  Query Match             99.1%;  Score 511.2;  DB 3;  Length 664;
  Best Local Similarity   99.4%;  Pred. No. 1.1e-114;
  Matches  513;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60
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Db         81 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 140

Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
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Db        141 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 200

Qy        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180
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Db        201 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 260

Qy        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        261 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 320

Qy        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300
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Db        321 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 380

Qy        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360
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Db        381 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 440

Qy        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420
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Db        441 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 500

Qy        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480
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Db        501 GTCTGGAAGTTCGCCGGCCTCAAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGG 560

Qy        481 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516
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Db        561 ATCTTTGAGGACGGACGGGAGACCTTGGGCGACAAA 596


RESULT 4
BM863340
LOCUS       BM863340                649 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm006xK09f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm006xK09 5', mRNA sequence.
ACCESSION   BM863340
VERSION     BM863340.2  GI:30391603
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 649)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19231022.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 361 5e-99
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm006  row: K  column: 09
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .649
                     /organism="Magnaporthe grisea"
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/mol_type="mRNA"
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/db_xref="taxon:148305"
/clone="mgcm006xK09"
/sex="Mat1-2 hermaphrodite"
/cell_type="mycelium"
/clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2: XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

ORIGIN

Query Match 98.8%; Score 509.6; DB 3; Length 649;
Best Local Similarity 99.2%; Pred. No. 2.6e-114;
Matches 512; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60
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Db         84 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 143

Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        144 ACTTGCGTCTATGAGTGGGCAGACAGCTACTACTCCAAGGACTGGGATAGGCTGCGAAAG 203

Qy        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 263

Qy        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        264 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 323

Qy        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 383

Qy        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 443

Qy        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        444 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTTACTGGTACAAGAAGATCGACGGC 503

Qy        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        504 GTCTGGAAGTTCGCCGGCCTCAAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGG 563

Qy        481 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516
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Db        564 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 599
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RESULT 5
BM863546
LOCUS BM863546 593 bp mRNA linear EST 06-MAY-2003
DEFINITION mgcm006xF04f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm006xF04 5', mRNA sequence.
ACCESSION BM863546
VERSION BM863546.2 GI:30391437
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE 1 (bases 1 to 593)
AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.
TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe grisea
JOURNAL Unpublished (2002)
COMMENT On Mar 7, 2002 this sequence version replaced gi:19231228.
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone dehydratase >gi|1127197|pdb|1STD|. . . 322 2e-87
PCR PRimers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgcm006 row: F column: 04
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .593
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="Guy11"
/db_xref="taxon:148305"
/clone="mgcm006xF04"
/sex="Mat1-2 hermaphrodite"
/cell_type="mycelium"
/clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2: XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

ORIGIN

Query Match 94.4%; Score 487; DB 3; Length 593;
Best Local Similarity 97.7%; Pred. No. 9.1e-109;
Matches 504; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

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Qy          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 138

Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 198

Qy        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180
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Db        199 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 258

Qy        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        259 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 318

Qy        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        319 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGAGAGAAGGTGTCCGAGGACGAGGTC 378

Qy        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
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Db        379 ATCGGCTACCACCAGCTGCGCGTGCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 438

Qy        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420
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Db        439 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 498

Qy        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480
              |||||||||||| |||||||||| ||||| |||| |||||||||||| ||||| |||||
Db        499 GTCTGGAAGTTNGCCGGCCTCAGCCCCGACATCCCGTGGGGCGAGTTCCACTTT-ACAGG 557

Qy        481 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516
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Db        558 ATCTTTGAGGGCGGACGGGAGACCTTTGGCGACAAA 593


RESULT 6
BM864156
LOCUS       BM864156                599 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm008xD02f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm008xD02 5', mRNA sequence.
ACCESSION   BM864156
VERSION     BM864156.2  GI:30390915
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 599)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19231838.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 302 3e-87
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm008  row: D  column: 02
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .599
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm008xD02"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN
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  Query Match           90.7%;  Score 468.2;  DB 3;  Length 599;
  Best Local Similarity  95.4%;  Pred. No. 3.8e-104;
  Matches  493;  Conservative    0;  Mismatches   23;  Indels    1;  Gaps    1;

Qy          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 138

Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 198

Qy        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 258

Qy        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        259 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 318

Qy        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 378

Qy        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        379 ATCGGCTACCACCAGCTGCGCGTTCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 438

Qy        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 498

Qy        421 GTCTGGAAGTTCGCCGGCC-TCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAG 479
              ||   |||||||    ||| | | |||||| |  |||||| |||||||||| |||||| |
Db        499 GTTCTGAAGTTCATGAGCCTTTACGCCCGACAGTCGCTGGCGCGAGTTCGAGTTTGACCG 558

Qy        480 GATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516
              || |||||| ||| ||  ||||||||||||| ||||||
Db        559 GAACTTTGACGACCGAACGGAGACCTTTGGGGACAAA 595


RESULT 7
BM863710
LOCUS       BM863710                571 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm007xE24f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm007xE24 5', mRNA sequence.
ACCESSION   BM863710
VERSION     BM863710.2  GI:30391295
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19231392.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 336 1e-91
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
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            Plate: mgcm007  row: E  column: 24
            Seq primer: T3.
FEATURES              Location/Qualifiers
     source           1. .571
                      /organism="Magnaporthe grisea"
                      /mol_type="mRNA"
                      /strain="Guy11"
                      /db_xref="taxon:148305"
                      /clone="mgcm007xE24"
                      /sex="Mat1-2 hermaphrodite"
                      /cell_type="mycelium"
                      /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                      /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                      XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                      predominantly 5' reads. T7 primer on XhoI side of insert.
                      Strain inoculated into complete medium grown for two days
                      at room temperature, 150 rpm, harvested, blended,
                      reinoculated into complete medium 24 h, room temperature,
                      150 rpm. Sequences were processed by one of two methods.
                      Where a full-length alignment to the M. grisea genome
                      sequence was available, the EST sequence was trimed
                      according to the alignment, otherwise sequence quality was
                      assessed using phredPhrap version 991019 and trimmed
                      according to phd files (0.05) and for vector seqs."
ORIGIN

  Query Match             89.3%;  Score 460.8;  DB 3;  Length 571;
  Best Local Similarity   97.5%;  Pred. No. 2.5e-102;
  Matches  468;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 151

Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 211

Qy        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 271

Qy        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        272 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 331

Qy        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 391

Qy        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360
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Db        392 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 451

Qy        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        452 GTCACCATGAAGGGCCACGCCCACTCGGGAAACCTTCACTGGTACAAGAAGATCGACGGG 511

Qy        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480
              || ||||||||  |||| |||||||||||| ||||| ||||||||  |||| |||||||||
Db        512 GTTTGGAAGTTTTCCGGTCTCAAGCCCGACATCCGGTGGGGCGAAGTCGATTTTGACAGG 571


RESULT 8
BM864467
LOCUS       BM864467                643 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm010xH12f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm010xH12 5', mRNA sequence.
ACCESSION   BM864467
VERSION     BM864467.2  GI:30390655
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 643)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19232149.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 320 8e-87
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm010  row: H  column: 12
            Seq primer: T3.
FEATURES              Location/Qualifiers
     source           1. .643
                      /organism="Magnaporthe grisea"
                      /mol_type="mRNA"
                      /strain="Guy11"
                      /db_xref="taxon:148305"
                      /clone="mgcm010xH12"
                      /sex="Mat1-2 hermaphrodite"
                      /cell_type="mycelium"
                      /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                      /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                      XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                      predominantly 5' reads. T7 primer on XhoI side of insert.
                      Strain inoculated into complete medium grown for two days
                      at room temperature, 150 rpm, harvested, blended,
                      reinoculated into complete medium 24 h, room temperature,
                      150 rpm. Sequences were processed by one of two methods.
                      Where a full-length alignment to the M. grisea genome
                      sequence was available, the EST sequence was trimed
                      according to the alignment, otherwise sequence quality was
                      assessed using phredPhrap version 991019 and trimmed
                      according to phd files (0.05) and for vector seqs."
ORIGIN

  Query Match             88.1%;  Score 454.4;  DB 3;  Length 643;
  Best Local Similarity   97.0%;  Pred. No. 9.3e-101;
  Matches  484;  Conservative    0;  Mismatches   12;  Indels    3;  Gaps    2;

Qy          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 204

Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 264

Qy        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 324

Qy        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        325 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 384

Qy        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 444

Qy        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360
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Db        445 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 504

Qy        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420
                ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        505 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTTACTGGTACAAGAAGATCGACGGC 564

Qy        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGC-TGGGGCGAGTTCGAC--TTTGAC 477
                || |||||||||||||||| || |||||| |||||| ||||||||||||||   |||
Db        565 GTTTGGAAGTTCGCCGGCCCCANGCCCGACATCCGCTTGGGGCGAGTTCGACTTTTTACA 624

Qy        478 AGGATCTTTGAGGACGGAC 496
                |  ||||||||||||||||
Db        625 GGATTCTTTGAGGACGGAC 643


RESULT 9
BM863558
LOCUS       BM863558                602 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm006xH04f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm006xH04 5', mRNA sequence.
ACCESSION   BM863558
VERSION     BM863558.2  GI:30391426
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 602)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19231240.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 272 3e-72
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm006  row: H  column: 04
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .602
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm006xH04"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN
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  Query Match           86.8%;  Score 448;  DB 3;  Length 602;
  Best Local Similarity   93.7%;  Pred. No. 3.4e-99;
  Matches  477;  Conservative    0;  Mismatches   31;  Indels    1;  Gaps    1;

Qy          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 154

Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        155 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 214

Qy        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 274

Qy        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        275 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 334

Qy        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        335 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGNGAGAAGGTGTCCGAGGACGAGGTC 394

Qy        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAA 454

Qy        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420
              ||||||||||||||| |||||||||||||||||||| ||| ||||||||||||||||||||
Db        455 GTCACCATGAAGGG-CACGCCCACTCGGCAAACCTTTACTTGTACAAGAAGATCGACGGC 513

Qy        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480
              | || | || |   ||| |  || |||    | || ||||||||||| | ||| |||||
Db        514 GGCTTGGAGGTTCGCGGGCCTAAACCCCGACTTCGGTGGGGCGAGTTCCAATTTTACAGG 573

Qy        481 ATCTTTGAGGACGGACGGGAGACCTTTGG 509
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Db        574 GTTCTTTAGGACGGACGGGAAACCCTTGG 602


RESULT 10
BM863209
LOCUS       BM863209                523 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm005xD02f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm005xD02 5', mRNA sequence.
ACCESSION   BM863209
VERSION     BM863209.2  GI:30391705
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 523)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19230891.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 308 3e-83
            PCR PRimers
            FORWARD: T3 primer
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            BACKWARD: T7 primer
            Plate: mgcm005  row: D  column: 02
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .523
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm005xD02"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

  Query Match             84.3%;  Score 434.8;  DB 3;  Length 523;
  Best Local Similarity   99.5%;  Pred. No. 5.8e-96;
  Matches  436;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 145

Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 205

Qy        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 265

Qy        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        266 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 325

Qy        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        326 CTCCGCACGCAGCACTTGATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 385

Qy        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        386 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 445

Qy        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        446 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 505

Qy        421 GTCTGGAAGTTCGCCGGC 438
              ||||||||||||||||||
Db        506 GTCTGGAAGTTCGCCGGC 523


RESULT 11
BM863639
LOCUS       BM863639                 486 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm007xG13f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm007xG13 5', mRNA sequence.
ACCESSION   BM863639
VERSION     BM863639.2  GI:30391353
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 486)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19231321.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 293 5e-79
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm007  row: G  column: 13
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .486
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm007xG13"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

  Query Match             81.9%;  Score 422.4;  DB 3;  Length 486;
  Best Local Similarity   98.6%;  Pred. No. 6.4e-93;
  Matches  426;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         55 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 114

Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
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Db        115 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 174

Qy        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 234

Qy        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        235 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 294

Qy        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 354
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Qy        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        355 ATCGGCTACCACCAGCTGCGCGTTCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 414

Qy        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420
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Db        415 GTCACCATGAAGGGCCCCGCCCACTCGGCAAACCTTCACTGTGACAAGAAGATCGACGGG 474

Qy        421 GTCTGGAAGTTC 432
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Db        475 GTCTGGAAGTTC 486


RESULT 12
BM864472
LOCUS       BM864472                600 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm010xJ04f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm010xJ04 5', mRNA sequence.
ACCESSION   BM864472
VERSION     BM864472.2  GI:30390651
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 600)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19232154.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 268 5e-71
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm010  row: J  column: 04
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .600
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm010xJ04"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

  Query Match             78.8%;  Score 406.4;  DB 3;  Length 600;
  Best Local Similarity   97.0%;  Pred. No. 5.6e-89;
  Matches  425;  Conservative    0;  Mismatches   11;  Indels    2;  Gaps    1;

Qy          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 204

Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 264

Qy        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 324

Qy        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        325 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 384

Qy        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 444

Qy        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360
              |||||||||||||||| |||||||||||||| |||||||||||||||||||||||||||
Db        445 ATCGGCTACCACCAGCTGGGCGTCCCGCACCAGAGGGACAAGGACACCACCATGAAGGAG 504

Qy        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420
              |||||||||||||||||||||||||||  ||||||    | | ||||||||||||||||
Db        505 GTCACCATGAAGGGCCACGCCCACTCGCAAAACCT--CATTGGACAAGAAGATCGACGGC 562

Qy        421 GTCTGGAAGTTCGCCGGC 438
              ||||| |||||||||| |
Db        563 GTCTGAAAGTTCGCCGCC 580


RESULT 13
BM864820/c
LOCUS       BM864820                781 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgap007xA05f.b Magnaporthe grisea Ap Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgap007xA05 5', mRNA sequence.
ACCESSION   BM864820
VERSION     BM864820.2  GI:30390364
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 781)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19232502.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 271 1e-71
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgap007  row: A  column: 05
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .781
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
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/strain="70-15"
/db_xref="taxon:148305"
/clone="mgap007xA05"
/sex="Mat1-2 hermaphrodite"
/cell_type="Appressorium"
/clone_lib="Magnaporthe grisea Ap Uni-Zap XR Library"
/note="Vector: pBluescriptSK+; Site_1: EcoRI; Site_2: XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Appressorium library. Conidia were germ inated on an inductive surface for 5-8 h. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

ORIGIN

Query Match 77.3%; Score 398.8; DB 3; Length 781;
Best Local Similarity 91.1%; Pred. No. 4.2e-87;
Matches 468; Conservative 0; Mismatches 42; Indels 4; Gaps 4;

```
Qy          4 GGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATGACT 63
              || | |  | ||| ||| | |||| | ||| | |    | |||||||||| ||||   ||
Db        723 GGGTTGTCAATTCCAAAAAACGATTAAATACCTTGTCCTGACTACCTGGG-CTCAATGCT 665

Qy         64 TGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTG-CGAAAGGT 122
              ||||| ||||||| |||||||||| |||| |||||||||||||||||||  ||||||| 
Db        664 TGCGTGTATGAGT-GGCAGACAGTTACGCCTCCAAGGACTGGGATAGGCTGAGGAAAGGT 606

Qy        123 CATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAAT 182
              ||| ||||   || || ||||||| | ||||||| |||||||||| | |||||| ||||
Db        605 CATGGCGCTATCTGTGGGCATTGAAT-CCGCTCCCTCCTCGACAAGTTTTGGGAGCCAAT 547

Qy        183 GCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCCACCCT 242
              |||| |  |||||||||||||||| |||||||||||| || ||||||||||||||||
Db        546 GCCGACGAAGGAGTTCGTCGGCATGTTCTCGAGCAAGCAGGTGGTGGGCGACCCCCACCCT 487

Qy        243 CCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCAT 302
              |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CCGCACGCAGCATTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCAT 427

Qy        303 CGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGT 362
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Qy        483 CTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516
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RESULT 14
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LOCUS BM863357 530 bp mRNA linear EST 06-MAY-2003
DEFINITION mgcm006xO05f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm006xO05 5', mRNA sequence.
ACCESSION BM863357
VERSION BM863357.1 GI:19231039
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE 1 (bases 1 to 530)
AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.
TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe grisea
JOURNAL Unpublished (2002)
COMMENT Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone dehydratase >gi|1127197|pdb|1STD|. . . 276 1e-73
PCR PRimers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgcm006 row: O column: 05
Seq primer: T3.
FEATURES Location/Qualifiers
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/strain="Guy11"
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/clone="mgcm006xO05"
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/note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2: XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

ORIGIN

Query Match 76.4%; Score 394.4; DB 3; Length 530;
Best Local Similarity 99.7%; Pred. No. 4.8e-86;
Matches 395; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db        143 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 202

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Db        203 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 262

Qy        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240
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Db        443 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTT 478


RESULT 15
BM863374
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DEFINITION  mgcm006xC10f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm006xC10 5', mRNA sequence.
ACCESSION   BM863374
VERSION     BM863374.2  GI:30391576
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 510)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19231056.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 276 1e-73
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm006  row: C  column: 10
            Seq primer: T3.
FEATURES             Location/Qualifiers
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                     /clone="mgcm006xC10"
                     /sex="Mat1-2 hermaphrodite"
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                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

  Query Match             76.1%;  Score 392.8;  DB 3;  Length 510;
  Best Local Similarity   99.5%;  Pred. No. 1.2e-85;
  Matches  394;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db         83 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 142

Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
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Db        143 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 202

Qy        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180
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Qy        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240
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Db        263 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 322

Qy        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 382

Qy        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 442

Qy        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTT 396
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Db        443 GTCACCATGAAGGGCCACGCTCACTCGGCAAACCTT 478


Search completed: December  4, 2006, 19:19:10
Job time : 2616 secs
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2006, 18:49:35 ; Search time 219 Seconds
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Title: US-10-507-132-1
Perfect score: 516
Sequence: 1 atgggttcgcaagttcaaaa.....gggagacctttggcgacaaa 516

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2931743 seqs, 1025338116 residues

Total number of hits satisfying chosen parameters: 5863486

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	4	514.4	99.7	610	6	US-10-507-132-16	Sequence 16, Appl
	5	504.8	97.8	538	6	US-10-507-132-15	Sequence 15, Appl
	6	504.8	97.8	545	6	US-10-507-132-14	Sequence 14, Appl
	7	377.8	73.2	729	6	US-10-507-132-18	Sequence 18, Appl
	8	373.8	72.4	732	6	US-10-507-132-17	Sequence 17, Appl
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ALIGNMENTS

RESULT 1
US-10-507-132-1
; Sequence 1, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
; APPLICANT: Koichiro KAKU et al.
; TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
; TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
; FILE REFERENCE: 1254-0258PUS1
; CURRENT APPLICATION NUMBER: US/10/507,132
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: JP 2002-66955
; PRIOR FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Pyricularia oryzae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(516)
US-10-507-132-1

Query Match 100.0%; Score 516; DB 6; Length 516;
Best Local Similarity 100.0%; Pred. No. 6.8e-113;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60
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Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
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RESULT 2
US-10-507-132-3
; Sequence 3, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU et al.
;  TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
;  TITLE OF INVENTION:  AGRICULTURAL FUNGICIDAL AGENT
;  FILE REFERENCE: 1254-0258PUS1
;  CURRENT APPLICATION NUMBER: US/10/507,132
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: JP 2002-66955
;  PRIOR FILING DATE: 2002-03-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 516
;   TYPE: DNA
;   ORGANISM: Pyricularia oryzae
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(516)
US-10-507-132-3

  Query Match             99.7%;  Score 514.4;  DB 6;  Length 516;
  Best Local Similarity   99.8%;  Pred. No. 1.6e-112;
  Matches  515;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
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Qy        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420
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Qy        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480

Qy        481 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516
              ||||||||||||||||||||||||||||||||||||
Db        481 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516


RESULT 3
US-10-507-132-13
; Sequence 13, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU et al.
;  TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
;  TITLE OF INVENTION:  AGRICULTURAL FUNGICIDAL AGENT
;  FILE REFERENCE: 1254-0258PUS1
;  CURRENT APPLICATION NUMBER: US/10/507,132
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: JP 2002-66955
;  PRIOR FILING DATE: 2002-03-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 600
;   TYPE: DNA
;   ORGANISM: Pyricularia oryzae
US-10-507-132-13

  Query Match             99.7%;  Score 514.4;  DB 6;  Length 600;
  Best Local Similarity   99.8%;  Pred. No. 1.7e-112;
  Matches  515;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 140

Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 200

Qy        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 260

Qy        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        261 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 320

Qy        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 380

Qy        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 440

Qy        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 500

Qy        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 560

Qy        481 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516
              ||||||||||||||||||||||||||||||||||||
Db        561 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 596
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RESULT 4
US-10-507-132-16
; Sequence 16, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU et al.
;  TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
;  TITLE OF INVENTION:  AGRICULTURAL FUNGICIDAL AGENT
;  FILE REFERENCE: 1254-0258PUS1
;  CURRENT APPLICATION NUMBER: US/10/507,132
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: JP 2002-66955
;  PRIOR FILING DATE: 2002-03-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 610
;   TYPE: DNA
;   ORGANISM: Pyricularia oryzae
US-10-507-132-16

  Query Match             99.7%;  Score 514.4;  DB 6;  Length 610;
  Best Local Similarity   99.8%;  Pred. No. 1.7e-112;
  Matches  515;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 140

Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 200

Qy        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 260

Qy        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        261 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 320

Qy        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 380

Qy        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 440

Qy        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 500

Qy        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 560

Qy        481 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516
              |||||||||||||||||||||||||||||||||||
Db        561 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 596


RESULT 5
US-10-507-132-15
; Sequence 15, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU et al.
;  TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
;  TITLE OF INVENTION:  AGRICULTURAL FUNGICIDAL AGENT
;  FILE REFERENCE: 1254-0258PUS1
;  CURRENT APPLICATION NUMBER: US/10/507,132
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: JP 2002-66955
;  PRIOR FILING DATE: 2002-03-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 538
;   TYPE: DNA
;   ORGANISM: Pyricularia oryzae
US-10-507-132-15

  Query Match             97.8%;  Score 504.8;  DB 6;  Length 538;
  Best Local Similarity   99.6%;  Pred. No. 3e-110;
  Matches  506;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 90

Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 150

Qy        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 210

Qy        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        211 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 270

Qy        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 330

Qy        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 390

Qy        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 450

Qy        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        451 GTCTGGAAGTTCGCCGGCCTCAAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGG 510

Qy        481 ATCTTTGAGGACGGACGGGAGACCTTTG 508
              ||||||||||||||||||||||||||||
Db        511 ATCTTTGAGGACGGACGGGAGACCTTTG 538


RESULT 6
US-10-507-132-14
; Sequence 14, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU et al.
;  TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
;  TITLE OF INVENTION:  AGRICULTURAL FUNGICIDAL AGENT
;  FILE REFERENCE: 1254-0258PUS1
;  CURRENT APPLICATION NUMBER: US/10/507,132
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: JP 2002-66955
;  PRIOR FILING DATE: 2002-03-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 545
;   TYPE: DNA
;   ORGANISM: Pyricularia oryzae
US-10-507-132-14
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  Query Match             97.8%;  Score 504.8;  DB 6;  Length 545;
  Best Local Similarity   99.6%;  Pred. No. 3e-110;
  Matches  506;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 97

Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 157

Qy        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 217

Qy        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        218 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 277

Qy        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 337

Qy        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 397

Qy        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 457

Qy        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        458 GTCTGGAAGTTCGCCGGCCTCAAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGG 517

Qy        481 ATCTTTGAGGACGGACGGGAGACCTTTG 508
              ||||||||||||||||||||||||||||
Db        518 ATCTTTGAGGACGGACGGGAGACCTTTG 545


RESULT 7
US-10-507-132-18
; Sequence 18, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU et al.
;  TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
;  TITLE OF INVENTION:  AGRICULTURAL FUNGICIDAL AGENT
;  FILE REFERENCE: 1254-0258PUS1
;  CURRENT APPLICATION NUMBER: US/10/507,132
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: JP 2002-66955
;  PRIOR FILING DATE: 2002-03-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 729
;   TYPE: DNA
;   ORGANISM: Pyricularia oryzae
US-10-507-132-18

  Query Match             73.2%;  Score 377.8;  DB 6;  Length 729;
  Best Local Similarity   84.5%;  Pred. No. 3.6e-80;
  Matches  474;  Conservative    0;  Mismatches    2;  Indels   85;  Gaps    1;

Qy         41 CAGACTACCTGGGCCTCATGACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGG 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 CAGACTACCTGGGCCTCATGACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGG 228

Qy        101 ACTGGGATAGGCTGCGAAAGGTCATTGCGCCTACTCTGCGC------------------- 141
              |||||||||||||||||||||||||||||||||||||||||
Db        229 ACTGGGATAGGCTGCGAAAGGTCATTGCGCCTACTCTGCGCGTATGTTCCGCCCTGCCAT 288

Qy        142 ------------------------------------------------------------ 141

Db        289 GTTTATTTTTACTTTCCCACACCAAATCCAGACTTTAACAGCGACGACCAAAAAAAAAAA 348

Qy        142 ------ATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAG 195
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 AAACAGATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAG 408

Qy        196 TTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCAC 255
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        409 TTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACCCTCCGCACGCAGCAC 468

Qy        256 TTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAG 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        469 TTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAG 528

Qy        316 CTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGC 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        529 CTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGC 588

Qy        376 CACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCC 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        589 CACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCC 648

Qy        436 GGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGGATCTTTGAGGACGGA 495
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        649 GGCCTCAAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGGATCTTTGAGGACGGA 708

Qy        496 CGGGAGACCTTTGGCGACAAA 516
              ||||||||||||||||||||||
Db        709 CGGGAGACCTTTGGCGACAAA 729


RESULT 8
US-10-507-132-17
; Sequence 17, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU et al.
;  TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
;  TITLE OF INVENTION:  AGRICULTURAL FUNGICIDAL AGENT
;  FILE REFERENCE: 1254-0258PUS1
;  CURRENT APPLICATION NUMBER: US/10/507,132
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: JP 2002-66955
;  PRIOR FILING DATE: 2002-03-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
;   LENGTH: 732
;   TYPE: DNA
;   ORGANISM: Pyricularia oryzae
US-10-507-132-17

  Query Match             72.4%;  Score 373.8;  DB 6;  Length 732;
  Best Local Similarity   83.9%;  Pred. No. 3.2e-79;
  Matches  474;  Conservative    0;  Mismatches    2;  Indels   89;  Gaps    1;

Qy         41 CAGACTACCTGGGCCTCATGACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGG 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 CAGACTACCTGGGCCTCATGACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGG 227

Qy        101 ACTGGGATAGGCTGCGAAAGGTCATTGCGCCTACTCTGCGC------------------- 141
              |||||||||||||||||||||||||||||||||||||||||
Db        228 ACTGGGATAGGCTGCGAAAGGTCATTGCGCCTACTCTGCGCGTATGTTCCGCCCTGCCAT 287

Qy        142 ------------------------------------------------------------ 141

Db        288 GTTTATTTTTACTTTCCCACACCAAATCCAGACTTTAACAGCGACGACCAAAAAAAAAAA 347

Qy        142 ----------ATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGA 191
                         ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        348 AAAAAAACAGATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGA 407

Qy        192 GGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCA 251
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        408 GGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACCCTCCGCACGCA 467

Qy        252 GCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCA 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 GCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCA 527

Qy        312 CCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAA 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        528 CCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAA 587

Qy        372 GGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTT 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        588 GGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTT 647

Qy        432 CGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGGATCTTTGAGGA 491
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        648 CGCCGGCCTCAAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGGATCTTTGAGGA 707

Qy        492 CGGACGGGAGACCTTTGGCGACAAA 516
              |||||||||||||||||||||||||
Db        708 CGGACGGGAGACCTTTGGCGACAAA 732


RESULT 9
US-10-449-902-18394
; Sequence 18394, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18394
;   LENGTH: 3067
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AK068793
;   DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-18394

  Query Match             10.0%;  Score 51.6;  DB 6;  Length 3067;
  Best Local Similarity   46.2%;  Pred. No. 0.0069;
  Matches  171;  Conservative    0;  Mismatches  199;  Indels    0;  Gaps    0;

Qy         79 GCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAGGTCATTGCGCCTACTCTG 138
              || | | ||  |    ||||||  | |   | ||    |  |||     |    |
Db        350 GCCGTCCGCACCATGAACAAGGAGGGCGGCGGCCTCGTCACCGTCGCCACCTTCGCCTCC 409

Qy        139 CGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTC 198
                | |   || |  || |  |  || ||| ||| || ||||  |   ||||   ||  ||
Db        410 ATCTTCTCCTCCTACTGCGCCAGCGGCAACCTCAGGAAGGCCGTCGAGGCCTTCGACGTC 469

Qy        199 GTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTC 258
              | || | | |       ||| |      | || || || |  || |        | |
Db        470 ATGGGGAAGTACGGCGTGGAGCCGGACGCCGTCGCCCTCAACTCCCTCCTCTCCGCCATG 529

Qy        259 ATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTG 318
                | ||||   | || | | ||| | |  ||||  | ||    ||  | |

Db        530 TGCCGCGGGGAGGGCCGCGCGCAGGCGGCGCAGGACCTGTTCGAGCGCACCAAGGCCACC 589

Qy        319 CGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCAC 378
              ||  ||  ||  |     |   |  |    | |  ||| |      |   ||||  ||
Db        590 GTCGCGCCCGACGCGGACACCTTCGGGATTCTCCTCGAGGCGTGGGAGAAAGAGGGGAAC 649

Qy        379 GCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGC 438
              |||||    || ||       ||     | ||| ||| | | |||||  |   |  |||||||
Db        650 GCCCAGCGCGCCAAGAGCACCTTCGGCGAGATGATTGTCCGCGTCGGCTGGGACGCCGGC 709

Qy        439 CTCAAGCCCG 448
                || |||||
Db        710 AACATGCCCG 719


RESULT 10
US-10-449-902-13052/c
; Sequence 13052, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13052
;   LENGTH: 3161
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AK110400
;   DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-13052

  Query Match             9.9%;  Score 51;  DB 6;  Length 3161;
  Best Local Similarity   47.3%;  Pred. No. 0.0097;
  Matches  187;  Conservative    0;  Mismatches  205;  Indels    3;  Gaps    1;

Qy         44 ACTACCTGGGCCTCATGACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACT 103
              ||| |  |  |  ||  |   ||| | | | |||    | ||||  |||| |||  |
Db        743 ACTCCGGGCTCTGCACCAAGGGCGGCGACGTGTGCTTCGTCAGCATCGACGCCAGCGGGA 684

Qy        104 GGGATAGGCTGCGAAAGGTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCG 163
              ||      | ||  |     | |   | |       | ||| ||  ||   | |    ||  |
Db        683 GGCCGGTGATGAGCGCCGACGAGGAGGAGGTGCAGCGGATGCACCGGCTCAAGCTCGCCA 624

Qy        164 ACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGA 223
              |  |||   || | |   | |||  | |  | |  | |||||||||  || |   | |
Db        623 TCGCGCTGCTGGTGACGGCGACGGTGGCGATGGTGCTGGGCATGGTCGGGATCCTACGGG 564

Qy        224 TGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGG 283
              ||  ||      || | || ||  | ||  |     |||||||  | || | ||   ||
Db        563 CGCGCGGGATGGGCATCGTCGGCGGGAAGGGCGGGCACGGCGGCGGGAGCAGCGACTCGG 504

Qy        284 TGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGG 343
              |||||  | |||   | | |   |  |     || |  |   |||  |||||  |   |
Db        503 AGTCCGGCGGCGA---CCTGGCGTGGCCGTGGCAGTTCACGCCGTTCCAGAAGCTGAGCT 447

Qy        344 ACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGT 403
              || |  |  | ||| |||   ||     | | |||||  ||         |    ||| |
Db        446 TCAGCGTCGAGCAGGTGGTGCGCAACCTCGTCGACGCCAACATCATCGGCAAGGGCTGCT 387

Qy        404 ACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGC 438
              |     | |  || ||||| |      | |||||
```

```
Db        386 CCGGCGTGGTGTACCGCGTCGGCCTCGACACCGGC 352


RESULT 11
US-11-056-355B-18159
; Sequence 18159, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 18159
;   LENGTH: 760
;   TYPE: DNA
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(760)
;   OTHER INFORMATION: Ceres Seq. ID no. 12416334
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(760)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 14306309
;   OTHER INFORMATION: as cited in SEQ ID NO 1394
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(760)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13595377
;   OTHER INFORMATION: as cited in SEQ ID NO 56088
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(760)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13598648
;   OTHER INFORMATION: as cited in SEQ ID NO 64497
US-11-056-355B-18159

  Query Match             9.7%;  Score 50;  DB 9;  Length 760;
  Best Local Similarity   47.7%;  Pred. No. 0.013;
  Matches  146;  Conservative    0;  Mismatches  160;  Indels    0;  Gaps    0;

Qy        207 GGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGG 266
              || | ||  |  | |||||| | | |     |  || |  |     | ||  |  |||| |
Db        130 GGCCGCGGACGCGGAGATGCAGAGGGTGTTCTGCCGCATCGACGCGGACGGCGACGGCCG 189

Qy        267 CACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCC 326
              |     |     | || || ||| ||    |  |  |  || ||  |    | ||  | |
Db        190 GATCTCCGCCTCGGAGCTGGCCGCGGTGACGCGCGCCATCTCCCCGCCAGCGAGCTCCTC 249

Qy        327 GCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTC 386
              ||||  | |   | |||   || ||||||| ||| |        | || || || |  ||
Db        250 GCACGGGCGCCGCGAGGTGGCCGCCATGATGGACGAGCTGGACACGGACCGCGACGGCTT 309

Qy        387 GGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCC 446
                |  ||||   |  || || |  | || |||    | |       || ||    | |
Db        310 CGTGGACCTCGGCGAGTTCAGGGCGTTCCACGCGCGCGGCGGCGGCGGCGTGGACGACGA 369

Qy        447 CGATATCCGCTGGGGCGAGTTCGACTTTGACAGGATCTTTGAGGACGGACGGGAGACCTT 506
              ||    | | | | ||  |||||| |  ||    ||   |  ||||| || |  ||
Db        370 CGCCGAGCTCCGCGCCGCCTTCGACGTCTACGACGTCGACGGCGACGGCCGCGTCACGGC 429

Qy        507 TGGCGA 512
                | |||
Db        430 GGCCGA 435


RESULT 12
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US-10-530-643-3
; Sequence 3, Application US/10530643
; Publication No. US20060259995A1
; GENERAL INFORMATION:
;  APPLICANT: CAYOUETTE, Michelle
;  APPLICANT:  HANSEN, Connie Jo
;  APPLICANT:  MCCLURE, Amy
;  APPLICANT:  SUN, May
;  APPLICANT:  GRAMATIKOVA, Svetlana
;  APPLICANT:  DYCAICO, Mark
;  APPLICANT:  BARTON, Nelson R.
;  APPLICANT:  STEGE, Justin T.
;  APPLICANT:  ABOUSHADI, Nahla M.
;  TITLE OF INVENTION: PROTEASES, NUCLEIC ACIDS ENCODING THEM
;  TITLE OF INVENTION:  AND METHODS FOR MAKING AND USING THEM
;  FILE REFERENCE: 564462004100
;  CURRENT APPLICATION NUMBER: US/10/530,643
;  CURRENT FILING DATE:  2006-04-07
;  PRIOR APPLICATION NUMBER: PCT/US03/32819
;  PRIOR FILING DATE: 2003-10-10
;  PRIOR APPLICATION NUMBER: 60/471,423
;  PRIOR FILING DATE: 2003-05-16
;  PRIOR APPLICATION NUMBER: 60/418,467
;  PRIOR FILING DATE: 2002-10-10
;  NUMBER OF SEQ ID NOS: 255
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1572
;   TYPE: DNA
;   ORGANISM: Bacteria
US-10-530-643-3

  Query Match             9.6%;  Score 49.4;  DB 6;  Length 1572;
  Best Local Similarity   48.7%;  Pred. No. 0.02;
  Matches  134;  Conservative    0;  Mismatches  141;  Indels    0;  Gaps    0;

Qy         85 AGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAGGTCATTGCGCCTACTCTGCGCATT 144
              | |  ||| |||  || |   |  ||       |  | ||  || ||  |    | |
Db       1276 ACCGTCGAGTCCCCGGTCACCGTCAGCGGCGTCAGCGGCAACGCCCCCGCCGCCCTCCAG 1335

Qy        145 GACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGC 204
              | |         | || || |||     |   |  |    | | |  | ||  | ||| |  |
Db       1336 GTCCCGGTGAACATCGTCCACACCTACATCGGTGACCTCCAGATCCAGCTGATCGCCCCC 1395

Qy        205 ATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGC 264
                | ||||    |   | ||  || |  |  ||||  | |||     | ||  |||| |
Db       1396 GACGGCTCGGCGTACACGCTGAAGGCCTTCGGCACCGGCGGCAGCTCGGACAACATCAAC 1455

Qy        265 GGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTC 324
                ||||  | | | ||| |  |||  ||| |  || ||||       |||| ||||||
Db       1456 ACCACGTACAGCGTGAACGCCTCCTCGGAGGTCGCCAACGGCACGTGGAAGCTCCGCGTC 1515

Qy        325 CCGCACCAGAGGTACAAGGACACCACCATGAAGGA 359
              || || |   | ||   ||||||  || ||  ||
Db       1516 ACGGACAACGCGAACGCCGACACCGGCAAGATCGA 1550


RESULT 13
US-11-218-305-7648
; Sequence 7648, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
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;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7648
;   LENGTH: 1000
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-218-305-7648

  Query Match             9.5%;  Score 49.2;  DB 9;  Length 1000;
  Best Local Similarity   48.6%;  Pred. No. 0.021;
  Matches  135;  Conservative    0;  Mismatches  143;  Indels    0;  Gaps    0;

Qy          82 GACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAGGTCATTGCGCCTACTCTGCGC 141
               ||| || ||    || ||  |  |||  ||| |     |  |   ||||   | | |
Db         552 GACCGCGACCTGGCCGAGTTCCTGGACCGGCGGGTGGCGCCCGACGCGCGGGCCCAGGAG 611

Qy         142 ATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTC 201
                 | || |  || |  || ||  |     |  | | |     | ||  |       ||  |
Db         612 GGGGTCTCCTCCTTCGACCACGTGATCGACACGTCGACCGGCCTGGAGGTCCGCATCTAC 671

Qy         202 GGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATC 261
                ||   | | | | |||  |        |||| | ||||||| | ||  | | ||||| ||
Db         672 CGCGCCGCCGCCAACAACAACGGCGGCGGCGGCGCCACCCTGCCCATCCTGGACTTCCTC 731

Qy         262 GGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGC 321
               ||||||||||    || | || | |   | |  |||||||  || |  |||      ||
Db         732 GGCGGCACGCCGGCGGCGGCGGCGGCGCCGTTCCCGGTCATCCTCTTCTTCCACGGCGGC 791

Qy         322 GTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGA 359
                 |.    ||   ||      | |||  ||||  | ||
Db         792 AGCTTCGCACACTCGTCGTCCGGCACGGCCATCTACGA 829


RESULT 14
US-10-449-902-23999
; Sequence 23999, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23999
;   LENGTH: 749
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AK099441
;   DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-23999

  Query Match             9.3%;  Score 48;  DB 6;  Length 749;
  Best Local Similarity   46.9%;  Pred. No. 0.037;
  Matches  150;  Conservative    0;  Mismatches  170;  Indels    0;  Gaps    0;

Qy         174 GGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGA 233
               ||||      | ||    |  | |  ||||||  | |    || ||   ||    | |||
Db         212 GGAGTACGCCCAGGTGACGCGGATGCTCGGCAACGGCCGCTGCGAGGCCATCTGCGTCGA 271

Qy         234 CCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGA 293
               |  ||||   |||      ||| ||  ||||   | || |  | ||  |  |  ||  |
Db         272 CGGCACCAAGCGCCTCTGCCACATCCGCGGCAAGATGCACAAGAAGGTGTGGATCGCCGC 331

Qy         294 CGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCAT 353
               || || ||||  |  |  |   || |||| |   ||  |       |   |||  || | |
Db         332 CGGGGACATCATCCTCGTCGGCCTCCGCGACTACCAGGACGACAAGGCCGACGTCATCCT 391

Qy         354 GAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGAT 413
               |||  |  | | |    |||  || |  || |  |||  ||    |      | | |   |
Db         392 CAAGTACATGAACGACGAGGCCCGCCTCCTCAAGGCCTACGGCGAGCTCCCCGACACCCT 451

Qy         414 CGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTT 473
               |     |  |  |    ||| || |  |  ||||||   | || | | | |   |||||
Db         452 CAGGCTCAACGAGGGCGTCGACGTCGACGGGCCCGAGGACGGCGGCGACCACGACGACTA 511

Qy         474 TGACAGGATCTTTGAGGACG 493
                  |  | ||   || || |
Db         512 CATCCAGTTCGAGGACGAGG 531


RESULT 15
US-10-953-349-26476
; Sequence 26476, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26476
;   LENGTH: 750
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
US-10-953-349-26476

  Query Match             9.3%;  Score 48;  DB 6;  Length 750;
  Best Local Similarity   46.9%;  Pred. No. 0.037;
  Matches  150;  Conservative    0;  Mismatches  170;  Indels    0;  Gaps    0;

Qy         174 GGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGA 233
               ||||      || ||    |  | |  ||||||  |       || ||   ||    | |||
Db         236 GGAGTACGCGCAGGTGACGCGGATGCTCGGCAACGGGCGCTGCGAGGCCATCTGCGTCGA 295

Qy         234 CCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGA 293
               |  ||||   |||      ||| ||   |||   | || |  | ||      |  ||  |
Db         296 CGGCACCAAGCGCCTCTGCCACATCCGGGGCAAGATGCACAAGAAGGTCTGGATCGCCGC 355

Qy         294 CGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCAT 353
               || || |||||  |  |  |   || |||| |   ||  |       |   |||  || | |
Db         356 CGGGGACATCGTCCTCGTCGGCCTCCGCGACTACCAGGACGACAAGGCCGACGTCATCCT 415

Qy         354 GAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGAT 413
               |||  |  | | |    |||  || |   | |  |||  ||    |      | | | | |
Db         416 CAAGTACATGAACGACGAGGCCCGCCTGCTCAAGGCCTACGGGGAGCTCCCCGACACGCT 475

Qy         414 CGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTT 473
               |  |  |  |  |    ||| || |  |   |||||      ||  |||||||   |||||
Db         476 CCGCCTCAACGAGGGCGTCGACGTCGACGGCCCCGAGGAGGGCGAGGGCGACAGCGACTA 535

Qy         474 TGACAGGATCTTTGAGGACG 493
                  |  | ||   || || |
Db         536 CATCCAGTTCGAGGACGAGG 555


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GenCore version 5.1.9

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(without alignments)
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Perfect score: 516
Sequence: 1 atgggttcgcaagttcaaaa.....gggagacctttggcgacaaa 516

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
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14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	58.6	11.4	1479	7	US-10-156-761-6148	Sequence 6148, Ap
	2	58.6	11.4	9025608	7	US-10-156-761-1	Sequence 1, Appli
	3	53.4	10.3	113193	12	US-10-478-943D-1	Sequence 1, Appli
	4	53	10.3	7407	7	US-10-246-330-3	Sequence 3, Appli
	5	53	10.3	7407	8	US-10-282-122A-30151	Sequence 30151, A
	6	52.2	10.1	791	8	US-10-437-963-23119	Sequence 23119, A
	7	52	10.1	1336	8	US-10-425-114-4414	Sequence 4414, Ap
	8	52	10.1	1394	8	US-10-425-114-29012	Sequence 29012, A
	9	52	10.1	1437	8	US-10-425-114-17854	Sequence 17854, A
	10	52	10.1	1598	8	US-10-425-114-29011	Sequence 29011, A
	11	51.4	10.0	2189	7	US-10-353-454-45	Sequence 45, Appl
	12	51.4	10.0	2346	7	US-10-353-445-4	Sequence 4, Appli
	13	51.4	10.0	2346	7	US-10-353-445-5	Sequence 5, Appli
	14	51.4	10.0	2346	7	US-10-353-445-8	Sequence 8, Appli
c	15	51.2	9.9	1536	8	US-10-767-701-14768	Sequence 14768, A
	16	51	9.9	3408	8	US-10-437-963-17000	Sequence 17000, A
	17	50.8	9.8	1605	10	US-10-858-730-137	Sequence 137, App
	18	50.4	9.8	1238	8	US-10-425-114-14248	Sequence 14248, A
	19	50.4	9.8	1329	7	US-10-156-761-6352	Sequence 6352, Ap
	20	50.4	9.8	1349	8	US-10-425-114-16604	Sequence 16604, A
	21	50.4	9.8	1352	8	US-10-425-114-4590	Sequence 4590, Ap
	22	50.4	9.8	1488	9	US-10-425-115-10066	Sequence 10066, A
	23	50.4	9.8	1492	9	US-10-425-115-10065	Sequence 10065, A
	24	50.4	9.8	1511	8	US-10-425-114-4356	Sequence 4356, Ap
	25	50.2	9.7	1177	8	US-10-425-114-17800	Sequence 17800, A
	26	50	9.7	1821	3	US-09-953-348-82	Sequence 82, Appl
	27	50	9.7	1821	7	US-10-267-255-82	Sequence 82, Appl
	28	50	9.7	2330	8	US-10-437-963-47924	Sequence 47924, A
	29	50	9.7	18034	3	US-09-953-348-75	Sequence 75, Appl
	30	50	9.7	18034	7	US-10-267-255-75	Sequence 75, Appl
	31	49.8	9.7	1388	8	US-10-425-114-4296	Sequence 4296, Ap
	32	49.6	9.6	2559	8	US-10-437-963-39180	Sequence 39180, A
	33	49.4	9.6	980	13	US-11-097-143-14525	Sequence 14525, A
	34	49.4	9.6	3665	13	US-11-097-143-14524	Sequence 14524, A
	35	49	9.5	699	6	US-10-006-922-41	Sequence 41, Appl
	36	48.8	9.5	1341	8	US-10-425-114-16569	Sequence 16569, A
	37	48.8	9.5	1434	8	US-10-425-114-4374	Sequence 4374, Ap
	38	48.8	9.5	1442	8	US-10-425-114-17865	Sequence 17865, A
	39	48.8	9.5	1443	8	US-10-425-114-16556	Sequence 16556, A
	40	48.8	9.5	1450	8	US-10-425-114-17863	Sequence 17863, A
	41	48.8	9.5	1454	8	US-10-425-114-28991	Sequence 28991, A
	42	48.8	9.5	1455	8	US-10-425-114-29006	Sequence 29006, A
	43	48.8	9.5	1632	7	US-10-369-493-41594	Sequence 41594, A
	44	48.8	9.5	1754	9	US-10-425-115-10067	Sequence 10067, A
	45	48.6	9.4	13631	13	US-11-097-143-27772	Sequence 27772, A

ALIGNMENTS

RESULT 1
US-10-156-761-6148
; Sequence 6148, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 6148
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1479)
US-10-156-761-6148

Query Match 11.4%; Score 58.6; DB 7; Length 1479;
Best Local Similarity 50.5%; Pred. No. 7.3e-07;
Matches 142; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

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Qy      148 TACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATG 207
            |||| || |  | ||||     ||   | ||      || ||   |||  | ||| || |
Db      835 TACCTCTTCCGCTTCGAGGGCTTCGACGTGGTCGGCTCGTCCCCCGAGGCCCTCGTCAAG 894

Qy      208 GTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGC 267
            |||  |  |  ||||  | ||| | ||||||  |    |||| | ||    |  ||    |
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Db        895 GTCGAGGACGGGCAGGCGATGGTCCACCCCATCGCGGGCACCCGGCCGCGCGGCGCGACC 954

Qy        268 ACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCG 327
              |||    ||| |||    || ||||||| |  | | | ||| | ||  ||||| |  |
Db        955 CCGCAGGAGGACCAGGCCCTCGCGGACGAGCTGCTGGCCGACCCCAAGGAGCGCGCCGAG 1014

Qy        328 CACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCG 387
              |||| || | |   |||          || ||  |      |    || |  ||   ||
Db       1015 CACCTGATGCTCGTCGACCTGGGGCGCAACGATCTGGGGCGGGTCTGCGAGCCCGGTTCC 1074

Qy        388 GCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAA 428
              |   |  |   |  | || ||  |||||  ||  || | |
Db       1075 GTCGAGGTCGTCGACTTCATGACCATCGAGCGCTACTCGCA 1115


RESULT 2
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
;  APPLICANT: OMURA, SATOSHI
;  APPLICANT:  IKEDA, HARUO
;  APPLICANT:  ISHIKAWA, JUN
;  APPLICANT:  HORIKAWA, HIROSHI
;  APPLICANT:  SHIBA, TADAYOSHI
;  APPLICANT:  SAKAKI, YOSHIYUKI
;  APPLICANT:  HATTORI, MASAHIRA
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;  FILE REFERENCE: 249-262
;  CURRENT APPLICATION NUMBER: US/10/156,761
;  CURRENT FILING DATE:  2002-05-29
;  PRIOR APPLICATION NUMBER: JP 2001-204089
;  PRIOR FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: JP 2001-272697
;  PRIOR FILING DATE: 2001-08-02
;  NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
;   LENGTH: 9025608
;   TYPE: DNA
;   ORGANISM: Streptomyces avermitilis
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4187715)
;   OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

  Query Match             11.4%;  Score 58.6;  DB 7;  Length 9025608;
  Best Local Similarity   50.5%;  Pred. No. 2.9e-06;
  Matches  142;  Conservative    0;  Mismatches  139;  Indels    0;  Gaps    0;

Qy        148 TACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATG 207
              |||| || |  | ||||      ||    | ||       || ||   |||  | ||| || |
Db    7418619 TACCTCTTCCGCTTCGAGGGCTTCGACGTGGTCGGCTCGTCCCCCGAGGCCCTCGTCAAG 7418678

Qy        208 GTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGC 267
              |||  |  |  ||||  | ||| | ||||||  |    ||||  | ||    |  ||    |
Db    7418679 GTCGAGGACGGGCAGGCGATGGTCCACCCCATCGCGGGCACCCGGCCGCGCGGCGCGACC 7418738

Qy        268 ACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCG 327
              |||    |||  |||    || ||||||| |  | | | ||| | ||  ||||| |  |
Db    7418739 CCGCAGGAGGACCAGGCCCTCGCGGACGAGCTGCTGGCCGACCCCAAGGAGCGCGCCGAG 7418798

Qy        328 CACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCG 387
              |||| || |  |   |||          || ||  |      |    || |  ||   ||
Db    7418799 CACCTGATGCTCGTCGACCTGGGGCGCAACGATCTGGGGCGGGTCTGCGAGCCCGGTTCC 7418858

Qy        388 GCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAA 428
              |   |  |   |  | || ||  |||||  ||  || | |
Db    7418859 GTCGAGGTCGTCGACTTCATGACCATCGAGCGCTACTCGCA 7418899


RESULT 3
US-10-478-943D-1
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; Sequence 1, Application US/10478943D
; Publication No. US20060073574A1
; GENERAL INFORMATION:
;  APPLICANT: University College Dublin, National University of Ireland
;  TITLE OF INVENTION: Engineered biosynthesis of novel polyenes
;  FILE REFERENCE: PC-1636US
;  CURRENT APPLICATION NUMBER: US/10/478,943D
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: S2001/0527
;  PRIOR FILING DATE: 2001-05-31
;  NUMBER OF SEQ ID NOS: 1
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
;   LENGTH: 113193
;   TYPE: DNA
;   ORGANISM: Streptomyces nodosus
US-10-478-943D-1

  Query Match             10.3%;  Score 53.4;  DB 12;  Length 113193;
  Best Local Similarity   47.5%;  Pred. No. 5e-05;
  Matches  159;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

Qy        136 CTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAG 195
              ||   ||  ||  ||||  ||||| ||||      ||   |  |  |||  |||  |
Db      72859 CTCGACACCGAGCACCGTGCCTTCATCGAGGTCAGCTCCCACCCGGTGCTCGCCATGTCC 72918

Qy        196 TTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCAC 255
              ||   | |||| ||      |        || | ||||   || ||  |  |  ||  |
Db      72919 GTCCAGGACATGATCGACGACGCCGGAGTGGTCGGCGTGGCCTCCGGCACCCTGCGCCGT 72978

Qy        256 TTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAG 315
              || |||||||      | |       | ||||||  | | ||||  |||     |  |
Db      72979 GACAACGGCGGCCTCGACCGCTTCCTGCTGTCCGCCGCCCAGGTGTTCGTGCGCGGCGTC 73038

Qy        316 CTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGC 375
              | |  || |  |  || |  || | ||| ||||  |  ||    ||||  | ||     |
Db      73039 CAGGTCGACTGGGCCCCGCTGTTCGAGGGCACCGGCGCGACCCGGGTCGACCTGCCCACC 73098

Qy        376 CACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCC 435
              |||||  |  |    | |   ||||| || |      || ||  | | |   | | ||
Db      73099 TACGCCTTCCAGCACGAGCGGTACTGGAACGACCGTGCCGTCGTGGACCGTTCGGCCTCC 73158

Qy        436 GGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGA 470
              |  |  | |  ||       |||||  |   ||||
Db      73159 GCGCCGATGGACGCCGAGTTCTGGGCGGCCGTCGA 73193


RESULT 4
US-10-246-330-3
; Sequence 3, Application US/10246330
; Publication No. US20030166030A1
; GENERAL INFORMATION:
;  APPLICANT: O'Toole, George A.
;  APPLICANT:  Mah, Thien-Fah
;  TITLE OF INVENTION: METHODS TO STUDY AND MECHANISMS OF
;  TITLE OF INVENTION:  BIOFILM-SPECIFIC ANTIBIOTIC RESISTANCE
;  FILE REFERENCE: 14537-002001
;  CURRENT APPLICATION NUMBER: US/10/246,330
;  CURRENT FILING DATE:  2002-09-18
;  PRIOR APPLICATION NUMBER: US 60/323,241
;  PRIOR FILING DATE: 2001-09-18
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 7407
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(7404)
US-10-246-330-3

  Query Match             10.3%;  Score 53;  DB 7;  Length 7407;
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  Best Local Similarity   48.5%;  Pred. No. 4.3e-05;
  Matches  146;  Conservative    0;  Mismatches  155;  Indels    0;  Gaps    0;

Qy        211 TCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACG 270
              ||  ||  |  |  |||||  ||  |  |||  |  |  |  ||  |||||  |||  |||||||
Db       6913 TCCGGCGACGACGTGCTGTCCGGCGCCAACGGCAGTTCGGAGCACATCAACGGCGGCGAC 6972

Qy        271 CGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCAC 330
               ||  |  ||    |  |  |  |  |  |     |  ||   ||      |    ||  |    ||
Db       6973 GGCAGCGACCTGATCTTCAACGTGGGCACCGGCGATCACGTGGTGGCCGGCAACGGCAAC 7032

Qy        331 CAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCA 390
               |  |     |  ||  ||||  |  |   |    ||||  |||  |  |||  ||||   |  |
Db       7033 GACACCATCCAGATCACCGCGACCGATTTCGTCAGCATCGATGGCGGCGCCGGGTTCGAC 7092

Qy        391 AACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGAT 450
              | |||    |  |  |||    ||||||  ||  ||   ||  ||||  ||    |
Db       7093 ACCCTGGTCCTGGCCAACGGCATCGACCTCGACTACAACGCCGTCGGCGTCGGCACGCTC 7152

Qy        451 ATCCGCTGGGGCGAGTTCGACTTTGACAGGATCTTTGAGGACGGACGGGAGACCTTTGGC 510
              |  |  |    |      |||||  |  |  ||  |  |  |  ||   |   |  ||||  |  |
Db       7153 AGCAACCTCGAGCGCATCGACCTCGGCAAGGGCGATTCGGGTAGCGTGCTGACCCTGACC 7212

Qy        511 G 511
              |
Db       7213 G 7213


RESULT 5
US-10-282-122A-30151
; Sequence 30151, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT:  Zamudio, Carlos
;  APPLICANT:  Malone, Cheryl
;  APPLICANT:  Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari
;  APPLICANT:  Zyskind, Judith
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John
;  APPLICANT:  Carr, Grant
;  APPLICANT:  Yamamoto, Robert
;  APPLICANT:  Forsyth, R.
;  APPLICANT:  Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30151
;  LENGTH: 7407
;  TYPE: DNA
;  ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-30151

  Query Match             10.3%;  Score 53;  DB 8;  Length 7407;
  Best Local Similarity   48.5%;  Pred. No. 4.3e-05;
  Matches  146;  Conservative    0;  Mismatches  155;  Indels    0;  Gaps    0;

Qy        211 TCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACG 270
              ||  ||  |  |  |||||  ||  |  |||  |  |  |  ||  |||||  |||  |||||||
Db       6913 TCCGGCGACGACGTGCTGTCCGGCGCCAACGGCAGTTCGGAGCACATCAACGGCGGCGAC 6972

Qy        271 CGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCAC 330
               ||  |  ||    |  |  |  |  |  |     |  ||   ||      |    ||  |    ||
Db       6973 GGCAGCGACCTGATCTTCAACGTGGGCACCGGCGATCACGTGGTGGCCGGCAACGGCAAC 7032

Qy        331 CAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCA 390
               |  |     |  ||  ||||  |  |   |    ||||  |||  |  |||  ||||   |  |
Db       7033 GACACCATCCAGATCACCGCGACCGATTTCGTCAGCATCGATGGCGGCGCCGGGTTCGAC 7092

Qy        391 AACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGAT 450
              | |||    |  |  |||    ||||||  ||  ||   ||  ||||  ||    |
Db       7093 ACCCTGGTCCTGGCCAACGGCATCGACCTCGACTACAACGCCGTCGGCGTCGGCACGCTC 7152

Qy        451 ATCCGCTGGGGCGAGTTCGACTTTGACAGGATCTTTGAGGACGGACGGGAGACCTTTGGC 510
              |  |  |    |      |||||  |  |  ||  |  |  |  ||   |   |  ||||  |  |
Db       7153 AGCAACCTCGAGCGCATCGACCTCGGCAAGGGCGATTCGGGTAGCGTGCTGACCCTGACC 7212

Qy        511 G 511
              |
Db       7213 G 7213


RESULT 6
US-10-437-963-23119
; Sequence 23119, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Wu, Wei
;  APPLICANT:  Boukharov, Andrey A.
;  APPLICANT:  Barbazuk, Brad
;  APPLICANT:  Li, Ping
;  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53221)B
;  CURRENT APPLICATION NUMBER: US/10/437,963
;  CURRENT FILING DATE:  2003-05-14
;  NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 23119
;   LENGTH: 791
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(791)
;   OTHER INFORMATION: unsure at all n locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_2822C.1
US-10-437-963-23119

  Query Match             10.1%;  Score 52.2;  DB 8;  Length 791;
  Best Local Similarity   46.2%;  Pred. No. 5.2e-05;
  Matches  171;  Conservative    0;  Mismatches  199;  Indels    0;  Gaps    0;

Qy         79 GCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAGGTCATTGCGCCTACTCTG 138
              ||  |  |  ||   |      ||||||  |  |   |  ||     |  |||     |      |
Db        404 GCCGTCCGCACCATGAACAAGGAGGGCGGCGGCCTCGTCACCGTCGCCACCTTCGCCTCC 463
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Qy        139 CGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTC 198
              | |   || |  || |  |  || ||| ||| || ||||  |   ||||   ||  ||
Db        464 ATCTTCTCCTCCTACTGCGCCAGCGGCAACCTCAGGAAGGCCGTCGAGGCCTTCGACGTC 523

Qy        199 GTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTC 258
              | || | |  |       ||| |       | || || || |  || |        | |
Db        524 ATGGGGAAGTACGGCGTGGAGCCGGACGCCGTCGCCCTCAACTCCCTCCTCTCCGCCATG 583

Qy        259 ATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTG 318
              | ||||   | || | | | ||| | |  |||||  | ||    ||  | |
Db        584 TGCCGCGGGGAGGGCCGCGCGCAGGCGGCGCAGGACCTGTTCGAGCGCACCAAGGCCACC 643

Qy        319 CGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCAC 378
              ||  ||  ||  |     |   |  |    | |  ||| |       |   ||||  ||
Db        644 GTCGCGCCCGACGCGGACACCTTCGGGATTCTCCTCGAGGCGTGNGAGAAAGAGGGGAAC 703

Qy        379 GCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGC 438
              |||||    || ||      ||    | ||| ||| | | |||||  |   |  |||||||
Db        704 GCCCAGCGCGCCAAGAGCACCTTCGGCGAGATGATTGTCCGCGTCGGCTGGGACGCCGGC 763

Qy        439 CTCAAGCCCG 448
              || |||||
Db        764 AACATGCCCG 773


RESULT 7
US-10-425-114-4414
; Sequence 4414, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 4414
;   LENGTH: 1336
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 700356834_FLI
US-10-425-114-4414

  Query Match             10.1%;  Score 52;  DB 8;  Length 1336;
  Best Local Similarity   47.1%;  Pred. No. 6.5e-05;
  Matches  160;  Conservative    0;  Mismatches  180;  Indels    0;  Gaps    0;

Qy        133 ACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAG 192
              | ||| ||| | ||  |||    | ||  || ||||       |    || || |
Db        372 ATTCTACGCGTGGATAACCTGGTCATCACCGGCAAGGGAAACCTTGACGGGCAGGGCCCA 431

Qy        193 GAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAG 252
              |   |      ||| |  |||  |||   ||| |   | | |   | ||| | ||    |
Db        432 GCCGTGTGGAGCAAGAACTCCTGCACCAAGAAGTACGACTGCAAGATCCTTCCCAACTCG 491

Qy        253 CACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCAC 312
              |   | || | |   |  | |  | | ||||||||| || |  | |  ||  || | |
Db        492 CTGGTGATGGACTTCGTGAACAACGGGGAGGTGTCCGGGGTCACGCTGCTCAACTCCAAG 551

Qy        313 CAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAG 372
              | | | |     |  ||| ||||||||     || ||||| || ||| ||| |
Db        552 TTCTTCCACATGAACATGTACCGGTGCAAGGACATGCTGATCAAGGACGTGACCGTGACG 611

Qy        373 GGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTC 432
              |  | ||   ||    | |||     |  |    | | | |  ||||      | |||    |
Db        612 GCGCCCGGGGACAGCCCCAACACGGATGGCATCCACATGGGCGACTCATCCGGGATCACC 671
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Qy        433 GCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACT 472
              |  |  ||     |  |  |  | | | ||| | |  ||
Db        672 ATCACCAACACCGTCATTGGCGTCGGCGACGACTGCATCT 711


RESULT 8
US-10-425-114-29012
; Sequence 29012, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 29012
;   LENGTH: 1394
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB4828-012-C2_FLI
US-10-425-114-29012

  Query Match             10.1%;  Score 52;  DB 8;  Length 1394;
  Best Local Similarity   47.1%;  Pred. No. 6.5e-05;
  Matches  160;  Conservative    0;  Mismatches  180;  Indels    0;  Gaps    0;

Qy        133 ACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAG 192
              | ||| ||| | ||  |||    | ||  || ||||       |    || || |
Db        361 ATTCTACGCGTGGATAACCTGGTCATCACCGGCAAGGGAAACCTTGACGGGCAGGGCCCA 420

Qy        193 GAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAG 252
              |   |      ||| |  |||  |||   ||| |   | | |   | ||| | ||    |
Db        421 GCTGTGTGGAGCAAGAACTCCTGCACCAAGAAGTACGACTGCAAGATCCTTCCCAACTCG 480

Qy        253 CACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCAC 312
              |   | || | |   |  | |  | | ||||||||| || |  | |  ||  || | |
Db        481 CTGGTGATGGACTTCGTGAACAACGGGGAGGTGTCCGGGGTCACGCTGCTCAACTCCAAG 540

Qy        313 CAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAG 372
              | | | |     |  ||| ||||||||     || ||||| || ||| ||| |
Db        541 TTCTTCCACATGAACATGTACCGGTGCAAGGACATGCTGATCAAGGACGTGACCGTGACG 600

Qy        373 GGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTC 432
              |  | ||   ||    | |||     |  |    | | | |  ||||      | |||    |
Db        601 GCGCCCGGGGACAGCCCCAACACGGATGGCATCCACATGGGCGACTCATCCGGGATCACC 660

Qy        433 GCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACT 472
              |  |  ||     |  |  |  | | | ||| | |  ||
Db        661 ATCACCAACACCGTCATTGGCGTCGGCGACGACTGCATCT 700


RESULT 9
US-10-425-114-17854
; Sequence 17854, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
```

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;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 17854
;   LENGTH: 1437
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB3075-048-C9_FLI
US-10-425-114-17854

  Query Match            10.1%;  Score 52;  DB 8;  Length 1437;
  Best Local Similarity   47.1%;  Pred. No. 6.6e-05;
  Matches  160;  Conservative    0;  Mismatches  180;  Indels    0;  Gaps    0;

Qy        133 ACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAG 192
              | ||| ||| | ||  |||     | ||  || ||||          |    || || |
Db        379 ATTCTACGCGTGGATAACCTGGTCATCACCGGCAAGGGAAACCTTGACGGGCAGGGCCCA 438

Qy        193 GAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAG 252
              |   |     ||| |  |||  |||    ||| |   | |   |   | ||| | ||    |
Db        439 GCCGTGTGGAGCAAGAACTCCTGCACCAAGAAGTACGACTGCAAGATCCTTCCCAACTCG 498

Qy        253 CACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCAC 312
              |    | || | |   | |   | | ||||||||| || |  | |   ||  || | |
Db        499 CTGGTGATGGACTTCGTGAACAACGGGGAGGTGTCCGGGGTCACGCTGCTCAACTCCAAG 558

Qy        313 CAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAG 372
              | | | |         | ||| ||||||||     || ||||| || ||| ||| |
Db        559 TTCTTCCACATGAACATGTACCGGTGCAAGGACATGCTGATCAAGGACGTGACCGTGACG 618

Qy        373 GGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTC 432
              |  | ||   ||    | |||    |  |   | | | |  ||||     | |||    |
Db        619 GCGCCCGGGGACAGCCCCAACACGGATGGCATCCACATGGGCGACTCATCCGGGATCACC 678

Qy        433 GCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACT 472
              |  |  ||    |  |  |  | | | ||| | |  ||
Db        679 ATCACCAACACCGTCATTGGCGTCGGCGACGACTGCATCT 718


RESULT 10
US-10-425-114-29011
; Sequence 29011, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 29011
;   LENGTH: 1598
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB4828-011-H12_FLI
US-10-425-114-29011

  Query Match            10.1%;  Score 52;  DB 8;  Length 1598;
  Best Local Similarity   47.1%;  Pred. No. 6.7e-05;
  Matches  160;  Conservative    0;  Mismatches  180;  Indels    0;  Gaps    0;

Qy        133 ACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAG 192
              | ||| ||| | ||  |||     | ||  || ||||          |    || || |
Db        395 ATTCTACGCGTGGATAACCTGGTCATCACCGGCAAGGGAAACCTTGACGGGCAGGGCCCA 454

Qy        193 GAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAG 252
              |   |     ||| |  |||  |||    ||| |   | |   |   | ||| | ||    |
Db        455 GCTGTGTGGAGCAAGAACTCCTGCACCAAGAAGTACGACTGCAAGATCCTTCCCAACTCG 514

Qy        253 CACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCAC 312
              |    | || | |   | |   | | ||||||||| || |  | |   ||  || | |
Db        515 CTGGTGATGGACTTCGTGAACAACGGGGAGGTGTCCGGGGTCACGCTGCTCAACTCCAAG 574

Qy        313 CAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAG 372
              | | | |         | ||| ||||||||     || ||||| || ||| ||| |
Db        575 TTCTTCCACATGAACATGTACCGGTGCAAGGACATGCTGATCAAGGACGTGACCGTGACG 634

Qy        373 GGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTC 432
              |  | ||   ||    | |||    |  |   | | | |  ||||     | |||    |
Db        635 GCGCCCGGGGACAGCCCCAACACGGATGGCATCCACATGGGCGACTCATCCGGGATCACC 694

Qy        433 GCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACT 472
              |  |  ||    |  |  |  | | | ||| | |  ||
Db        695 ATCACCAACACCGTCATTGGCGTCGGCGACGACTGCATCT 734


RESULT 11
US-10-353-454-45
; Sequence 45, Application US/10353454
; Publication No. US20030194809A1
; GENERAL INFORMATION:
;  APPLICANT: E.I. DuPont de Nemours & Company
;  APPLICANT:  Yadav, Narendra
;  TITLE OF INVENTION: METHOD OF CONTROLLING SITE-SPECIFIC RECOMBINATION
;  FILE REFERENCE: CL1975 US NA
;  CURRENT APPLICATION NUMBER: US/10/353,454
;  CURRENT FILING DATE:  2003-01-29
;  NUMBER OF SEQ ID NOS: 59
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 45
;   LENGTH: 2189
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Sequence of 2189 bp Bgl II-Hind III fragment containing
;   OTHER INFORMATION: SCP:Flp:3'pin gene in plasmid pPH12891
US-10-353-454-45

  Query Match            10.0%;  Score 51.4;  DB 7;  Length 2189;
  Best Local Similarity   47.1%;  Pred. No. 0.00011;
  Matches  157;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

Qy        156 CTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAG 215
              | ||   | |   |||  | ||   || || |||  |||||||  |  |||   ||
Db        859 CCTCGAGGCCTCCCTCAAGAAGCTCATCCCCGCCTGGGAGTTCACCATCATCCCCTACTA 918

Qy        216 CAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGCTG 275
              |   |||| ||       | || |  |  ||    |  | | ||       |  | |
Db        919 CGGCCAGAAGCACCAGTCCGACATCACCGACATCGTGTCATCCCTCCAGCTTCAGTTCGA 978

Qy        276 GGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAG 335
              |      | |   |  ||| ||| || |  | ||  | ||  |    |   |  ||
Db        979 GTCCTCCGAGGAGGCTGACAAGGGCAACTCCCACTCCAAGAAGATGCTGAAGGCCCTCCT 1038

Qy        336 GTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCT 395
              | | ||| |     ||||  |||| ||||  ||||  || |  |  ||   |   ||
Db       1039 CTCCGAGGGCGAGTCCATCTGGGAGATCACCGAGAAGATCCTCAACTCCTTCGAGTACAC 1098

Qy        396 TCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCG 455
              | ||| ||  |||| | |   | |||   |||||  |  ||||    ||   |||
Db       1099 CTCCAGGTTCACTAAGACCAAGACCCTCTACCAGTTCCTCTTCCTCGCCACCTTCATCAA 1158

Qy        456 CTGGGGCGAGTTCGACTTTGACAGGATCTTTGA 488
              ||| |||  ||||        || || | | ||
Db       1159 CTGCGGCAGGTTCTCAGACATCAAGAACGTGGA 1191
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RESULT 12
US-10-353-445-4
; Sequence 4, Application US/10353445
; Publication No. US20030119166A1
; GENERAL INFORMATION:
;  APPLICANT: Baszczynski, Christopher L.
;  APPLICANT:  Lyznik, Leszek A.
;  APPLICANT:  Gordon-Kamm, William J.
;  APPLICANT:  Guan, Xueni
;  APPLICANT:  Rao, Guru
;  APPLICANT:  Tagliani, Laura A.
;  TITLE OF INVENTION: A No. US20030119166A1el Method For The Integration Of Foreign DNA
;  TITLE OF INVENTION:  Eukaryotic Genomes
;  FILE REFERENCE: 5718-66 (amended listing)
;  CURRENT APPLICATION NUMBER: US/10/353,445
;  CURRENT FILING DATE:  2003-01-29
;  PRIOR APPLICATION NUMBER: US/09/193,503B
;  PRIOR FILING DATE: 1998-11-17
;  PRIOR APPLICATION NUMBER: 60/099,435
;  PRIOR FILING DATE: 1998-09-08
;  PRIOR APPLICATION NUMBER: 60/056,627
;  PRIOR FILING DATE: 1997-11-18
;  PRIOR APPLICATION NUMBER: 60/065,613
;  PRIOR FILING DATE: 1997-11-18
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 2346
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Nucleotide
;   OTHER INFORMATION: sequence encoding a Cre:FLPm  polypeptide, Cre
;   OTHER INFORMATION: from Bacteriophage P1 and FLP (Maize preferred
;   OTHER INFORMATION: codons) from Saccharomyces
US-10-353-445-4

  Query Match             10.0%;  Score 51.4;  DB 7;  Length 2346;
  Best Local Similarity   47.1%;  Pred. No. 0.00011;
  Matches  157;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

Qy        156 CTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAG 215
              | ||   | |   |||  | ||   || || |||  |||||||  |  |||   ||
Db       1338 CCTCGAGGCCTCCCTCAAGAAGCTCATCCCCGCCTGGGAGTTCACCATCATCCCCTACTA 1397

Qy        216 CAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGCTG 275
              |   |||| ||       |  || |  |  ||    |   | | ||       |  |
Db       1398 CGGCCAGAAGCACCAGTCCGACATCACCGACATCGTGTCATCCCTCCAGCTTCAGTTCGA 1457

Qy        276 GGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAG 335
              |       | |   | ||| ||| || |  | ||  | ||  |    |   |  ||
Db       1458 GTCCTCCGAGGAGGCTGACAAGGGCAACTCCCACTCCAAGAAGATGCTGAAGGCCCTCCT 1517

Qy        336 GTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCT 395
               | | ||| |    ||||   |||| ||||  ||||  || |  |  ||  |   ||
Db       1518 CTCCGAGGGCGAGTCCATCTGGGAGATCACCGAGAAGATCCTCAACTCCTTCGAGTACAC 1577

Qy        396 TCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCG 455
                | ||| ||  |||| | |   | |||   |||||  |  ||||    ||   |||
Db       1578 CTCCAGGTTCACTAAGACCAAGACCCTCTACCAGTTCCTCTTCCTCGCCACCTTCATCAA 1637

Qy        456 CTGGGGCGAGTTCGACTTTGACAGGATCTTTGA 488
              |||  |||  ||||         || || | | ||
Db       1638 CTGCGGCAGGTTCTCAGACATCAAGAACGTGGA 1670


RESULT 13
US-10-353-445-5
; Sequence 5, Application US/10353445
; Publication No. US20030119166A1
; GENERAL INFORMATION:
;  APPLICANT: Baszczynski, Christopher L.
;  APPLICANT:  Lyznik, Leszek A.
;  APPLICANT:  Gordon-Kamm, William J.
;  APPLICANT:  Guan, Xueni
;  APPLICANT:  Rao, Guru
;  APPLICANT:  Tagliani, Laura A.
;  TITLE OF INVENTION: A No. US20030119166A1el Method For The Integration Of Foreign DNA
;  TITLE OF INVENTION:  Eukaryotic Genomes
;  FILE REFERENCE: 5718-66 (amended listing)
;  CURRENT APPLICATION NUMBER: US/10/353,445
;  CURRENT FILING DATE:  2003-01-29
;  PRIOR APPLICATION NUMBER: US/09/193,503B
;  PRIOR FILING DATE: 1998-11-17
;  PRIOR APPLICATION NUMBER: 60/099,435
;  PRIOR FILING DATE: 1998-09-08
;  PRIOR APPLICATION NUMBER: 60/056,627
;  PRIOR FILING DATE: 1997-11-18
;  PRIOR APPLICATION NUMBER: 60/065,613
;  PRIOR FILING DATE: 1997-11-18
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 2346
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: sequence
;   OTHER INFORMATION: encoding moCre:FLPm, Cre from Bacteriophage P1 and
;   OTHER INFORMATION: FLP from Saccharomyces, both maize preferred
;   OTHER INFORMATION: codons
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2346)
US-10-353-445-5

  Query Match             10.0%;  Score 51.4;  DB 7;  Length 2346;
  Best Local Similarity   47.1%;  Pred. No. 0.00011;
  Matches  157;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

Qy        156 CTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAG 215
              | ||   | |   |||  | ||   || || |||  |||||||  |  |||   ||
Db       1338 CCTCGAGGCCTCCCTCAAGAAGCTCATCCCCGCCTGGGAGTTCACCATCATCCCCTACTA 1397

Qy        216 CAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGCTG 275
              |   |||| ||       |  || |  |  ||    |   | | ||       |  |
Db       1398 CGGCCAGAAGCACCAGTCCGACATCACCGACATCGTGTCATCCCTCCAGCTTCAGTTCGA 1457

Qy        276 GGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAG 335
              |       | |   | ||| ||| || |  | ||  | ||  |    |   |  ||
Db       1458 GTCCTCCGAGGAGGCTGACAAGGGCAACTCCCACTCCAAGAAGATGCTGAAGGCCCTCCT 1517

Qy        336 GTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCT 395
               | | ||| |    ||||   |||| ||||  ||||  || |  |  ||  |   ||
Db       1518 CTCCGAGGGCGAGTCCATCTGGGAGATCACCGAGAAGATCCTCAACTCCTTCGAGTACAC 1577

Qy        396 TCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCG 455
                | ||| ||  |||| | |   | |||   |||||  |  ||||    ||   |||
Db       1578 CTCCAGGTTCACTAAGACCAAGACCCTCTACCAGTTCCTCTTCCTCGCCACCTTCATCAA 1637

Qy        456 CTGGGGCGAGTTCGACTTTGACAGGATCTTTGA 488
              |||  |||  ||||         || || | | ||
Db       1638 CTGCGGCAGGTTCTCAGACATCAAGAACGTGGA 1670


RESULT 14
US-10-353-445-8
; Sequence 8, Application US/10353445
; Publication No. US20030119166A1
; GENERAL INFORMATION:
;  APPLICANT: Baszczynski, Christopher L.
;  APPLICANT:  Lyznik, Leszek A.
;  APPLICANT:  Gordon-Kamm, William J.
;  APPLICANT:  Guan, Xueni
;  APPLICANT:  Rao, Guru
;  APPLICANT:  Tagliani, Laura A.
```

; TITLE OF INVENTION: A No. US20030119166A1el Method For The Integration Of Foreign DNA
; TITLE OF INVENTION: Eukaryotic Genomes
; FILE REFERENCE: 5718-66 (amended listing)
; CURRENT APPLICATION NUMBER: US/10/353,445
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US/09/193,503B
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence
; OTHER INFORMATION: encoding a FLPm:Cre polypeptide, FLP from
; OTHER INFORMATION: Saccharomyces (maize preferred codons), and Cre
; OTHER INFORMATION: from Bacteriophage P1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2346)
US-10-353-445-8

Query Match 10.0%; Score 51.4; DB 7; Length 2346;
Best Local Similarity 47.1%; Pred. No. 0.00011;
Matches 157; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

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Qy        156 CTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAG 215
              | ||   | |   |||  | ||   || || |||  |||||||  |  |||   ||
Db        264 CCTCGAGGCCTCCCTCAAGAAGCTCATCCCCGCCTGGGAGTTCACCATCATCCCCTACTA 323

Qy        216 CAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGCTG 275
              |   |||| ||        |  || |  |  ||     |   | | ||         |  |
Db        324 CGGCCAGAAGCACCAGTCCGACATCACCGACATCGTGTCATCCCTCCAGCTTCAGTTCGA 383

Qy        276 GGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAG 335
              |       | |   |  ||| ||| || |  | ||  | ||  |    |    |  ||
Db        384 GTCCTCCGAGGAGGCTGACAAGGGCAACTCCCACTCCAAGAAGATGCTGAAGGCCCTCCT 443

Qy        336 GTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCT 395
              | | ||| |    ||||  |||| ||||  ||||  || |  |  ||  |   ||
Db        444 CTCCGAGGGCGAGTCCATCTGGGAGATCACCGAGAAGATCCTCAACTCCTTCGAGTACAC 503

Qy        396 TCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCG 455
                | ||| ||  |||| | |   | |||   |||||  |  ||||    ||   |||
Db        504 CTCCAGGTTCACTAAGACCAAGACCCTCTACCAGTTCCTCTTCCTCGCCACCTTCATCAA 563

Qy        456 CTGGGGCGAGTTCGACTTTGACAGGATCTTTGA 488
              ||| |||  ||||       || || | | ||
Db        564 CTGCGGCAGGTTCTCAGACATCAAGAACGTGGA 596
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RESULT 15
US-10-767-701-14768/c
; Sequence 14768, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 14768
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS2086_1
US-10-767-701-14768

Query Match 9.9%; Score 51.2; DB 8; Length 1536;
Best Local Similarity 50.4%; Pred. No. 0.00011;
Matches 125; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

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Qy        137 TGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGT 196
              ||   || | || ||||  ||||||| |   |    ||| ||| | |   ||||    |
Db       1136 TGGTGATGGCCTGCCGCGACTTCCTCAAGGCGGCGCGGGCGGCCAAGGGCGCCGGCATGG 1077

Qy        197 TCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACT 256
              | |||||     | | | || |||  ||       | | ||  |  | ||  || ||| |
Db       1076 CGGACGGCAGCTACACCATCATGCACCTGGACCTGGCCTCCCTCGACAGCGTGCGGCAGT 1017

Qy        257 TCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGC 316
              || |||    |  ||||  |  | || || ||   ||||  ||  || || ||  |
Db       1016 TCGTCGAGAACGTGCGCCAGCTGGAGATGCCCATCGACGTCGTGGTCTGCAACGCCGCCG 957

Qy        317 TGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCC 376
              ||  |   ||   |   | | ||  |  |  ||||    | |   ||   ||||  | |
Db        956 TGTACCGGCCCACCGCCACGGACCCGTCCTACACCGCCGACGGCTTCGAGATGAGCGTCG 897

Qy        377 ACGCCCAC 384
              || | ||
Db        896 GCGTCAAC 889
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Job time : 1116 secs

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: December 4, 2006, 18:35:54 ; Search time 139 Seconds
(without alignments)
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Title: US-10-507-132-1
Perfect score: 516
Sequence: 1 atgggttcgcaagttcaaaa.....gggagacctttggcgacaaa 516

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	52.4	10.2	4451	3	US-08-717-294-42	Sequence 42, Appl
	2	52	10.1	1820	2	US-08-173-508-7	Sequence 7, Appli
	3	52	10.1	1821	2	US-08-265-310-7	Sequence 7, Appli
	4	52	10.1	1821	3	US-08-951-742-7	Sequence 7, Appli
	5	51.4	10.0	1272	2	US-08-972-258-1	Sequence 1, Appli
	6	51.4	10.0	1272	3	US-09-263-128-1	Sequence 1, Appli
	7	51.4	10.0	1272	3	US-09-641-111A-1	Sequence 1, Appli
	8	51.4	10.0	2346	3	US-09-193-503B-4	Sequence 4, Appli
	9	51.4	10.0	2346	3	US-09-193-503B-5	Sequence 5, Appli
	10	51.4	10.0	2346	3	US-09-193-503B-8	Sequence 8, Appli
	11	51.4	10.0	2346	3	US-09-415-839-4	Sequence 4, Appli
	12	51.4	10.0	2346	3	US-09-415-839-5	Sequence 5, Appli
	13	51.4	10.0	2346	3	US-09-415-839-8	Sequence 8, Appli
c	14	51.4	10.0	4131	3	US-09-252-991A-13773	Sequence 13773, A
	15	51.4	10.0	8211	3	US-09-252-991A-13656	Sequence 13656, A
	16	50.8	9.8	561	3	US-09-252-991A-13572	Sequence 13572, A
	17	50.6	9.8	1062	3	US-09-902-540-8032	Sequence 8032, Ap
	18	50.6	9.8	6715	3	US-09-902-540-818	Sequence 818, App
	19	50	9.7	1821	3	US-09-266-965-82	Sequence 82, Appl
	20	50	9.7	18034	3	US-09-266-965-75	Sequence 75, Appl
	21	48.2	9.3	510	3	US-09-252-991A-15512	Sequence 15512, A
c	22	48.2	9.3	1989	3	US-09-252-991A-15371	Sequence 15371, A
	23	48.2	9.3	2058	3	US-09-252-991A-15462	Sequence 15462, A
	24	48.2	9.3	2637	3	US-09-252-991A-15403	Sequence 15403, A
	25	47.4	9.2	654	4	US-10-081-864A-23	Sequence 23, Appl
	26	47.4	9.2	707	4	US-10-081-864A-21	Sequence 21, Appl
	27	47.4	9.2	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	28	47.4	9.2	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	29	46.8	9.1	1365	3	US-09-030-995-1	Sequence 1, Appli
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c	31	46.6	9.0	13706	3	US-09-902-540-1124	Sequence 1124, Ap
	32	46.4	9.0	2208	3	US-09-902-540-3493	Sequence 3493, Ap
	33	46.4	9.0	18471	3	US-09-902-540-1167	Sequence 1167, Ap
	34	46.2	9.0	3282	3	US-09-902-540-6552	Sequence 6552, Ap
	35	46.2	9.0	3666	3	US-09-902-540-484	Sequence 484, App
	36	46.2	9.0	44377	2	US-08-804-227C-7	Sequence 7, Appli
	37	46.2	9.0	44377	2	US-08-804-198-1	Sequence 1, Appli
	38	45.6	8.8	2016	4	US-10-632-694A-4	Sequence 4, Appli
	39	45.6	8.8	2016	4	US-10-632-694A-5	Sequence 5, Appli
	40	45.6	8.8	2595	3	US-10-132-350-11	Sequence 11, Appl
	41	45.6	8.8	3007	3	US-10-132-350-9	Sequence 9, Appli
	42	45	8.7	3401	3	US-09-907-794A-249	Sequence 249, App
	43	45	8.7	3401	3	US-09-905-125A-249	Sequence 249, App
	44	45	8.7	3401	3	US-09-902-775A-249	Sequence 249, App
	45	45	8.7	3401	3	US-09-906-700-249	Sequence 249, App

ALIGNMENTS

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RESULT 1
US-08-717-294-42
; Sequence 42, Application US/08717294
; Patent No. 6114148
;  GENERAL INFORMATION:
;    APPLICANT:  SEED, BRIAN
;    APPLICANT:  HAAS, JURGEN
;    TITLE OF INVENTION:  HIGH LEVEL EXPRESSION OF
;    TITLE OF INVENTION:  PROTEINS
;    NUMBER OF SEQUENCES:  110
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Clark & Elbing LLP
;      STREET:  176 Federal Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/717,294
;      FILING DATE:  20-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elbing, Karen L
;      REGISTRATION NUMBER:  35,238
;      REFERENCE/DOCKET NUMBER:  00786/345001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-428-0200
;      TELEFAX:  617-428-7045
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4451 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-717-294-42
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  Query Match           10.2%;  Score 52.4;  DB 3;  Length 4451;
  Best Local Similarity   52.8%;  Pred. No. 0.0026;
  Matches  113;  Conservative    0;  Mismatches  101;  Indels    0;  Gaps    0;

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Db       2323 GCCACCCCAGCACGCGTCAGAAGCAGTTCAACGCCACCCCCCCCGTGCTGAAGCGCCACC 2382

Qy        290 AGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCA 349
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Qy        350 CCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGA 409
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RESULT 2
US-08-173-508-7
; Sequence 7, Application US/08173508
; Patent No. 5616485
;  GENERAL INFORMATION:
;    APPLICANT:  Bartfeld, Daniel
;    APPLICANT:  Butler, Michael J.
;    APPLICANT:  Hadary, Dany
;    APPLICANT:  Jenish, David
;    APPLICANT:  Krieger, Timothy
;    TITLE OF INVENTION:  STREPTOMYCES PROTEASES AND IMPROVED
;    TITLE OF INVENTION:  STREPTOMYCES STRAINS FOR EXPRESSION OF PEPTIDES AND
;    TITLE OF INVENTION:  POLYPEPTIDES
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W.
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/173,508
;      FILING DATE:  23-DEC-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  18740/125/CACO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202 672 5300
;      TELEFAX:  202 672 5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1820 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  104..1720
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  104..244
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  245..1720

US-08-173-508-7

  Query Match           10.1%;  Score 52;  DB 2;  Length 1820;
  Best Local Similarity   49.3%;  Pred. No. 0.0027;
  Matches  136;  Conservative    0;  Mismatches  140;  Indels    0;  Gaps    0;

Qy        148 TACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATG 207
              ||| || ||||||| | |  |  ||  |  |   ||    ||||   |   | | || ||
Db        848 TACGGCACCTTCCTGGGCGCGACCTACGCCGGTCTGTTCCCCGACCGGACGGGCCGCCTG 907

Qy        208 GTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGC 267
              |||  |  |     ||||     |   |   ||  ||||   | | || |
Db        908 GTCCTGGACGGCGCGATGGACCCCTCGCTGCCCGCCCGCCGCCTGAACCTGGAGCAGACG 967

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              | |||  |||| || || | ||  |   |  |  | || |    ||| ||  | |
Db        968 GAGGGCTTCGAGACGGCGTTCCAGTCCTTCGCGAAGGACTGCGTGAAGCAGCCGGACTGC 1027

Qy        328 CACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCG 387
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Qy        388 GCAAACCTTCACTGGTACAAGAAGATCGACGGCGTC 423
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RESULT 3
US-08-265-310-7
; Sequence 7, Application US/08265310
; Patent No. 5856166
;  GENERAL INFORMATION:
;    APPLICANT:  Bartfeld, Daniel
;    APPLICANT:  Butler, Michael J.
;    APPLICANT:  Hadary, Dany
;    APPLICANT:  Jenish, David
;    APPLICANT:  Krieger, Timothy
;    APPLICANT:  Malek, Lawrence T.
;    APPLICANT:  Soostmeyer, Gisela
;    APPLICANT:  Walczyk, Eva
;    APPLICANT:  Krygsman, Phyllis
;    APPLICANT:  Garven, Shelia
;    TITLE OF INVENTION:  STREPTOMYCES PROTEASES AND IMPROVED
;    TITLE OF INVENTION:  STREPTOMYCES STRAINS FOR EXPRESSION OF PEPTIDES AND
;    TITLE OF INVENTION:  POLYPEPTIDES
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W.
;      CITY:  Washington, D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,310
;      FILING DATE:  24-JUN-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/173,508
;      FILING DATE:  23-DEC-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  18740/133/CACO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202 672 5300
;      TELEFAX:  202 672 5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  7:
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;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1821 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  104..1720
;     FEATURE:
;       NAME/KEY:  sig_peptide
;       LOCATION:  104..244
;     FEATURE:
;       NAME/KEY:  mat_peptide
;       LOCATION:  245..1720
US-08-265-310-7

  Query Match             10.1%;  Score 52;  DB 2;  Length 1821;
  Best Local Similarity   49.3%;  Pred. No. 0.0027;
  Matches  136;  Conservative    0;  Mismatches  140;  Indels    0;  Gaps    0;

Qy        148 TACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATG 207
              ||| || ||||||| | |  |  ||  |  |   ||    ||||   |   | | || ||
Db        848 TACGGCACCTTCCTGGGCGCGACCTACGCCGGTCTGTTCCCCGACCGGACGGGCCGCCTG 907

Qy        208 GTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGC 267
              |||  |  |      ||||      |   |   ||  ||||   | | || |
Db        908 GTCCTGGACGGCGCGATGGACCCCTCGCTGCCCGCCCGCCGCCTGAACCTGGAGCAGACG 967

Qy        268 ACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCG 327
                | |||  |||| || || | ||  |   |  |  | || |    ||| ||  | |
Db        968 GAGGGCTTCGAGACGGCGTTCCAGTCCTTCGCGAAGGACTGCGTGAAGCAGCCGGACTGC 1027

Qy        328 CACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCG 387
              | ||   | ||||||||||||||    |  |||||  || |||   | |  ||  ||
Db       1028 CCCCTCGGCGACAAGGACACCACCCCCGACCAGGTCGGCAAGAACCTCAAGTCCTTCTTC 1087

Qy        388 GCAAACCTTCACTGGTACAAGAAGATCGACGGCGTC 423
              |  ||||  ||  | |       |  || ||||| |
Db       1088 GACGACCTGGACGCGAAGCCCCTGCCCGCCGGCGAC 1123


RESULT 4
US-08-951-742-7
; Sequence 7, Application US/08951742
; Patent No. 6127144
;  GENERAL INFORMATION:
;     APPLICANT:  Bartfeld, Daniel
;     APPLICANT:  Michael J. Butler
;     APPLICANT:  Dany Hadary
;     APPLICANT:  David Jenish
;     APPLICANT:  Tim Krieger
;     APPLICANT:  Lawrence T. Malek
;     APPLICANT:  Gisela Soostmeyer
;     APPLICANT:  Eva Walczyk
;     APPLICANT:  Phyllis Krygsman
;     APPLICANT:  Sheila Garven
;     TITLE OF INVENTION:  METHOD FOR EXPRESSION OF PROTEINS IN
;     TITLE OF INVENTION:  BACTERIAL HOST CELLS
;     NUMBER OF SEQUENCES:  25
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Foley & Lardner
;       STREET:  3000 K Street, N.W., Suite 500
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20007-5109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/951,742
;       FILING DATE:  16-OCT-1997
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Bent, Stephen A.
;       REGISTRATION NUMBER:  29,768
;       REFERENCE/DOCKET NUMBER:  0189740/0140
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202)672-5300
;       TELEFAX:  (202)672-5399
;       TELEX:  904136
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1821 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  104..1720
;     FEATURE:
;       NAME/KEY:  sig_peptide
;       LOCATION:  104..244
;     FEATURE:
;       NAME/KEY:  mat_peptide
;       LOCATION:  245..1720
US-08-951-742-7

  Query Match             10.1%;  Score 52;  DB 3;  Length 1821;
  Best Local Similarity   49.3%;  Pred. No. 0.0027;
  Matches  136;  Conservative    0;  Mismatches  140;  Indels    0;  Gaps    0;

Qy        148 TACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATG 207
              ||| || ||||||| | |  |  ||  |  |   ||    ||||   |   | | || ||
Db        848 TACGGCACCTTCCTGGGCGCGACCTACGCCGGTCTGTTCCCCGACCGGACGGGCCGCCTG 907

Qy        208 GTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGC 267
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Db        908 GTCCTGGACGGCGCGATGGACCCCTCGCTGCCCGCCCGCCGCCTGAACCTGGAGCAGACG 967

Qy        268 ACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCG 327
                | |||  |||| || || | ||  |   |  |  | || |    ||| ||  | |
Db        968 GAGGGCTTCGAGACGGCGTTCCAGTCCTTCGCGAAGGACTGCGTGAAGCAGCCGGACTGC 1027

Qy        328 CACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCG 387
              | ||   | ||||||||||||||    |  |||||  || |||   | |  ||  ||
Db       1028 CCCCTCGGCGACAAGGACACCACCCCCGACCAGGTCGGCAAGAACCTCAAGTCCTTCTTC 1087

Qy        388 GCAAACCTTCACTGGTACAAGAAGATCGACGGCGTC 423
              |  ||||  ||  | |       |  || ||||| |
Db       1088 GACGACCTGGACGCGAAGCCCCTGCCCGCCGGCGAC 1123


RESULT 5
US-08-972-258-1
; Sequence 1, Application US/08972258
; Patent No. 5929301
;  GENERAL INFORMATION:
;     APPLICANT:  Baszczynski, Chris
;     APPLICANT:  Bowen, Benjamin A.
;     APPLICANT:  Drummond, Bruce J.
;     APPLICANT:  Gordon-Kamm, William J.
;     APPLICANT:  Peterson, David J.
;     APPLICANT:  Sandahl, Gary A.
;     APPLICANT:  Tagliani, Laura A.
;     APPLICANT:  Zhao, Zuo-Yu
;     TITLE OF INVENTION:  No. 5929301el Nucleic Acid Sequence Encoding FLP
; Patent No. 5929301
;     TITLE OF INVENTION:  Recombinase and Method of Using Same
;     NUMBER OF SEQUENCES:  4
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  W. Murray Spruill
;       STREET:  3605 Glenwood Ave.  Suite 310
;       CITY:  Raleigh
```

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;       STATE:  NC
;       COUNTRY:  US
;       ZIP:  27622
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/972,258
;       FILING DATE:
;       CLASSIFICATION:  800
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Spruill, W. Murray
;       REGISTRATION NUMBER:  32,943
;       REFERENCE/DOCKET NUMBER:  5718-28
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  919 420 2202
;       TELEFAX:  919 881 3175
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1272 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     ORIGINAL SOURCE:
;       ORGANISM:  Synthetic sequence (optimized)
US-08-972-258-1

  Query Match             10.0%;  Score 51.4;  DB 2;  Length 1272;
  Best Local Similarity   47.1%;  Pred. No. 0.0035;
  Matches  157;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

Qy        156 CTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAG 215
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Db        264 CCTCGAGGCCTCCCTCAAGAAGCTCATCCCCGCCTGGGAGTTCACCATCATCCCCTACTA 323

Qy        216 CAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGCTG 275
              |   |||| ||       |  || |  |  ||    |   | | ||        | |
Db        324 CGGCCAGAAGCACCAGTCCGACATCACCGACATCGTGTCATCCCTCCAGCTTCAGTTCGA 383

Qy        276 GGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAG 335
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Db        384 GTCCTCCGAGGAGGCTGACAAGGGCAACTCCCACTCCAAGAAGATGCTGAAGGCCCTCCT 443

Qy        336 GTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCT 395
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Qy        396 TCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCG 455
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Db        504 CTCCAGGTTCACTAAGACCAAGACCCTCTACCAGTTCCTCTTCCTCGCCACCTTCATCAA 563

Qy        456 CTGGGGCGAGTTCGACTTTGACAGGATCTTTGA 488
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Db        564 CTGCGGCAGGTTCTCAGACATCAAGAACGTGGA 596


RESULT 6
US-09-263-128-1
; Sequence 1, Application US/09263128
; Patent No. 6175058
;  GENERAL INFORMATION:
;    APPLICANT:  Baszczynski, Chris
;    APPLICANT:  Bowen, Benjamin A.
;    APPLICANT:  Drummond, Bruce J.
;    APPLICANT:  Gordon-Kamm, William J.
;    APPLICANT:  Peterson, David J.
;    APPLICANT:  Sandahl, Gary A.
;    APPLICANT:  Tagliani, Laura A.
;    APPLICANT:  Zhao, Zuo-Yu
;    TITLE OF INVENTION:  No. 6175058el Nucleic Acid Sequence Encoding FLP
; Patent No. 6175058
;    TITLE OF INVENTION:  Recombinase and Method of Using Same
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  W. Murray Spruill
;      STREET:  3605 Glenwood Ave.  Suite 310
;      CITY:  Raleigh
;      STATE:  NC
;      COUNTRY:  US
;      ZIP:  27622
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,128
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/972,258
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Spruill, W. Murray
;      REGISTRATION NUMBER:  32,943
;      REFERENCE/DOCKET NUMBER:  5718-28
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919 420 2202
;      TELEFAX:  919 881 3175
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1272 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      ORGANISM:  Synthetic sequence (optimized)
US-09-263-128-1

  Query Match             10.0%;  Score 51.4;  DB 3;  Length 1272;
  Best Local Similarity   47.1%;  Pred. No. 0.0035;
  Matches  157;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

Qy        156 CTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAG 215
              | ||   | |   |||  | ||   || || |||  |||||||  |  |||   ||
Db        264 CCTCGAGGCCTCCCTCAAGAAGCTCATCCCCGCCTGGGAGTTCACCATCATCCCCTACTA 323

Qy        216 CAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGCTG 275
              |   |||| ||       |  || |  |  ||    |   | | ||        | |
Db        324 CGGCCAGAAGCACCAGTCCGACATCACCGACATCGTGTCATCCCTCCAGCTTCAGTTCGA 383

Qy        276 GGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAG 335
              |      | |   | ||| ||| || |  | ||  | ||  |    |  |  ||
Db        384 GTCCTCCGAGGAGGCTGACAAGGGCAACTCCCACTCCAAGAAGATGCTGAAGGCCCTCCT 443

Qy        336 GTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCT 395
              | | ||| |    ||||  |||| ||||| |||| || |  |  ||  |   ||
Db        444 CTCCGAGGGCGAGTCCATCTGGGAGATCACCGAGAAGATCCTCAACTCCTTCGAGTACAC 503

Qy        396 TCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCG 455
              | ||| ||  |||| | |   | |||   |||||  |  ||||   ||  |||
Db        504 CTCCAGGTTCACTAAGACCAAGACCCTCTACCAGTTCCTCTTCCTCGCCACCTTCATCAA 563

Qy        456 CTGGGGCGAGTTCGACTTTGACAGGATCTTTGA 488
              ||| |||  ||||       || || | | ||
Db        564 CTGCGGCAGGTTCTCAGACATCAAGAACGTGGA 596


RESULT 7
US-09-641-111A-1
; Sequence 1, Application US/09641111A
; Patent No. 6720475
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; GENERAL INFORMATION:
;  APPLICANT: Baszczynski, Christopher L.
;  APPLICANT:  Bowen, Benjamin A.
;  APPLICANT:  Drummond, Bruce J.
;  APPLICANT:  Gordon-Kamm, William J.
;  APPLICANT:  Peterson, David J.
;  APPLICANT:  Sandahl, Gary A.
;  APPLICANT:  Tagliani, Laura A.
;  APPLICANT:  Zhao, Zuo-Yu
;  APPLICANT:  St. Clair, Grace Marie
;  TITLE OF INVENTION: No. 6720475el Nucleic Acid Sequence Encoding FLP
; Patent No. 6720475
;  TITLE OF INVENTION:  Recombinase and Method of Using Same
;  FILE REFERENCE: 35718/201942
;  CURRENT APPLICATION NUMBER: US/09/641,111A
;  CURRENT FILING DATE:  2000-08-17
;  PRIOR APPLICATION NUMBER: 09/263,128
;  PRIOR FILING DATE: 1999-04-05
;  PRIOR APPLICATION NUMBER: 08/972,258
;  PRIOR FILING DATE: 1997-11-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1272
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1272)
;   OTHER INFORMATION: Optimized sequence
US-09-641-111A-1

  Query Match             10.0%;  Score 51.4;  DB 3;  Length 1272;
  Best Local Similarity   47.1%;  Pred. No. 0.0035;
  Matches  157;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

Qy        156 CTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAG 215
              | ||   | |   |||  | ||   || || |||  |||||||  |  |||   ||
Db        264 CCTCGAGGCCTCCCTCAAGAAGCTCATCCCCGCCTGGGAGTTCACCATCATCCCCTACTA 323

Qy        216 CAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGCTG 275
              |   |||| ||        |  || |  |  ||     |   | | ||        | |
Db        324 CGGCCAGAAGCACCAGTCCGACATCACCGACATCGTGTCATCCCTCCAGCTTCAGTTCGA 383

Qy        276 GGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAG 335
              |      | |   |  ||| ||| || |  | ||  | ||  |    |   |  ||
Db        384 GTCCTCCGAGGAGGCTGACAAGGGCAACTCCCACTCCAAGAAGATGCTGAAGGCCCTCCT 443

Qy        336 GTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCT 395
              | | ||| |    ||||   |||| |||||  ||||  || |  |  ||  |   ||
Db        444 CTCCGAGGGCGAGTCCATCTGGGAGATCACCGAGAAGATCCTCAACTCCTTCGAGTACAC 503

Qy        396 TCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCG 455
              | ||| ||  |||| | |   | |||   |||||  |  ||||    ||   |||
Db        504 CTCCAGGTTCACTAAGACCAAGACCCTCTACCAGTTCCTCTTCCTCGCCACCTTCATCAA 563

Qy        456 CTGGGGCGAGTTCGACTTTGACAGGATCTTTGA 488
              ||| |||  ||||        || || | | ||
Db        564 CTGCGGCAGGTTCTCAGACATCAAGAACGTGGA 596


RESULT 8
US-09-193-503B-4
; Sequence 4, Application US/09193503B
; Patent No. 6262341
; GENERAL INFORMATION:
;  APPLICANT:  Baszczynski, Christopher L.
;  APPLICANT:  Lyznik, Leszek A.
;  APPLICANT:  Gordon-Kamm, William J.
;  APPLICANT:  Guan, Xueni
;  APPLICANT:  Rao, Guru
;  APPLICANT:  Tagliani, Laura A.
;  TITLE OF INVENTION:  A No. 6262341el Method For The Integration Of Foreign DNA Into
;  TITLE OF INVENTION:  Eukaryotic Genomes
;  FILE REFERENCE:  5718-66 (amended listing)
;  CURRENT APPLICATION NUMBER: US/09/193,503B
;  CURRENT FILING DATE:  1998-11-17
;  PRIOR APPLICATION NUMBER:  60/099,435
;  PRIOR FILING DATE:  1998-09-08
;  PRIOR APPLICATION NUMBER:  60/056,627
;  PRIOR FILING DATE:  1997-11-18
;  PRIOR APPLICATION NUMBER:  60/065,613
;  PRIOR FILING DATE:  1997-11-18
;  NUMBER OF SEQ ID NOS:  11
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 2346
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Nucleotide
;   OTHER INFORMATION: sequence encoding a Cre:FLPm  polypeptide, Cre
;   OTHER INFORMATION: from Bacteriophage P1 and FLP (Maize preferred
;   OTHER INFORMATION: codons) from Saccharomyces
US-09-193-503B-4

  Query Match             10.0%;  Score 51.4;  DB 3;  Length 2346;
  Best Local Similarity   47.1%;  Pred. No. 0.004;
  Matches  157;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

Qy        156 CTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAG 215
              | ||   | |   |||  | ||   || || |||  |||||||  |  |||   ||
Db       1338 CCTCGAGGCCTCCCTCAAGAAGCTCATCCCCGCCTGGGAGTTCACCATCATCCCCTACTA 1397

Qy        216 CAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGCTG 275
              |   |||| ||        |  || |  |  ||     |   | | ||        | |
Db       1398 CGGCCAGAAGCACCAGTCCGACATCACCGACATCGTGTCATCCCTCCAGCTTCAGTTCGA 1457

Qy        276 GGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAG 335
              |      | |   |  ||| ||| || |  | ||  | ||  |    |   |  ||
Db       1458 GTCCTCCGAGGAGGCTGACAAGGGCAACTCCCACTCCAAGAAGATGCTGAAGGCCCTCCT 1517

Qy        336 GTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCT 395
              | | ||| |    ||||   |||| |||||  ||||  || |  |  ||  |   ||
Db       1518 CTCCGAGGGCGAGTCCATCTGGGAGATCACCGAGAAGATCCTCAACTCCTTCGAGTACAC 1577

Qy        396 TCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCG 455
              | ||| ||  |||| | |   | |||   |||||  |  ||||    ||   |||
Db       1578 CTCCAGGTTCACTAAGACCAAGACCCTCTACCAGTTCCTCTTCCTCGCCACCTTCATCAA 1637

Qy        456 CTGGGGCGAGTTCGACTTTGACAGGATCTTTGA 488
              ||| |||  ||||        || || | | ||
Db       1638 CTGCGGCAGGTTCTCAGACATCAAGAACGTGGA 1670


RESULT 9
US-09-193-503B-5
; Sequence 5, Application US/09193503B
; Patent No. 6262341
; GENERAL INFORMATION:
;  APPLICANT:  Baszczynski, Christopher L.
;  APPLICANT:  Lyznik, Leszek A.
;  APPLICANT:  Gordon-Kamm, William J.
;  APPLICANT:  Guan, Xueni
;  APPLICANT:  Rao, Guru
;  APPLICANT:  Tagliani, Laura A.
;  TITLE OF INVENTION:  A No. 6262341el Method For The Integration Of Foreign DNA Into
;  TITLE OF INVENTION:  Eukaryotic Genomes
;  FILE REFERENCE:  5718-66 (amended listing)
;  CURRENT APPLICATION NUMBER: US/09/193,503B
;  CURRENT FILING DATE:  1998-11-17
;  PRIOR APPLICATION NUMBER:  60/099,435
;  PRIOR FILING DATE:  1998-09-08
;  PRIOR APPLICATION NUMBER:  60/056,627
;  PRIOR FILING DATE:  1997-11-18
;  PRIOR APPLICATION NUMBER:  60/065,613
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;  PRIOR FILING DATE:  1997-11-18
;  NUMBER OF SEQ ID NOS:  11
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 2346
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: sequence
;   OTHER INFORMATION: encoding moCre:FLPm, Cre from Bacteriophage P1 and
;   OTHER INFORMATION: FLP from Saccharomyces, both maize preferred
;   OTHER INFORMATION: codons
;   NAME/KEY: CDS
;   LOCATION: (1)..(2346)
US-09-193-503B-5

  Query Match           10.0%;  Score 51.4;  DB 3;  Length 2346;
  Best Local Similarity   47.1%;  Pred. No. 0.004;
  Matches  157;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

Qy        156 CTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAG 215
              | ||   | |   |||  | ||   || || |||  |||||||  |  |||   ||
Db       1338 CCTCGAGGCCTCCCTCAAGAAGCTCATCCCCGCCTGGGAGTTCACCATCATCCCCTACTA 1397

Qy        216 CAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGCTG 275
              |   |||| ||        |  || |  |  ||     |   | | ||         |  |
Db       1398 CGGCCAGAAGCACCAGTCCGACATCACCGACATCGTGTCATCCCTCCAGCTTCAGTTCGA 1457

Qy        276 GGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAG 335
              |       | |   |  ||| ||| || |  | ||  | ||  |    |   |  ||
Db       1458 GTCCTCCGAGGAGGCTGACAAGGGCAACTCCCACTCCAAGAAGATGCTGAAGGCCCTCCT 1517

Qy        336 GTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCT 395
              | | ||| |    ||||   |||| |||||  ||||  || |  |  ||  |   ||
Db       1518 CTCCGAGGGCGAGTCCATCTGGGAGATCACCGAGAAGATCCTCAACTCCTTCGAGTACAC 1577

Qy        396 TCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCG 455
                | ||| ||  |||| | |   | |||   |||||  |  ||||    ||   |||
Db       1578 CTCCAGGTTCACTAAGACCAAGACCCTCTACCAGTTCCTCTTCCTCGCCACCTTCATCAA 1637

Qy        456 CTGGGGCGAGTTCGACTTTGACAGGATCTTTGA 488
              ||| |||  ||||        || || | | ||
Db       1638 CTGCGGCAGGTTCTCAGACATCAAGAACGTGGA 1670


RESULT 10
US-09-193-503B-8
; Sequence 8, Application US/09193503B
; Patent No. 6262341
; GENERAL INFORMATION:
;  APPLICANT:  Baszczynski, Christopher L.
;  APPLICANT:  Lyznik, Leszek A.
;  APPLICANT:  Gordon-Kamm, William J.
;  APPLICANT:  Guan, Xueni
;  APPLICANT:  Rao, Guru
;  APPLICANT:  Tagliani, Laura A.
;  TITLE OF INVENTION:  A No. 6262341el Method For The Integration Of Foreign DNA Into
;  TITLE OF INVENTION:  Eukaryotic Genomes
;  FILE REFERENCE:  5718-66 (amended listing)
;  CURRENT APPLICATION NUMBER: US/09/193,503B
;  CURRENT FILING DATE:  1998-11-17
;  PRIOR APPLICATION NUMBER:  60/099,435
;  PRIOR FILING DATE:  1998-09-08
;  PRIOR APPLICATION NUMBER:  60/056,627
;  PRIOR FILING DATE:  1997-11-18
;  PRIOR APPLICATION NUMBER:  60/065,613
;  PRIOR FILING DATE:  1997-11-18
;  NUMBER OF SEQ ID NOS:  11
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 2346
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Sequence
;   OTHER INFORMATION: encoding a FLPm:Cre polypeptide, FLP from
;   OTHER INFORMATION: Saccharomyces (maize preferred codons), and Cre
;   OTHER INFORMATION: from Bacteriophage P1
;   NAME/KEY: CDS
;   LOCATION: (1)..(2346)
US-09-193-503B-8

  Query Match           10.0%;  Score 51.4;  DB 3;  Length 2346;
  Best Local Similarity   47.1%;  Pred. No. 0.004;
  Matches  157;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

Qy        156 CTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAG 215
              | ||   | |   |||  | ||   || || |||  |||||||  |  |||   ||
Db        264 CCTCGAGGCCTCCCTCAAGAAGCTCATCCCCGCCTGGGAGTTCACCATCATCCCCTACTA 323

Qy        216 CAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGCTG 275
              |   |||| ||        |  || |  |  ||     |   | | ||         |  |
Db        324 CGGCCAGAAGCACCAGTCCGACATCACCGACATCGTGTCATCCCTCCAGCTTCAGTTCGA 383

Qy        276 GGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAG 335
              |       | |   |  ||| ||| || |  | ||  | ||  |    |   |  ||
Db        384 GTCCTCCGAGGAGGCTGACAAGGGCAACTCCCACTCCAAGAAGATGCTGAAGGCCCTCCT 443

Qy        336 GTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCT 395
              | | ||| |    ||||   |||| |||||  ||||  || |  |  ||  |   ||
Db        444 CTCCGAGGGCGAGTCCATCTGGGAGATCACCGAGAAGATCCTCAACTCCTTCGAGTACAC 503

Qy        396 TCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCG 455
                | ||| ||  |||| | |   | |||   |||||  |  ||||    ||   |||
Db        504 CTCCAGGTTCACTAAGACCAAGACCCTCTACCAGTTCCTCTTCCTCGCCACCTTCATCAA 563

Qy        456 CTGGGGCGAGTTCGACTTTGACAGGATCTTTGA 488
              ||| |||  ||||        || || | | ||
Db        564 CTGCGGCAGGTTCTCAGACATCAAGAACGTGGA 596


RESULT 11
US-09-415-839-4
; Sequence 4, Application US/09415839
; Patent No. 6541231
; GENERAL INFORMATION:
;  APPLICANT: Baszczynski, Christopher L.
;  APPLICANT:  Lyznik, Leszek A.
;  APPLICANT:  Gordon-Kamm, William J.
;  APPLICANT:  Guan, Xueni
;  APPLICANT:  Rao, Guru
;  APPLICANT:  Tagliani, Laura A.
;  TITLE OF INVENTION: A No. 6541231el Method For The Integration Of Foreign DNA
;  TITLE OF INVENTION:  Into
;  TITLE OF INVENTION:  Eukaryotic Genomes
;  FILE REFERENCE: 5718-66 (amended listing)
;  CURRENT APPLICATION NUMBER: US/09/415,839
;  CURRENT FILING DATE:  1999-10-12
;  PRIOR APPLICATION NUMBER: US/09/193,503
;  PRIOR FILING DATE: 1998-11-17
;  PRIOR APPLICATION NUMBER: 60/099,435
;  PRIOR FILING DATE: 1998-09-08
;  PRIOR APPLICATION NUMBER: 60/056,627
;  PRIOR FILING DATE: 1997-11-18
;  PRIOR APPLICATION NUMBER: 60/065,613
;  PRIOR FILING DATE: 1997-11-18
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 2346
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Nucleotide
;   OTHER INFORMATION: sequence encoding a Cre:FLPm  polypeptide, Cre
;   OTHER INFORMATION: from Bacteriophage P1 and FLP (Maize preferred
```

; OTHER INFORMATION: codons) from Saccharomyces
US-09-415-839-4

Query Match 10.0%; Score 51.4; DB 3; Length 2346;
Best Local Similarity 47.1%; Pred. No. 0.004;
Matches 157; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

```
Qy        156 CTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAG 215
              | ||   | |   |||  | ||   || || |||  |||||||  |  |||   ||
Db       1338 CCTCGAGGCCTCCCTCAAGAAGCTCATCCCCGCCTGGGAGTTCACCATCATCCCCTACTA 1397

Qy        216 CAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGCTG 275
              |   |||| ||       |  || |  |  ||   |  | | ||        |  |
Db       1398 CGGCCAGAAGCACCAGTCCGACATCACCGACATCGTGTCATCCCTCCAGCTTCAGTTCGA 1457

Qy        276 GGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAG 335
              |      | |   | ||| ||| || |  | ||  | ||  |    |   |  ||
Db       1458 GTCCTCCGAGGAGGCTGACAAGGGCAACTCCCACTCCAAGAAGATGCTGAAGGCCCTCCT 1517

Qy        336 GTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCT 395
              | | ||| |    ||||   |||| |||||  |||   || |  |  ||  |   ||
Db       1518 CTCCGAGGGCGAGTCCATCTGGGAGATCACCGAGAAGATCCTCAACTCCTTCGAGTACAC 1577

Qy        396 TCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCG 455
              | ||| ||  |||| | |   | |||   |||||  |  ||||    ||   |||
Db       1578 CTCCAGGTTCACTAAGACCAAGACCCTCTACCAGTTCCTCTTCCTCGCCACCTTCATCAA 1637

Qy        456 CTGGGGCGAGTTCGACTTTGACAGGATCTTTGA 488
              ||| |||  ||||        || || | | ||
Db       1638 CTGCGGCAGGTTCTCAGACATCAAGAACGTGGA 1670
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RESULT 12
US-09-415-839-5
; Sequence 5, Application US/09415839
; Patent No. 6541231
; GENERAL INFORMATION:
; APPLICANT: Baszczynski, Christopher L.
; APPLICANT: Lyznik, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Guan, Xueni
; APPLICANT: Rao, Guru
; APPLICANT: Tagliani, Laura A.
; TITLE OF INVENTION: A No. 6541231el Method For The Integration Of Foreign DNA
; TITLE OF INVENTION: Into
; TITLE OF INVENTION: Eukaryotic Genomes
; FILE REFERENCE: 5718-66 (amended listing)
; CURRENT APPLICATION NUMBER: US/09/415,839
; CURRENT FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: US/09/193,503
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence
; OTHER INFORMATION: encoding moCre:FLPm, Cre from Bacteriophage P1 and
; OTHER INFORMATION: FLP from Saccharomyces, both maize preferred
; OTHER INFORMATION: codons
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2346)
US-09-415-839-5

Query Match 10.0%; Score 51.4; DB 3; Length 2346;
Best Local Similarity 47.1%; Pred. No. 0.004;
Matches 157; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

```
Qy        156 CTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAG 215
              | ||   | |   |||  | ||   || || |||  |||||||  |  |||   ||
Db       1338 CCTCGAGGCCTCCCTCAAGAAGCTCATCCCCGCCTGGGAGTTCACCATCATCCCCTACTA 1397

Qy        216 CAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGCTG 275
              |   |||| ||       |  || |  |  ||   |  | | ||        |  |
Db       1398 CGGCCAGAAGCACCAGTCCGACATCACCGACATCGTGTCATCCCTCCAGCTTCAGTTCGA 1457

Qy        276 GGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAG 335
              |      | |   | ||| ||| || |  | ||  | ||  |    |   |  ||
Db       1458 GTCCTCCGAGGAGGCTGACAAGGGCAACTCCCACTCCAAGAAGATGCTGAAGGCCCTCCT 1517

Qy        336 GTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCT 395
              | | ||| |    ||||   |||| |||||  |||   || |  |  ||  |   ||
Db       1518 CTCCGAGGGCGAGTCCATCTGGGAGATCACCGAGAAGATCCTCAACTCCTTCGAGTACAC 1577

Qy        396 TCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCG 455
              | ||| ||  |||| | |   | |||   |||||  |  ||||    ||   |||
Db       1578 CTCCAGGTTCACTAAGACCAAGACCCTCTACCAGTTCCTCTTCCTCGCCACCTTCATCAA 1637

Qy        456 CTGGGGCGAGTTCGACTTTGACAGGATCTTTGA 488
              ||| |||  ||||        || || | | ||
Db       1638 CTGCGGCAGGTTCTCAGACATCAAGAACGTGGA 1670
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RESULT 13
US-09-415-839-8
; Sequence 8, Application US/09415839
; Patent No. 6541231
; GENERAL INFORMATION:
; APPLICANT: Baszczynski, Christopher L.
; APPLICANT: Lyznik, Leszek A.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Guan, Xueni
; APPLICANT: Rao, Guru
; APPLICANT: Tagliani, Laura A.
; TITLE OF INVENTION: A No. 6541231el Method For The Integration Of Foreign DNA
; TITLE OF INVENTION: Into
; TITLE OF INVENTION: Eukaryotic Genomes
; FILE REFERENCE: 5718-66 (amended listing)
; CURRENT APPLICATION NUMBER: US/09/415,839
; CURRENT FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: US/09/193,503
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/099,435
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/056,627
; PRIOR FILING DATE: 1997-11-18
; PRIOR APPLICATION NUMBER: 60/065,613
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence
; OTHER INFORMATION: encoding a FLPm:Cre polypeptide, FLP from
; OTHER INFORMATION: Saccharomyces (maize preferred codons), and Cre
; OTHER INFORMATION: from Bacteriophage P1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2346)
US-09-415-839-8

Query Match 10.0%; Score 51.4; DB 3; Length 2346;
Best Local Similarity 47.1%; Pred. No. 0.004;
Matches 157; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

```
Qy        156 CTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAG 215
              | ||   | |   |||  | ||   || || |||  |||||||  |  |||   ||
Db        264 CCTCGAGGCCTCCCTCAAGAAGCTCATCCCCGCCTGGGAGTTCACCATCATCCCCTACTA 323

Qy        216 CAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGCTG 275
              |   |||| ||       |  || |  |  ||    |  | | ||          |  |
Db        324 CGGCCAGAAGCACCAGTCCGACATCACCGACATCGTGTCATCCCTCCAGCTTCAGTTCGA 383

Qy        276 GGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAG 335
              |      | |   | ||| ||| || |  | ||  | ||  |    |   |  ||
Db        384 GTCCTCCGAGGAGGCTGACAAGGGCAACTCCCACTCCAAGAAGATGCTGAAGGCCCTCCT 443

Qy        336 GTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCT 395
              | | ||| |    ||||   |||| ||||  ||||  || |  |  ||  |   ||
Db        444 CTCCGAGGGCGAGTCCATCTGGGAGATCACCGAGAAGATCCTCAACTCCTTCGAGTACAC 503

Qy        396 TCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCG 455
              |·||| ||  |||| | |   | |||   |||||  |  ||||   ||   |||
Db        504 CTCCAGGTTCACTAAGACCAAGACCCTCTACCAGTTCCTCTTCCTCGCCACCTTCATCAA 563

Qy        456 CTGGGGCGAGTTCGACTTTGACAGGATCTTTGA 488
              ||| |||  ||||        || || | | ||
Db        564 CTGCGGCAGGTTCTCAGACATCAAGAACGTGGA 596
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RESULT 14
US-09-252-991A-13773/c
; Sequence 13773, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13773
; LENGTH: 4131
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13773

Query Match 10.0%; Score 51.4; DB 3; Length 4131;
Best Local Similarity 48.2%; Pred. No. 0.0044;
Matches 145; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

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Qy        211 TCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACG 270
              ||  || |  |  ||||| || | ||| |  | |  || ||||| ||| |||||||
Db        609 TCCGGCGACGACGTGCTGTCCGGCGCCAACGGCAGTTCGGAGCACATCAACGGCGGCGAC 550

Qy        271 CGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCAC 330
              || | ||   | | | | | |  |    |  ||   ||      |    ||  |    ||
Db        549 GGCAGCGACCTGATCTTCAACGTGGGCACCGGCGATCACGTGGTGGCCGGCAACGGCAAC 490

Qy        331 CAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCA 390
              | |    | ||  |||| | |   |    |||| |||  | |||  ||||   |  |
Db        489 GACACCATCCAGATCACCGCGACCGATTTCGTCAGCATCGATGGCGGCGCCGGGTTCGAC 430

Qy        391 AACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGAT 450
              | |||   |  |  |||    ||||||  || ||  ||   || |||| ||    |
Db        429 ACCCTGGTCCTGGCCAACGGCATCGACCTCGACTACAACGCCGTCGGCGTCGGCACGCTC 370

Qy        451 ATCCGCTGGGGCGAGTTCGACTTTGACAGGATCTTTGAGGACGGACGGGAGACCTTTGGC 510
              | |  |   |      ||||| | | || |  |      ||   |   | |||| |   |
Db        369 AGCAACCTCGAGCGCATCGACCTCGGCAAGGGCGACTCGGGTAGCGTGCTGACCCTGACC 310

Qy        511 G 511
              |
Db        309 G 309
```

RESULT 15
US-09-252-991A-13656
; Sequence 13656, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13656
; LENGTH: 8211
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13656

Query Match 10.0%; Score 51.4; DB 3; Length 8211;
Best Local Similarity 48.2%; Pred. No. 0.0051;
Matches 145; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

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Qy        211 TCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACG 270
              ||  || |  |  ||||| || | ||| |  | |  || ||||| ||| |||||||
Db       7717 TCCGGCGACGACGTGCTGTCCGGCGCCAACGGCAGTTCGGAGCACATCAACGGCGGCGAC 7776

Qy        271 CGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCAC 330
              || | ||   | | | | | |  |    |  ||   ||      |    ||  |    ||
Db       7777 GGCAGCGACCTGATCTTCAACGTGGGCACCGGCGATCACGTGGTGGCCGGCAACGGCAAC 7836

Qy        331 CAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCA 390
              | |    | ||  |||| | |   |    |||| |||  | |||  ||||   |  |
Db       7837 GACACCATCCAGATCACCGCGACCGATTTCGTCAGCATCGATGGCGGCGCCGGGTTCGAC 7896

Qy        391 AACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGAT 450
              | |||   |  |  |||    ||||||  || ||  ||   || |||| ||    |
Db       7897 ACCCTGGTCCTGGCCAACGGCATCGACCTCGACTACAACGCCGTCGGCGTCGGCACGCTC 7956

Qy        451 ATCCGCTGGGGCGAGTTCGACTTTGACAGGATCTTTGAGGACGGACGGGAGACCTTTGGC 510
              | |  |   |      ||||| | | || |  |      ||   |   | |||| |   |
Db       7957 AGCAACCTCGAGCGCATCGACCTCGGCAAGGGCGACTCGGGTAGCGTGCTGACCCTGACC 8016

Qy        511 G 511
              |
Db       8017 G 8017
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Search completed: December 4, 2006, 18:41:29
Job time : 142 secs

GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: December 4, 2006, 17:46:54 ; Search time 360 Seconds
(without alignments)
9993.556 Million cell updates/sec

Title: US-10-507-132-1
Perfect score: 516
Sequence: 1 atgggttcgcaagttcaaaa.....gggagacctttggcgacaaa 516

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	516	100.0	516	10	ADC16590	Adc16590 Scytalone
2	514.4	99.7	516	10	ADC16592	Adc16592 Scytalone
3	514.4	99.7	600	10	ADC16602	Adc16602 Scytalone
4	514.4	99.7	610	10	ADC16603	Adc16603 Scytalone
5	53.4	10.3	113193	8	AAD54645	Aad54645 Streptomy
6	53	10.3	7407	8	ACA42281	Aca42281 Prokaryot
7	53	10.3	7407	9	ACC59398	Acc59398 Microbial
8	52.4	10.2	4451	2	AAV23288	Aav23288 Synthetic
9	52	10.1	1336	13	ADX09839	Adx09839 Plant ful
10	52	10.1	1394	13	ADX54272	Adx54272 Plant ful
11	52	10.1	1437	13	ADX35034	Adx35034 Plant ful
12	52	10.1	1598	13	ADX54271	Adx54271 Plant ful
13	52	10.1	1821	2	AAQ99366	Aaq99366 S. livida
14	52	10.1	1821	2	AAV84068	Aav84068 Clone P5-
15	52	10.1	1821	3	AAC61406	Aac61406 cDNA enco
16	51.6	10.0	1395	11	ACL29101	Acl29101 Rice abio
17	51.4	10.0	1272	2	AAX61296	Aax61296 Yeast moF
18	51.4	10.0	2189	10	AAD63718	Aad63718 pPH12891
19	51.4	10.0	2346	4	AAD10219	Aad10219 Chimeric
20	51.4	10.0	2346	4	AAD10217	Aad10217 Chimeric
21	51.4	10.0	2346	4	AAD10216	Aad10216 Chimeric
22	51.4	10.0	2346	9	ACD26378	Acd26378 DNA encod
23	51.4	10.0	2346	9	ACD26379	Acd26379 DNA encod
24	51.4	10.0	2346	9	ACD26381	Acd26381 DNA encod
25	51.4	10.0	2346	10	AAD65095	Aad65095 Cre:FLPm
26	51.4	10.0	2346	10	AAD65097	Aad65097 FLPm:Cre
27	51.4	10.0	2346	10	AAD65094	Aad65094 Cre:FLPm
c 28	51.4	10.0	4131	11	ABD15169	Abd15169 Pseudomon
29	51.4	10.0	8211	11	ABD15052	Abd15052 Pseudomon
30	50.8	9.8	561	11	ABD14968	Abd14968 Pseudomon
31	50.6	9.8	1062	14	ACL71569	Acl71569 M. xanthu
32	50.6	9.8	6715	14	ACL64355	Acl64355 M. xanthu
33	50.4	9.8	1238	13	ADX31428	Adx31428 Plant ful
34	50.4	9.8	1349	13	ADX33784	Adx33784 Plant ful
35	50.4	9.8	1352	13	ADX10015	Adx10015 Plant ful
36	50.4	9.8	1511	13	ADX09781	Adx09781 Plant ful
37	50.2	9.7	1177	13	ADX34980	Adx34980 Plant ful
38	50	9.7	585	11	ACL34434	Acl34434 Rice abio
39	50	9.7	1821	3	AAC55846	Aac55846 Mitomycin
40	50	9.7	1821	10	ADE10327	Ade10327 S. lavend
41	50	9.7	18034	3	AAC55841	Aac55841 Complete
42	50	9.7	18034	10	ADE10260	Ade10260 S. lavend
43	49.8	9.7	1388	13	ADX09721	Adx09721 Plant ful
44	49.4	9.6	980	4	ABL11523	Abl11523 Drosophil
45	49.4	9.6	1572	12	ADM99120	Adm99120 Bacterial

ALIGNMENTS

RESULT 1
ADC16590
ID ADC16590 standard; DNA; 516 BP.
XX
AC ADC16590;
XX
DT 18-DEC-2003 (first entry)
XX
DE Scytalone dehydrogenase gene #SEQ ID 1.
XX
KW Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor;
KW gene; ds.
XX
OS Magnaporthe grisea.
XX
FH Key Location/Qualifiers
FT CDS 1. .516
FT /*tag= a
FT /product= "scytalone dehydrogenase"
FT /partial
FT /note= "no stop codon"
XX
PN WO2003076628-A1.
XX
PD 18-SEP-2003.
XX
PF 24-FEB-2003; 2003WO-JP001980.
XX
PR 12-MAR-2002; 2002JP-00066955.
XX
PA (TSUB) KUMIAI CHEM IND CO LTD.
XX
PI Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;
XX
DR WPI; 2003-748394/70.
DR P-PSDB; ADC16591.
XX
PT Gene encoding for scytalone dehydrogenase (SCDH), useful for screening
PT for SCDH inhibitors and evaluating sensitivity to them.
XX
PS Example 2; SEQ ID NO 1; 50pp; Japanese.

```
XX
CC   The invention relates to a gene encoding scytalone dehydrogenase (SCDH),
CC   that functions in the presence of an inhibitor, comprising an optionally
CC   mutated, defined amino acid sequence given in the specification. Also
CC   disclosed is a method for evaluating rice blast fungus (Pyricularia
CC   oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase
CC   inhibitors. The gene is useful for screening for new SCDH inhibitors and
CC   evaluating sensitivity to them. The current sequence represents the
CC   Scytalone dehydrogenase gene sequence.
XX
SQ   Sequence 516 BP; 119 A; 151 C; 155 G; 91 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 516;  DB 10;  Length 516;
  Best Local Similarity  100.0%;  Pred. No. 9.5e-108;
  Matches  516;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60

Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120

Qy        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180

Qy        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240

Qy        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300

Qy        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360

Qy        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420

Qy        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480

Qy        481 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516
              ||||||||||||||||||||||||||||||||||||
Db        481 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516


RESULT 2
ADC16592
ID   ADC16592 standard; DNA; 516 BP.
XX
AC   ADC16592;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Scytalone dehydrogenase gene #SEQ ID 3.
XX
KW   Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor;
KW   gene; ds.
XX
OS   Magnaporthe grisea.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .516
FT                   /*tag=  a
FT                   /product= "scytalone dehydrogenase"
FT                   /partial
FT                   /note= "no stop codon"
XX
PN   WO2003076628-A1.
XX
PD   18-SEP-2003.
XX
PF   24-FEB-2003; 2003WO-JP001980.
XX
PR   12-MAR-2002; 2002JP-00066955.
XX
PA   (TSUB ) KUMIAI CHEM IND CO LTD.
XX
PI   Kaku K,  Watanabe S,  Kawai K,  Shimizu T,  Nagayama K;
XX
DR   WPI; 2003-748394/70.
DR   P-PSDB; ADC16593.
XX
PT   Gene encoding for scytalone dehydrogenase (SCDH), useful for screening
PT   for SCDH inhibitors and evaluating sensitivity to them.
XX
PS   Example 2; SEQ ID NO 3; 50pp; Japanese.
XX
CC   The invention relates to a gene encoding scytalone dehydrogenase (SCDH),
CC   that functions in the presence of an inhibitor, comprising an optionally
CC   mutated, defined amino acid sequence given in the specification. Also
CC   disclosed is a method for evaluating rice blast fungus (Pyricularia
CC   oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase
CC   inhibitors. The gene is useful for screening for new SCDH inhibitors and
CC   evaluating sensitivity to them. The current sequence represents the
CC   Scytalone dehydrogenase gene sequence.
XX
SQ   Sequence 516 BP; 118 A; 151 C; 156 G; 91 T; 0 U; 0 Other;

  Query Match            99.7%;  Score 514.4;  DB 10;  Length 516;
  Best Local Similarity  99.8%;  Pred. No. 2.2e-107;
  Matches  515;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60

Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120

Qy        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180

Qy        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 240

Qy        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300

Qy        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360

Qy        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420

Qy        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480

Qy        481 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516
              ||||||||||||||||||||||||||||||||||||
Db        481 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516
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```
RESULT 3
ADC16602
ID   ADC16602 standard; DNA; 600 BP.
XX
AC   ADC16602;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Scytalone dehydrogenase DNA #1.
XX
KW   Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor;
KW   gene; ds.
XX
OS   Magnaporthe grisea.
XX
PN   WO2003076628-A1.
XX
PD   18-SEP-2003.
XX
PF   24-FEB-2003; 2003WO-JP001980.
XX
PR   12-MAR-2002; 2002JP-00066955.
XX
PA   (TSUB ) KUMIAI CHEM IND CO LTD.
XX
PI   Kaku K,  Watanabe S,  Kawai K,  Shimizu T,  Nagayama K;
XX
DR   WPI; 2003-748394/70.
XX
PT   Gene encoding for scytalone dehydrogenase (SCDH), useful for screening
PT   for SCDH inhibitors and evaluating sensitivity to them.
XX
PS   Example 2; Fig 3; 50pp; Japanese.
XX
CC   The invention relates to a gene encoding scytalone dehydrogenase (SCDH),
CC   that functions in the presence of an inhibitor, comprising an optionally
CC   mutated, defined amino acid sequence given in the specification. Also
CC   disclosed is a method for evaluating rice blast fungus (Pyricularia
CC   oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase
CC   inhibitors. The gene is useful for screening for new SCDH inhibitors and
CC   evaluating sensitivity to them. The current sequence represents the
CC   Scytalone dehydrogenase DNA sequence. Note: gene sequence from this is
CC   given in ADC16590.
XX
SQ   Sequence 600 BP; 146 A; 176 C; 168 G; 110 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 514.4;  DB 10;  Length 600;
  Best Local Similarity   99.8%;  Pred. No. 2.2e-107;
  Matches  515;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 140

Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 200

Qy        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 260

Qy        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        261 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 320

Qy        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 380

Qy        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 440

Qy        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 500

Qy        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 560

Qy        481 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516
              |||||||||||||||||||||||||||||||||||
Db        561 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 596


RESULT 4
ADC16603
ID   ADC16603 standard; DNA; 610 BP.
XX
AC   ADC16603;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Scytalone dehydrogenase DNA #2.
XX
KW   Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor;
KW   gene; ds.
XX
OS   Magnaporthe grisea.
XX
PN   WO2003076628-A1.
XX
PD   18-SEP-2003.
XX
PF   24-FEB-2003; 2003WO-JP001980.
XX
PR   12-MAR-2002; 2002JP-00066955.
XX
PA   (TSUB ) KUMIAI CHEM IND CO LTD.
XX
PI   Kaku K,  Watanabe S,  Kawai K,  Shimizu T,  Nagayama K;
XX
DR   WPI; 2003-748394/70.
XX
PT   Gene encoding for scytalone dehydrogenase (SCDH), useful for screening
PT   for SCDH inhibitors and evaluating sensitivity to them.
XX
PS   Example 2; Fig 4; 50pp; Japanese.
XX
CC   The invention relates to a gene encoding scytalone dehydrogenase (SCDH),
CC   that functions in the presence of an inhibitor, comprising an optionally
CC   mutated, defined amino acid sequence given in the specification. Also
CC   disclosed is a method for evaluating rice blast fungus (Pyricularia
CC   oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase
CC   inhibitors. The gene is useful for screening for new SCDH inhibitors and
CC   evaluating sensitivity to them. The current sequence represents the
CC   Scytalone dehydrogenase DNA sequence. Note: gene sequence from this is
CC   given in ADC16592.
XX
SQ   Sequence 610 BP; 148 A; 179 C; 170 G; 113 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 514.4;  DB 10;  Length 610;
  Best Local Similarity   99.8%;  Pred. No. 2.3e-107;
  Matches  515;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 140

Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 200
```

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Qy        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 260

Qy        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        261 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 320

Qy        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 380

Qy        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 440

Qy        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 500

Qy        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 560

Qy        481 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516
              ||||||||||||||||||||||||||||||||||||
Db        561 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 596
```

```
RESULT 5
AAD54645
ID   AAD54645 standard; DNA; 113193 BP.
XX
AC   AAD54645;
XX
DT   26-JUN-2003  (first entry)
XX
DE   Streptomyces nodosus amphotericin (amph) biosynthetic gene cluster.
XX
KW   Polyene; antibiotic; amphotericin; amph; polyketide; enzyme; gene; ds.
XX
OS   Streptomyces nodosus.
XX
FH   Key             Location/Qualifiers
FT   CDS             complement(4. .1824)
FT                   /*tag=  a
FT                   /product= "ABC transporter encoded by S. nodosus amphG
FT                   gene"
FT   CDS             complement(1805. .3628)
FT                   /*tag=  b
FT                   /product= "ABC transporter encoded by S. nodosus amphH
FT                   gene"
FT   CDS             3840. .4874
FT                   /*tag=  c
FT                   /product= "GDP-mannose dehydratase encoded by S. nodosus
FT                   amphDIII gene"
FT   CDS             5042. .33574
FT                   /*tag=  d
FT                   /product= "Polyketide synthase multienzyme housing
FT                   extension modules 9, 10, 11, 12, 13 and 14 encoded by S.
FT                   nodosus amphI gene"
FT   CDS             33584. .50518
FT                   /*tag=  e
FT                   /product= "Polyketide synthase multienzyme housing
FT                   extension modules 15, 16 and 17 encoded by S. nodosus
FT                   amphJ gene"
FT   CDS             50571. .56675
FT                   /*tag=  f
FT                   /product= "Polyketide synthase multienzyme housing
FT                   extension modules 18 and thioesterase encoded by S.
FT                   nodosus amphK gene"
FT   CDS             56829. .58019
FT                   /*tag=  g
FT                   /product= "Cytochrome P450 encoded by S. nodosus amphL
FT                   gene"
FT   CDS             58139. .58648
FT                   /*tag=  h
FT                   /product= "ORF1, hypothetical protein"
FT   CDS             complement(58756. .59610)
FT                   /*tag=  i
FT                   /product= "ORF2, hypothetical protein"
FT   CDS             59869. .61470
FT                   /*tag=  j
FT                   /product= "ORF3, hypothetical protein"
FT                   /transl_except= (pos:59869. .59871, aa:Met)
FT   CDS             complement(61798. .61995)
FT                   /*tag=  k
FT                   /product= "Ferredoxin encoded by S. nodosus amphM gene"
FT   CDS             complement(62051. .63250)
FT                   /*tag=  l
FT                   /product= "Cytochrome P450 encoded by S. nodosus amphN
FT                   gene"
FT   CDS             complement(63250. .64308)
FT                   /*tag=  m
FT                   /product= "NDP-sugar aminotransferase encoded by S.
FT                   nodosus amphDII gene"
FT   CDS             complement(64324. .65775)
FT                   /*tag=  n
FT                   /product= "Glycosyl transferase encoded by S. nodosus
FT                   amphDI gene"
FT                   /transl_except= (pos:65773. .65775, aa:Met)
FT   CDS             66081. .70319
FT                   /*tag=  o
FT                   /product= "Polyketide synthase multienzyme housing
FT                   loading module encoded by S. nodosus amphA gene"
FT   CDS             70366. .79938
FT                   /*tag=  p
FT                   /product= "Polyketide synthase multienzyme housing
FT                   extension modules 1 and 2 encoded by S. nodosus by amphB
FT                   gene"
FT   CDS             79956. .112709
FT                   /*tag=  q
FT                   /product= "Polyketide synthase multienzyme housing
FT                   extension modules 3, 4, 5, 6, 7 and 8 encoded by S.
FT                   nodosus by amphC gene"
XX
PN   WO200297082-A2.
XX
PD   05-DEC-2002.
XX
PF   27-MAY-2002; 2002WO-IE000071.
XX
PR   31-MAY-2001; 2001IE-00000527.
XX
PA   (UYDU-) UNIV COLLEGE DUBLIN.
XX
PI   Caffrey JP;
XX
DR   WPI; 2003-201271/19.
DR   P-PSDB; AAE36116, AAE36117, AAE36118, AAE36119, AAE36120, AAE36121,
DR   AAE36122, AAE36123, AAE36124, AAE36125, AAE36126, AAE36127, AAE36128,
DR   AAE36129, AAE36130, AAE36131, AAE36132.
XX
PT   Novel cytochrome P450 enzyme and nucleotides encoding the enzyme, useful
PT   for preparing amphotericin derivative or analog antibiotic agent with
PT   altered properties, in biosynthesis of polyketide other than
PT   amphotericin.
XX
PS   Claim 1; Page 52-114; 276pp; English.
XX
CC   The invention relates to the gene cluster encoding the polypeptides
CC   responsible for the biosynthesis of the polyene antibiotic amphotericin
CC   (amph) of Streptomyces nodosus. Polynucleotides of the invention are
CC   useful for preparing amphotericin derivatives or analogue antibiotic
CC   agents with altered properties and in the biosynthesis of polyketides
CC   other than amphotericin. amphDIII, amphDII or amphDI mutants are useful
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CC   for producing amphotericin derivatives glycosylated with alternative
CC   sugars; amphDIII or amphDII gene sequences are useful in engineered
CC   biosynthesis of perosaminyl-amphoteronolide B; amphDIII or amphDII and
CC   amphN gene sequences are useful in the engineered biosynthesis of
CC   perosaminyl-16-descarboxyl-16-methyl amphoteronolide B; amphDIII, amphDII
CC   and amphDI gene sequences are useful for preparing polypeptides capable
CC   of addition of mycosamine to a polyketide other than amphoteronolide A or
CC   B or for preparing polypeptides for in vitro synthesis of GDP-mycosamine.
CC   The present sequence is S. nodosus amph biosynthetic gene cluster
XX
SQ   Sequence 113193 BP; 14248 A; 45141 C; 38354 G; 15450 T; 0 U; 0 Other;

  Query Match            10.3%;  Score 53.4;  DB 8;  Length 113193;
  Best Local Similarity   47.5%;  Pred. No. 0.031;
  Matches  159;  Conservative    0;  Mismatches  176;  Indels    0;  Gaps    0;

Qy        136 CTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAG 195
              ||   ||  ||  ||||  ||||| ||||      ||   |  | |||  |||  |
Db      72859 CTCGACACCGAGCACCGTGCCTTCATCGAGGTCAGCTCCCACCCGGTGCTCGCCATGTCC 72918

Qy        196 TTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCAC 255
              ||   | |||| ||       |       || | ||||   || ||  |  |  ||  |
Db      72919 GTCCAGGACATGATCGACGACGCCGGAGTGGTCGGCGTGGCCTCCGGCACCCTGCGCCGT 72978

Qy        256 TTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAG 315
              || |||||||     | |       | ||||||  | | ||||  |||    |  |
Db      72979 GACAACGGCGGCCTCGACCGCTTCCTGCTGTCCGCCGCCCAGGTGTTCGTGCGCGGCGTC 73038

Qy        316 CTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGC 375
              | |  || |  |  || |  || | ||| ||||  |  ||     ||||  | ||     |
Db      73039 CAGGTCGACTGGGCCCCGCTGTTCGAGGGCACCGGCGCGACCCGGGTCGACCTGCCCACC 73098

Qy        376 CACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCC 435
              |||||  |  |    | |  ||||| || |       || ||  | | |   |  | ||
Db      73099 TACGCCTTCCAGCACGAGCGGTACTGGAACGACCGTGCCGTCGTGGACCGTTCGGCCTCC 73158

Qy        436 GGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGA 470
              |  |  | |  ||       |||||  |   ||||
Db      73159 GCGCCGATGGACGCCGAGTTCTGGGCGGCCGTCGA 73193


RESULT 6
ACA42281
ID   ACA42281 standard; DNA; 7407 BP.
XX
AC   ACA42281;
XX
DT   19-JUN-2003  (first entry)
XX
DE   Prokaryotic essential gene #23938.
XX
KW   Antisense; ds; prokaryotic essential gene; cell proliferation;
KW   drug design; gene.
XX
OS   Pseudomonas aeruginosa.
XX
PN   WO200277183-A2.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2002; 2002WO-US009107.
XX
PR   21-MAR-2001; 2001US-00815242.
PR   06-SEP-2001; 2001US-00948993.
PR   25-OCT-2001; 2001US-0342923P.
PR   08-FEB-2002; 2002US-00072851.
PR   06-MAR-2002; 2002US-0362699P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Wang L,  Zamudio C,  Malone C,  Haselbeck R,  Ohlsen KL,  Zyskind JW;
PI   Wall D,  Trawick JD,  Carr GJ,  Yamamoto R,  Forsyth RA,  Xu HH;
XX
DR   WPI; 2003-029926/02.
DR   P-PSDB; ABU38411.
XX
PT   New antisense nucleic acids, useful for identifying proteins or screening
PT   for homologous nucleic acids required for cellular proliferation to
PT   isolate candidate molecules for rational drug discovery programs.
XX
PS   Claim 14; SEQ ID NO 30151; 1766pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising any one of
CC   the 6213 antisense sequences given in the specification where expression
CC   of the nucleic acid inhibits proliferation of a cell. Also included are:
CC   (1) a vector comprising a promoter operably linked to the nucleic acid
CC   encoding a polypeptide whose expression is inhibited by the antisense
CC   nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC   polypeptide or its fragment whose expression is inhibited by the
CC   antisense nucleic acid; (4) an antibody capable of specifically binding
CC   the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC   proliferation or the activity of a gene in an operon required for
CC   proliferation; (7) identifying a compound that influences the activity of
CC   the gene product or that has an activity against a biological pathway
CC   required for proliferation, or that inhibits cellular proliferation; (8)
CC   identifying a gene required for cellular proliferation or the biological
CC   pathway in which a proliferation-required gene or its gene product lies
CC   or a gene on which the test compound that inhibits proliferation of an
CC   organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC   compound's activity; (11) a culture comprising strains in which the gene
CC   product is overexpressed or underexpressed; (12) determining the extent
CC   to which each of the strains is present in a culture or collection of
CC   strains; or (13) identifying the target of a compound that inhibits the
CC   proliferation of an organism. The antisense nucleic acids are useful for
CC   identifying proteins or screening for homologous nucleic acids required
CC   for cellular proliferation to isolate candidate molecules for rational
CC   drug discovery programs, or for screening homologous nucleic acids
CC   required for proliferation in cells other than S. aureus, S. typhimurium,
CC   K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC   prokaryotic essential genes. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 7407 BP; 1387 A; 2763 C; 2378 G; 879 T; 0 U; 0 Other;

  Query Match            10.3%;  Score 53;  DB 8;  Length 7407;
  Best Local Similarity   48.5%;  Pred. No. 0.026;
  Matches  146;  Conservative    0;  Mismatches  155;  Indels    0;  Gaps    0;

Qy      .  211 TCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACG 270
              ||  || |  |  |||||  || | ||| |  | |  || ||||| ||| |||||||
Db       6913 TCCGGCGACGACGTGCTGTCCGGCGCCAACGGCAGTTCGGAGCACATCAACGGCGGCGAC 6972

Qy        271 CGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCAC 330
              || | ||   | | | | | |  |     |  ||   ||      |    ||  |    ||
Db       6973 GGCAGCGACCTGATCTTCAACGTGGGCACCGGCGATCACGTGGTGGCCGGCAACGGCAAC 7032

Qy        331 CAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCA 390
              | |     | ||  |||| | |    |     |||| |||  | |||  ||||    |  |
Db       7033 GACACCATCCAGATCACCGCGACCGATTTCGTCAGCATCGATGGCGGCGCCGGGTTCGAC 7092

Qy        391 AACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGAT 450
              | |||    |  |  |||     ||||||  || ||  ||    || |||| ||     |
Db       7093 ACCCTGGTCCTGGCCAACGGCATCGACCTCGACTACAACGCCGTCGGCGTCGGCACGCTC 7152

Qy        451 ATCCGCTGGGGCGAGTTCGACTTTGACAGGATCTTTGAGGACGGACGGGAGACCTTTGGC 510
              | |  |    |       |||||  | | || |  |  |  ||   |    |  |||| |   |
Db       7153 AGCAACCTCGAGCGCATCGACCTCGGCAAGGGCGATTCGGGTAGCGTGCTGACCCTGACC 7212

Qy        511 G 511
              |
Db       7213 G 7213


RESULT 7
```

ACC59398
ID ACC59398 standard; DNA; 7407 BP.
XX
AC ACC59398;
XX
DT 28-AUG-2003 (first entry)
XX
DE Microbial resistance gene PA1874 coding sequence.
XX
KW Biofilm; microbial resistance; gene; ds.
XX
OS Unidentified.
XX
PN WO2003041483-A2.
XX
PD 22-MAY-2003.
XX
PF 18-SEP-2002; 2002WO-US029565.
XX
PR 18-SEP-2001; 2001US-0323241P.
XX
PA (DART-) DARTMOUTH COLLEGE.
XX
PI O'toole GA, Mah T;
XX
DR WPI; 2003-468567/44.
DR P-PSDB; ABP59933.
XX
PT Identifying modulators of microbial resistance of organisms in biofilms,
PT e.g. inhibitor of biofilm formation, by employing expression controls, or
PT efflux pumps containing polypeptides, of genes associated with biofilm
PT resistance.
XX
PS Disclosure; Fig 7; 102pp; English.
XX
CC The present invention relates to a method of identifying a compound
CC capable of altering the sensitivity of a microorganism to an
CC antimicrobial agent by employing efflux pumps comprising polypeptides
CC encoded by the following genes: PA1874, PA4142, PA2389, PA1876, PA4143,
CC PA2390 or PA1163. The method is useful for identifying modulators of
CC microbial resistance of an organism in a biofilm. The methods are also
CC useful for identifying genes that encode proteins that play a role in
CC biofilm resistance. The method is particularly useful for screening
CC compounds or discovering compositions that will inhibit biofilm formation
CC and overcome their resistance mechanisms. These methods are particularly
CC useful in medical, industrial or natural settings, where formation of
CC biofilms can have serious negative consequences and result in high costs
CC both in human health and economic terms. The present sequence is a
CC coding/control sequence shown in the exemplification of the invention
XX
SQ Sequence 7407 BP; 1387 A; 2763 C; 2378 G; 879 T; 0 U; 0 Other;

Query Match 10.3%; Score 53; DB 9; Length 7407;
Best Local Similarity 48.5%; Pred. No. 0.026;
Matches 146; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

Qy 211 TCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACG 270
Db 6913 TCCGGCGACGACGTGCTGTCCGGCGCCAACGGCAGTTCGGAGCACATCAACGGCGGCGAC 6972

Qy 271 CGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCAC 330
Db 6973 GGCAGCGACCTGATCTTCAACGTGGGCACCGGCGATCACGTGGTGGCCGGCAACGGCAAC 7032

Qy 331 CAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCA 390
Db 7033 GACACCATCCAGATCACCGCGACCGATTTCGTCAGCATCGATGGCGGCGCCGGGTTCGAC 7092

Qy 391 AACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGAT 450
Db 7093 ACCCTGGTCCTGGCCAACGGCATCGACCTCGACTACAACGCCGTCGGCGTCGGCACGCTC 7152

Qy 451 ATCCGCTGGGGCGAGTTCGACTTTGACAGGATCTTTGAGGACGGACGGGAGACCTTTGGC 510

Db 7153 AGCAACCTCGAGCGCATCGACCTCGGCAAGGGCGATTCGGGTAGCGTGCTGACCCTGACC 7212

Qy 511 G 511
Db 7213 G 7213

RESULT 8
AAV23288
ID AAV23288 standard; DNA; 4451 BP.
XX
AC AAV23288;
XX
DT 17-AUG-1998 (first entry)
XX
DE Synthetic human Factor-VIII gene lacking central B domain.
XX
KW Factor-VIII; blood clotting; human; synthetic gene; codon usage; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9812207-A1.
XX
PD 26-MAR-1998.
XX
PF 18-SEP-1997; 97WO-US016639.
XX
PR 20-SEP-1996; 96US-00717294.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Seed B, Haas J;
XX
DR WPI; 1998-217200/19.
XX
PT New synthetic eukaryotic gene(s) - in which non-preferred or less
PT preferred codon(s) are replaced to provide high level expression in
PT mammalian cell(s).
XX
PS Claim 20; Fig 13; 92pp; English.
XX
CC This synthetic gene codes for a human Factor-VIII protein that lacks the
CC central B domain (amino acids 760-1639) of the native protein. In the
CC synthetic gene, non-preferred or less preferred codons of the native gene
CC (see AAV23339) are replaced by codons favored by highly expressed human
CC genes to provide high-level expression in mammalian cells. The synthetic
CC gene was assembled from 29 pairs of oligonucleotides (see AAV23340-97)
CC which served as PCR templates. Synthetic genes of the invention (see also
CC AAV23289-91) are used for production of recombinant proteins in mammalian
CC cells at levels of at least 500% of those obtained using the natural
CC genes. They can also be used in gene therapy. An expression vector
CC comprising a synthetic gene and a mammalian cell harboring a synthetic
CC gene are also claimed
XX
SQ Sequence 4451 BP; 972 A; 1568 C; 1234 G; 677 T; 0 U; 0 Other;

Query Match 10.2%; Score 52.4; DB 2; Length 4451;
Best Local Similarity 52.8%; Pred. No. 0.033;
Matches 113; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Qy 230 GCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCG 289
Db 2323 GCCACCCCAGCACGCGTCAGAAGCAGTTCAACGCCACCCCCCCCGTGCTGAAGCGCCACC 2382

Qy 290 AGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCA 349
Db 2383 AGCGCGAGATCACCCGCACCACCCTGCAAAGCGACCAGGAGGAGATCGACTACGACGACA 2442

Qy 350 CCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGA 409
Db 2443 CCATCAGCGTGGAGATGAAGAAGGAGGACTTCGACATCTACGACGAGGACGAGAACCAGA 2502

```
Qy        410 AGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAA 443
              |  |  | ||   |||    || ||| | |
Db       2503 GCCCCCGCTCCTTCCAAAAGAAAACCCGCCACTA 2536
```

RESULT 9
ADX09839
ID ADX09839 standard; cDNA; 1336 BP.
XX
AC ADX09839;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 4414.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
DR WPI; 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 4414; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX

SQ Sequence 1336 BP; 331 A; 405 C; 358 G; 242 T; 0 U; 0 Other;

  Query Match   10.1%; Score 52; DB 13; Length 1336;
  Best Local Similarity 47.1%; Pred. No. 0.034;
  Matches 160; Conservative   0; Mismatches 180; Indels   0; Gaps   0;

```
Qy        133 ACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAG 192
              | ||| ||| | ||  |||    | ||  || ||||          |    || || |
Db        372 ATTCTACGCGTGGATAACCTGGTCATCACCGGCAAGGGAAACCTTGACGGGCAGGGCCCA 431

Qy        193 GAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAG 252
              |   |     ||| |  |||  |||   ||| |   | |  |   | ||| | ||    |
Db        432 GCCGTGTGGAGCAAGAACTCCTGCACCAAGAAGTACGACTGCAAGATCCTTCCCAACTCG 491

Qy        253 CACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCAC 312
              |   | || | |  |  |  |   | | ||||||||| || |  | |  ||  || | |
Db        492 CTGGTGATGGACTTCGTGAACAACGGGGAGGTGTCCGGGGTCACGCTGCTCAACTCCAAG 551

Qy        313 CAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAG 372
              | | | |         |  ||| ||||||||     || ||||| || ||| ||| |
Db        552 TTCTTCCACATGAACATGTACCGGTGCAAGGACATGCTGATCAAGGACGTGACCGTGACG 611

Qy        373 GGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTC 432
              | | ||   ||    | |||    |  |   | | | |  ||||     | |||    |
Db        612 GCGCCCGGGGACAGCCCCAACACGGATGGCATCCACATGGGCGACTCATCCGGGATCACC 671

Qy        433 GCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACT 472
              |  | ||    |  |  |  | | | ||| | |  ||
Db        672 ATCACCAACACCGTCATTGGCGTCGGCGACGACTGCATCT 711
```

RESULT 10
ADX54272
ID ADX54272 standard; cDNA; 1394 BP.
XX
AC ADX54272;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 29012.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
DR WPI; 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to

PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 29012; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 1394 BP; 349 A; 418 C; 365 G; 262 T; 0 U; 0 Other;

Query Match 10.1%; Score 52; DB 13; Length 1394;
Best Local Similarity 47.1%; Pred. No. 0.034;
Matches 160; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

Qy 133 ACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAG 192
Db 361 ATTCTACGCGTGGATAACCTGGTCATCACCGGCAAGGGAAACCTTGACGGGCAGGGCCCA 420

Qy 193 GAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAG 252
Db 421 GCTGTGTGGAGCAAGAACTCCTGCACCAAGAAGTACGACTGCAAGATCCTTCCCAACTCG 480

Qy 253 CACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCAC 312
Db 481 CTGGTGATGGACTTCGTGAACAACGGGGAGGTGTCCGGGGTCACGCTGCTCAACTCCAAG 540

Qy 313 CAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAG 372
Db 541 TTCTTCCACATGAACATGTACCGGTGCAAGGACATGCTGATCAAGGACGTGACCGTGACG 600

Qy 373 GGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTC 432
Db 601 GCGCCCGGGGACAGCCCCAACACGGATGGCATCCACATGGGCGACTCATCCGGGATCACC 660

Qy 433 GCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACT 472
Db 661 ATCACCAACACCGTCATTGGCGTCGGCGACGACTGCATCT 700

RESULT 11
ADX35034
ID ADX35034 standard; cDNA; 1437 BP.
XX
AC ADX35034;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 17854.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
DR WPI; 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 17854; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 1437 BP; 364 A; 426 C; 375 G; 272 T; 0 U; 0 Other;

Query Match 10.1%; Score 52; DB 13; Length 1437;
Best Local Similarity 47.1%; Pred. No. 0.035;
Matches 160; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

Qy 133 ACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAG 192
Db 379 ATTCTACGCGTGGATAACCTGGTCATCACCGGCAAGGGAAACCTTGACGGGCAGGGCCCA 438

Qy 193 GAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAG 252
Db 439 GCCGTGTGGAGCAAGAACTCCTGCACCAAGAAGTACGACTGCAAGATCCTTCCCAACTCG 498

Qy 253 CACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCAC 312
Db 499 CTGGTGATGGACTTCGTGAACAACGGGGAGGTGTCCGGGGTCACGCTGCTCAACTCCAAG 558

Qy 313 CAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAG 372
Db 559 TTCTTCCACATGAACATGTACCGGTGCAAGGACATGCTGATCAAGGACGTGACCGTGACG 618

Qy 373 GGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTC 432

```
Db        619 GCGCCCGGGGACAGCCCCAACACGGATGGCATCCACATGGGCGACTCATCCGGGATCACC 678

Qy        433 GCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACT 472
              |  |  ||    |  |  |  | | | ||| | |  ||
Db        679 ATCACCAACACCGTCATTGGCGTCGGCGACGACTGCATCT 718
```

RESULT 12
ADX54271
ID ADX54271 standard; cDNA; 1598 BP.
XX
AC ADX54271;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 29011.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
DR WPI; 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 29011; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 1598 BP; 408 A; 453 C; 400 G; 337 T; 0 U; 0 Other;

  Query Match   10.1%; Score 52; DB 13; Length 1598;
  Best Local Similarity   47.1%; Pred. No. 0.035;
  Matches 160; Conservative   0; Mismatches 180; Indels   0; Gaps   0;

```
Qy        133 ACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAG 192
              | ||| ||| | ||  |||    | ||  || ||||         |    || || |
Db        395 ATTCTACGCGTGGATAACCTGGTCATCACCGGCAAGGGAAACCTTGACGGGCAGGGCCCA 454

Qy        193 GAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAG 252
              |    |      ||| |  |||  |||   ||| |   | |  |   | ||| | ||    |
Db        455 GCTGTGTGGAGCAAGAACTCCTGCACCAAGAAGTACGACTGCAAGATCCTTCCCAACTCG 514

Qy        253 CACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCAC 312
              |   | || | |  |  |  |  | | |||||||||| || |  | |  ||  || | |
Db        515 CTGGTGATGGACTTCGTGAACAACGGGGAGGTGTCCGGGGTCACGCTGCTCAACTCCAAG 574

Qy        313 CAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAG 372
              | | | |        |  ||| ||||||||     || ||||| || ||| ||| | |
Db        575 TTCTTCCACATGAACATGTACCGGTGCAAGGACATGCTGATCAAGGACGTGACCGTGACG 634

Qy        373 GGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTC 432
              | | ||   ||    | |||    |  |   | | | |  ||||     | |||    |
Db        635 GCGCCCGGGGACAGCCCCAACACGGATGGCATCCACATGGGCGACTCATCCGGGATCACC 694

Qy        433 GCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACT 472
              |  |  ||    |  |  |  | | | ||| | |  ||
Db        695 ATCACCAACACCGTCATTGGCGTCGGCGACGACTGCATCT 734
```

RESULT 13
AAQ99366
ID AAQ99366 standard; DNA; 1821 BP.
XX
AC AAQ99366;
XX
DT 25-MAR-2003 (revised)
DT 04-DEC-1995 (first entry)
XX
DE S. lividans protease P5-6 gene.
XX
KW Protease; metalloendoproteinase; tripeptidyl aminopeptidase;
KW protease-deficiency; protein secretion; ds.
XX
OS Streptomyces lividans.
XX
FH Key   Location/Qualifiers
FT CDS   104. .1723
FT   /*tag= a
FT sig_peptide   104. .244
FT   /*tag= b
FT mat_peptide   245. .1720
FT   /*tag= c
FT   /product= "P5-6."
XX
PN WO9517512-A2.
XX
PD 29-JUN-1995.
XX
PF 22-DEC-1994; 94WO-US014772.
XX
PR 23-DEC-1993; 93US-00173508.
XX
PA (CANG-) CANGENE CORP.
XX
PI Bartfeld D, Butler MJ, Hadary D, Jenish DL, Krieger TJ, Malek LT;
PI Walcyzk E, Soostmeyer G;
XX
DR WPI; 1995-240673/31.
DR P-PSDB; AAR80506.

```
XX
PT   Endogenous Streptomyces protease(s), opt. having impaired activity -
PT   useful in prodn. of exogenous proteins with reduced proteolytic
PT   degradation.
XX
PS   Claim 7; Fig 14; 142pp; English.
XX
CC   Protease Tap-negative cells were transformed with a S. lividans 66
CC   genomic library and screened with APA-beta-naphthylamide to isolate
CC   colonies contg. genes (AAQ99365-68) for novel proteases P5-4, P5-6, P5-10
CC   and P8-2 (AAR80505-08). Impaired expression of such proteases by
CC   Streptomyces hosts improves the quality, quantity and stability of
CC   exogenous gene products. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 1821 BP; 283 A; 715 C; 602 G; 221 T; 0 U; 0 Other;

  Query Match             10.1%;  Score 52;  DB 2;  Length 1821;
  Best Local Similarity   49.3%;  Pred. No. 0.036;
  Matches  136;  Conservative    0;  Mismatches  140;  Indels    0;  Gaps    0;

Qy        148 TACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATG 207
              ||| || ||||||| | |  |  ||  |  |   ||     ||||    |   | | || ||
Db        848 TACGGCACCTTCCTGGGCGCGACCTACGCCGGTCTGTTCCCCGACCGGACGGGCCGCCTG 907

Qy        208 GTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGC 267
              |||  |  |      ||||      |   |   ||  ||||   | | || |
Db        908 GTCCTGGACGGCGCGATGGACCCCTCGCTGCCCGCCCGCCGCCTGAACCTGGAGCAGACG 967

Qy        268 ACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCG 327
                | |||  |||| || || | ||  |   |  |  | || |     ||| ||  | |
Db        968 GAGGGCTTCGAGACGGCGTTCCAGTCCTTCGCGAAGGACTGCGTGAAGCAGCCGGACTGC 1027

Qy        328 CACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCG 387
              | ||   |  ||||||||||||||    |  |||||  || |||   | |  ||  ||
Db       1028 CCCCTCGGCGACAAGGACACCACCCCCGACCAGGTCGGCAAGAACCTCAAGTCCTTCTTC 1087

Qy        388 GCAAACCTTCACTGGTACAAGAAGATCGACGGCGTC 423
              |   ||||  ||  | |      |  || ||||| |
Db       1088 GACGACCTGGACGCGAAGCCCCTGCCCGCCGGCGAC 1123


RESULT 14
AAV84068
ID   AAV84068 standard; DNA; 1821 BP.
XX
AC   AAV84068;
XX
DT   19-MAR-1999  (first entry)
XX
DE   Clone P5-6 encoding an aminopeptidase designated SlpD.
XX
KW   Tripeptidyl aminopeptidase; TAP; N-terminal cleavage; protein production;
KW   GM-CSF; interleukin-3; IL-3; IL-6; EPO; tumour necrosis factor; TNF; SCF;
KW   IL-7; IL-2; P5-6; SlpD; ds.
XX
OS   Streptomyces lividans.
XX
FH   Key             Location/Qualifiers
FT   CDS             104. .1723
FT                   /*tag=  a
FT                   /product= "protease"
FT   sig_peptide     104. .244
FT                   /*tag=  b
FT   mat_peptide     245. .1720
FT                   /*tag=  c
XX
PN   US5856166-A.
XX
PD   05-JAN-1999.
XX
PF   24-JUN-1994;   94US-00265310.
XX
PR   23-DEC-1993;   93US-00173508.
XX
PA   (CANG-) CANGENE CORP.
XX
PI   Bartfeld D,  Malek LT,  Jenish DL,  Walczyk E,  Hadary D,  Garven S;
PI   Soostmeyer G,  Butler MJ,  Krygsman P,  Krieger TJ;
XX
DR   WPI; 1999-105117/09.
DR   P-PSDB; AAW87799.
XX
PT   Streptomyces tri:peptidyl aminopeptidase - useful for removing N-terminal
PT   pro-peptide from secreted proteins.
XX
PS   Example 25; Fig 25A-C; 83pp; English.
XX
CC   The present sequence encodes an aminopeptidase designated SlpD. The
CC   specification also describes a tripeptidyl aminopeptidase (TAP) of
CC   Streptomyces. The aminopeptidase is endogenous to Streptomyces and
CC   cleaves an N-terminal sequence of X-Pro-Y, where X is an aliphatic or
CC   hydroxy amino acid and Y is an aliphatic, hydroxy or sulphur-containing
CC   amino acid. The TAP of Streptomyces are useful in the production of
CC   proteins, such as GM-CSF, interleukin-3 (IL-3), IL-6, EPO, tumour
CC   necrosis factor (TNF) SCF, IL-7 and IL-2
XX
SQ   Sequence 1821 BP; 283 A; 715 C; 602 G; 221 T; 0 U; 0 Other;

  Query Match             10.1%;  Score 52;  DB 2;  Length 1821;
  Best Local Similarity   49.3%;  Pred. No. 0.036;
  Matches  136;  Conservative    0;  Mismatches  140;  Indels    0;  Gaps    0;

Qy        148 TACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATG 207
              ||| || ||||||| | |  |  ||  |  |   ||     ||||    |   | | || ||
Db        848 TACGGCACCTTCCTGGGCGCGACCTACGCCGGTCTGTTCCCCGACCGGACGGGCCGCCTG 907

Qy        208 GTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGC 267
              |||  |  |      ||||      |   |   ||  ||||   | | || |
Db        908 GTCCTGGACGGCGCGATGGACCCCTCGCTGCCCGCCCGCCGCCTGAACCTGGAGCAGACG 967

Qy        268 ACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCG 327
                | |||  |||| || || | ||  |   |  |  | || |     ||| ||  | |
Db        968 GAGGGCTTCGAGACGGCGTTCCAGTCCTTCGCGAAGGACTGCGTGAAGCAGCCGGACTGC 1027

Qy        328 CACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCG 387
              | ||   |  ||||||||||||||    |  |||||  || |||   | |  ||  ||
Db       1028 CCCCTCGGCGACAAGGACACCACCCCCGACCAGGTCGGCAAGAACCTCAAGTCCTTCTTC 1087

Qy        388 GCAAACCTTCACTGGTACAAGAAGATCGACGGCGTC 423
              |   ||||  ||  | |      |  || ||||| |
Db       1088 GACGACCTGGACGCGAAGCCCCTGCCCGCCGGCGAC 1123


RESULT 15
AAC61406
ID   AAC61406 standard; cDNA; 1821 BP.
XX
AC   AAC61406;
XX
DT   19-FEB-2001  (first entry)
XX
DE   cDNA encoding a subtilisin-like polypeptide (Ssp) desiganted P5-6.
XX
KW   Subtilisin-like polypeptide; protein production; GM-CSF;
KW   chloromethylketone aminopeptidase inhibitor; stem cell factor;
KW   granulocyte macrophage-colony stimulating factor; interleukin-3; IL-3;
KW   IL-6; erythropoietin; EPO; SCF; IL-7; IL-2; ds.
XX
OS   Streptomyces lividans.
XX
FH   Key             Location/Qualifiers
FT   CDS             104. .1723
FT                   /*tag=  a
FT                   /product= "subtilisin-like polypeptide"
FT   sig_peptide     104. .244
FT                   /*tag=  b
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FT   mat_peptide     245. .1720
FT                   /*tag=  c
XX
PN   US6127144-A.
XX
PD   03-OCT-2000.
XX
PF   16-OCT-1997;   97US-00951742.
XX
PR   23-DEC-1993;   93US-00173508.
PR   24-JUN-1994;   94US-00265310.
XX
PA   (CANG-) CANGENE CORP.
XX
PI   Bartfeld D,  Butler MJ,  Hadary D,  Krieger TJ,  Malek LT;
PI   Soostmeyer G,  Krygsman P,  Garven S,  Walczyk E,  Jenish DL;
XX
DR   WPI; 2000-655618/63.
DR   P-PSDB; AAB19231.
XX
PT   Producing a heterologous protein such as interleukins or growth factors
PT   involves incubating a transformed Streptomyces host cell in the presence
PT   of peptide-substituted chloromethylketone aminopeptidase inhibitor.
XX
PS   Example 21; Fig 25A-C; 87pp; English.
XX
CC   The present sequence encodes a subtilisin-like polypeptide (Ssp). The
CC   polypeptide is a protease, and was used to identify inhibitors, which
CC   were then used in the method of the invention. The specification
CC   describes a method for producing a heterologous protein. The method
CC   involves incubating a Streptomyces host cell transformed nucleic acid
CC   sequence encoding the heterologous protein, in the presence of a peptide-
CC   substituted chloromethylketone aminopeptidase inhibitor. The inhibitor
CC   has the structure X-proline-Y-chlromethylketone, where X is an aliphatic
CC   or hydroxy amino acid and Y is an aliphatic hydroxy or sulphur-containing
CC   amino acid. Alternately, X and Y are non-polar amino acids. Use of the
CC   inhibitor inhibits degradation of the heterologous protein by
CC   aminopeptidases. The method is useful for producing granulocyte
CC   macrophage-colony stimulating factor (GM-CSF), interleukin-3 (IL-3), IL-
CC   6, erythropoietin (EPO), stem cell factor (SCF), IL-7, and IL-2 which are
CC   secreted from the host cell
XX
SQ   Sequence 1821 BP; 283 A; 715 C; 602 G; 221 T; 0 U; 0 Other;

  Query Match             10.1%;  Score 52;  DB 3;  Length 1821;
  Best Local Similarity   49.3%;  Pred. No. 0.036;
  Matches  136;  Conservative    0;  Mismatches  140;  Indels    0;  Gaps    0;

Qy        148 TACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATG 207
              ||| || ||||||| | |  |  ||  |  |   ||    ||||   |   | | || ||
Db        848 TACGGCACCTTCCTGGGCGCGACCTACGCCGGTCTGTTCCCCGACCGGACGGGCCGCCTG 907

Qy        208 GTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGC 267
              |||  |  |     ||||     |   |   ||  ||||   | | || |
Db        908 GTCCTGGACGGCGCGATGGACCCCTCGCTGCCCGCCCGCCGCCTGAACCTGGAGCAGACG 967

Qy        268 ACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCG 327
                | |||  |||| || || | ||  |   |  | | || |    ||| ||  | |
Db        968 GAGGGCTTCGAGACGGCGTTCCAGTCCTTCGCGAAGGACTGCGTGAAGCAGCCGGACTGC 1027

Qy        328 CACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCG 387
              | ||   |  ||||||||||||||    |  |||||  || |||   | |  ||  ||
Db       1028 CCCCTCGGCGACAAGGACACCACCCCCGACCAGGTCGGCAAGAACCTCAAGTCCTTCTTC 1087

Qy        388 GCAAACCTTCACTGGTACAAGAAGATCGACGGCGTC 423
              |   ||||  ||  | |      |  || ||||| |
Db       1088 GACGACCTGGACGCGAAGCCCCTGCCCGCCGGCGAC 1123


Search completed: December  4, 2006, 17:53:08
Job time : 363 secs
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GenCore version 5.1.9

OM nucleic - nucleic search, using sw model

Run on: December 4, 2006, 17:53:24 ; Search time 2492 Seconds
(without alignments)
13241.119 Million cell updates/sec

Title: US-10-507-132-1
Perfect score: 516
Sequence: 1 atgggttcgcaagttcaaaa.....gggagacctttggcgacaaa 516

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	514.4	99.7	807	4	AB004741	AB004741 Magnaport
2	251.2	48.7	770	4	AB100172	AB100172 Bipolaris
3	234.8	45.5	1151	4	COGSCD1	D86079 Colletotric
4	219	42.4	1477	4	AF316575	AF316575 Ophiostom
5	192	37.2	415	4	AY098662	AY098662 Ophiostom
6	191.8	37.2	1215	4	AY214004	AY214004 Ceratocys
7	190	36.8	414	4	AY098664	AY098664 Ophiostom
8	189.4	36.7	414	4	AY098663	AY098663 Ophiostom
9	187.8	36.4	433	4	AY098658	AY098658 Ophiostom
10	185.6	36.0	427	4	AY098656	AY098656 Ophiostom
11	182.6	35.4	424	4	AY098657	AY098657 Ophiostom
12	182.4	35.3	428	4	AY098659	AY098659 Ophiostom
13	179.2	34.7	421	4	AY098661	AY098661 Ophiostom
14	179.2	34.7	423	4	AY098660	AY098660 Ophiostom
15	179.2	34.7	423	4	AY098666	AY098666 Ophiostom
16	171.8	33.3	422	4	AY098665	AY098665 Ophiostom
17	167.8	32.5	573	4	SMA575152	AJ575152 Sordaria
18	162.4	31.5	1447	4	AFU95042	U95042 Aspergillus
19	160	31.0	433	4	AY098655	AY098655 Ceratocys
20	155.8	30.2	432	4	AY098654	AY098654 Ceratocys
21	58.6	11.4	110000	15	BA000030_74	Continuation (75 o
22	55.2	10.7	110000	15	AP006840_16	Continuation (17 o
c 23	54.4	10.5	110000	15	CR555306_37	Continuation (38 o
24	53.6	10.4	110000	15	CP000251_10	Continuation (11 o
25	53.4	10.3	110000	4	AP008209_139	Continuation (140
26	53.4	10.3	113193	2	AX703543	AX703543 Sequence
27	53.4	10.3	113193	15	AF357202	AF357202 Streptomy
c 28	53.4	10.3	161676	4	AC135907	AC135907 Genomic s
c 29	53.4	10.3	295150	15	SCO939126	AL939126 Streptomy
30	53	10.3	20342	15	AE004613	AE004613 Pseudomon
31	52.4	10.2	4451	2	AR110041	AR110041 Sequence
32	52.4	10.2	4451	2	BD008905	BD008905 High leve
33	52.2	10.1	110000	15	AE016825_06	Continuation (7 of
34	52.2	10.1	110000	15	AP006618_19	Continuation (20 o
35	52	10.1	1233	4	ZMPGAL17	X62385 Z.mays gene
36	52	10.1	1562	4	ZMPGAL2	X57628 Z.mays mRNA
37	52	10.1	1820	2	I38962	I38962 Sequence 7
38	52	10.1	1820	15	STMSLPD	L42758 Streptomyce
39	52	10.1	1821	2	AR027260	AR027260 Sequence
40	52	10.1	1821	2	AR111405	AR111405 Sequence
c 41	52	10.1	293050	15	SCO939116	AL939116 Streptomy
42	51.8	10.0	1144	15	AB014943	AB014943 Rubrobact
43	51.6	10.0	3067	4	AK068793	AK068793 Oryza sat
c 44	51.6	10.0	66135	15	AP006840_35	Continuation (36 o
45	51.6	10.0	110000	4	AP008210_260	Continuation (261

ALIGNMENTS

RESULT 1
AB004741
LOCUS AB004741 807 bp mRNA linear PLN 13-NOV-1998
DEFINITION Magnaporthe grisea mRNA for scytalone dehydratase, complete cds.
ACCESSION AB004741
VERSION AB004741.1 GI:3798733
KEYWORDS scytalone dehydratase; sdh1.
SOURCE Magnaporthe grisea
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE 1 (sites)
AUTHORS Motoyama,T., Imanishi,K. and Yamaguchi,I.
TITLE cDNA cloning, expression, and mutagenesis of scytalone dehydratase needed for pathogenicity of the rice blast fungus, Pyricularia oryzae
JOURNAL Biosci. Biotechnol. Biochem. 62 (3), 564-566 (1998)
PUBMED 9571787
REFERENCE 2 (bases 1 to 807)
AUTHORS Motoyama,T.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-1997) Takayuki Motoyama, The Institute of Physical and Chemical Research (RIKEN), Miclobial Toxicology Lab.; 2-1 Hirosawa, Wako-shi, Saitama 351-0198, Japan
(E-mail:tmotoyam@postman.riken.go.jp, Tel:+81-48-467-9518)
COMMENT Sequence updated (27-Oct-1998).
FEATURES Location/Qualifiers
source 1. .807
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/db_xref="taxon:148305"
/note="sequence obtained from anamorph Pyricularia oryzae whose telemorphic form is unknown"
gene 1. .807
/gene="Sdh1"
CDS 81. .599
/gene="Sdh1"
/codon_start=1
/product="scytalone dehydratase"
/protein_id="BAA34046.1"
/db_xref="GI:3798734"

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                     TLRIDYRSFLDKLWEAMPAEEFVGMVSSKQVLGDPTLRTQHFIGGTRWEKVSEDEVIG
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                     IFEDGRETFGDK"
ORIGIN

  Query Match             99.7%;  Score 514.4;  DB 4;  Length 807;
  Best Local Similarity   99.8%;  Pred. No. 2.2e-118;
  Matches  515;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 140

Qy         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 200

Qy        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 260

Qy        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCCACC 320

Qy        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 380

Qy        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 440

Qy        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 500

Qy        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 560

Qy        481 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516
              ||||||||||||||||||||||||||||||||||||
Db        561 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 596


RESULT 2
AB100172
LOCUS       AB100172                 770 bp    DNA     linear   PLN 01-APR-2004
DEFINITION  Bipolaris oryzae BSCD1gene for scytalone dehydratase, complete cds.
ACCESSION   AB100172
VERSION     AB100172.1  GI:32879676
KEYWORDS    .
SOURCE      Bipolaris oryzae
  ORGANISM  Bipolaris oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
            Pleosporales; Pleosporaceae; mitosporic Cochliobolus; Bipolaris.
REFERENCE   1
  AUTHORS   Kihara,J., Moriwaki,A., Ueno,M., Tokunaga,T., Arase,S. and Honda,Y.
  TITLE     Cloning, functional analysis and expression of a scytalone
            dehydratase gene (SCD1) involved in melanin biosynthesis of the
            phytopathogenic fungus Bipolaris oryzae
  JOURNAL   Curr. Genet. 45 (4), 197-204 (2004)
    PUBMED  14716498
REFERENCE   2  (bases 1 to 770)
  AUTHORS   Kihara,J. and Moriwaki,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JAN-2003) Junichi Kihara, Shimane University, Faculty
            of Life and Environmental Science; Nishikawatsu 1060, Matsue,
            Shimane 690-8504, Japan (E-mail:j-kihara@life.shimane-u.ac.jp,
            Tel:81-852-32-6520, Fax:81-852-32-6597)
FEATURES             Location/Qualifiers
     source          1. .770
                     /organism="Bipolaris oryzae"
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                     /db_xref="taxon:33195"
     gene            join(34. .70,125. .645)
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                     AEGREQLGEAKAAAGIPETAPGQAV"
ORIGIN

  Query Match             48.7%;  Score 251.2;  DB 4;  Length 770;
  Best Local Similarity   70.8%;  Pred. No. 3.1e-52;
  Matches  334;  Conservative    0;  Mismatches  138;  Indels    0;  Gaps    0;

Qy         41 CAGACTACCTGGGCCTCATGACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGG 100
              ||||  | |||||     |     ||| || ||||||||||||||||||  |||||
Db        122 CAGAGGTCATGGGCTGTCAATCGGCATGCTACGAATGGGCAGACAGCTACGACAGCAAGG 181

Qy        101 ACTGGGATAGGCTGCGAAAGGTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCC 160
              |||||||  | |||||  |||  | | || || ||||||   ||||||||||| ||||||
Db        182 ACTGGGAGCGTCTGCGCAAGTGCGTCGCTCCGACTCTGAAGATTGACTACCGGTCCTTCT 241

Qy        161 TCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGC 220
              | ||||||  | ||||||||  |||||  || ||  |||||  ||  |  |||||  |||    |
Db        242 TGGACAAGATATGGGAGGCGATGCCAGCGGATGAGTTTGTGGCCATGGCCTCTGACCCTG 301

Qy        221 AGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGA 280
              | ||||  |||  |||||   ||||    ||  ||||||||||||||||||  ||  ||  |||||||
Db        302 CGGTGCTCGGCAACCCCCTCCTCAAGACACAGCACTTCATCGGCGGAACACGGTGGGAGA 361

Qy        281 AGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACA 340
              ||  | |||||||  |||  | |  ||  |||||||||||||||  ||  ||  ||||||  | ||||
Db        362 AGACGGCCGAGGATGAGATTACGGGATACCACCAGCTGCGAGTGCCTCACCAGCGATACA 421

Qy        341 AGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACT 400
              |||      |   |  |  |||  |  | ||||||||||||||||      |||   ||||
Db        422 CGGATGAGTCACGGGCGACGGTGGCAGTCAAGGGCCACGCCCACAGCTTCAACACGCACT 481

Qy        401 GGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGG 460
              |||||||  |||||  |||||||  ||||||||  |||||  || || || || ||  | |||
Db        482 GGTACAAAAAGATTGACGGCGAGTGGAAGTTTGCCGGGCTGAACCCGGACATTAGGTGGT 541

Qy        461 GCGAGTTCGACTTTGACAGGATCTTTGAGGACGGACGGGAGACCTTTGGCGA 512
              |||||  ||||||||||  | |  ||||  || || || |||     | |||||
Db        542 ACGAGTATGACTTTGACAAGGTGTTTGCAGAGGGCCGCGAGCAGCTGGGCGA 593


RESULT 3
COGSCD1
LOCUS       COGSCD1                  1151 bp    DNA     linear   PLN 25-DEC-2002
DEFINITION  Colletotrichum lagenarium DNA for scytalone dehydratase, complete
            cds.
ACCESSION   D86079
VERSION     D86079.1  GI:1395159
KEYWORDS    melanin biosynthesis; scytalone dehydratase.
SOURCE      Colletotrichum lagenarium
  ORGANISM  Colletotrichum lagenarium
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
            mitosporic Phyllachoraceae; Colletotrichum.
REFERENCE   1
  AUTHORS   Kubo,Y., Takano,Y., Endo,N., Yasuda,N., Tajima,S. and Furusawa,I.
  TITLE     Cloning and structural analysis of the melanin biosynthesis gene
            SCD1 encoding scytalone dehydratase in Colletotrichum lagenarium
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  JOURNAL   Appl. Environ. Microbiol. 62 (12), 4340-4344 (1996)
   PUBMED   8953707
REFERENCE   2  (bases 1 to 1151)
  AUTHORS   Kubo,Y., Takano,Y., Noriko,E., Yasuda,N., Tajima,S. and Furusawa,I.
  TITLE     Cloning and structural analysis of the melanin biosynthesis gene
            encoding scytalone dehydratase of Colletotrichum lagenarium
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1151)
  AUTHORS   Kubo,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-JUN-1996) Yasuyuki Kubo, Laboratory of Plant
            Pathology, Faculty of Agriculture, Kyoto Prefectural University;
            Shimogamo, Kyoto, Kyoto 606, Japan (E-mail:y_kubo@kpu.ac.jp,
            Tel:075-702-0957, Fax:075-702-0957)
FEATURES             Location/Qualifiers
     source          1. .1151
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                     /mol_type="genomic DNA"
                     /isolate="104-T"
                     /db_xref="taxon:5462"
     TATA_signal     117. .121
     gene            join(233. .266,324. .421,489. .923)
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     CDS             join(233. .266,324. .421,489. .923)
                     /gene="SCD1"
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     intron          267. .323
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     exon            324. .421
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     intron          422. .488
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ORIGIN

  Query Match             45.5%;  Score 234.8;  DB 4;  Length 1151;
  Best Local Similarity   76.7%;  Pred. No. 4.2e-48;
  Matches  287;  Conservative    0;  Mismatches   87;  Indels    0;  Gaps    0;

Qy        142 ATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTC 201
              || |||||||||||||||||||||||| |||||||||| ||||| |||||||||||| ||
Db        489 ATCGACTACCGCTCCTTCCTCGACAAGATCTGGGAGGCCATGCCCGCCGAGGAGTTCATC 548

Qy        202 GGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATC 261
              | |||| |||||  ||||    | || ||| ||||   ||||   ||||||||||||||
Db        549 GCCATGATCTCGGACAAGTCCGTCCTCGGCAACCCGCTCCTCAAGACGCAGCACTTCATC 608

Qy        262 GGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGC 321
              |||||| | |||||||| ||||| || ||    |||||||||||| ||||||||||||||
Db        609 GGCGGCTCCCGCTGGGAAAAGGTCTCGGACACGGAGGTCATCGGCCACCACCAGCTGCGC 668

Qy        322 GTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCC 381
              || |||||||| | |||||  ||| || |    |  |||||| || | ||||||||||||
Db        669 GTGCCGCACCAAAAGTACACCGACGCCTCGCGCACCGAGGTCGCCGTCAAGGGCCACGCC 728

Qy        382 CACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTC 441
              |||      ||| | |||||||||   ||| || ||||||| ||||||||||||| ||
Db        729 CACAGCTACAACATGCACTGGTACCGCAAGGTCAACGGCGTGTGGAAGTTCGCCGGTCTG 788

Qy        442 AAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGGATCTTTGAGGACGGACGGGAG 501
              || ||||| ||||| ||| ||||| |||||||||||    |||| |  ||||| || ||
Db        789 AACCCCGAGATCCGGTGGTCCGAGTACGACTTTGACGCCGTCTTCGCCGACGGCCGCGAC 848

Qy        502 ACCTTTGGCGACAA 515
              | |  |||  | |
Db        849 TCGTACGGCACCGA 862


RESULT 4
AF316575
LOCUS       AF316575               1477 bp    DNA     linear   PLN 22-MAY-2002
DEFINITION  Ophiostoma floccosum strain 387N scytalone dehydratase (OSD1) gene,
            complete cds.
ACCESSION   AF316575
VERSION     AF316575.1  GI:12964737
KEYWORDS    .
SOURCE      Ophiostoma floccosum
  ORGANISM  Ophiostoma floccosum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE   1  (bases 1 to 1477)
  AUTHORS   Wang,H.L., Kim,S.H. and Breuil,C.
  TITLE     A scytalone dehydratase gene from Ophiostoma floccosum restores the
            melanization and pathogenicity phenotypes of a melanin-deficient
            Colletotrichum lagenarium mutant
  JOURNAL   Mol. Genet. Genomics 266 (1), 126-132 (2001)
   PUBMED   11589570
REFERENCE   2  (bases 1 to 1477)
  AUTHORS   Wang,H. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-OCT-2000) Wood Science, University of British
            Columbia, 2424 Main Mall, Vancouver, BC V6T 1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .1477
                     /organism="Ophiostoma floccosum"
                     /mol_type="genomic DNA"
                     /strain="387N"
                     /db_xref="taxon:104300"
     gene            <316. .>1105
                     /gene="OSD1"
     mRNA            join(<316. .394,471. .571,635. .>1105)
                     /gene="OSD1"
                     /product="scytalone dehydratase"
     CDS             join(316. .394,471. .571,635. .1105)
                     /gene="OSD1"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAK11296.1"
                     /db_xref="GI:12964738"
                     /translation="MGLNISSLTSTTSSAPKTTGSDISFEDYMGLCSAAYEWADSYDS
                     KDWDRLRKCIAPTLRIDYRSFLNKLWEAMPAEEFIGMISDPSVLGNPLLRTQHFFGAS
                     RWERISDTEVVGYHQLRVPHQVYTDTTLTQVAVKGHAHSANTHWYRKVDGVWKFAGLD
                     PKIRWFEYDFDKVFASGRDQFGTEEKAAATAGPELLAKDKVQSAIASAQRAVAVSA"
ORIGIN

  Query Match             42.4%;  Score 219;  DB 4;  Length 1477;
  Best Local Similarity   74.4%;  Pred. No. 4e-44;
  Matches  276;  Conservative    0;  Mismatches   95;  Indels    0;  Gaps    0;

Qy        145 GACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGC 204
              |||||||||| |||||  ||||||| |||||||| |||||||||| |||||  |||||
Db        635 GACTACCGCTCGTTCCTGAACAAGCTGTGGGAGGCCATGCCGGCCGAAGAGTTTATCGGC 694

Qy        205 ATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGC 264
              ||| ||||   |       | || ||| |||||   || ||||| || |||||| |||||
Db        695 ATGATCTCCGACCCCAGCGTTCTCGGCAACCCCCTGCTGCGCACACAACACTTCTTCGGC 754

Qy        265 GGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTC 324
              | | ||||||||||||    | |||||   ||||||| | |||||||| ||||||||||||
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Db        755 GCCTCGCGCTGGGAGCGCATCTCCGACACCGAGGTCGTGGGCTACCATCAGCTGCGCGTC 814

Qy        325 CCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCAC 384
              || ||||||   ||||  || |||||  | |   | ||  || | ||||||||||||||||
Db        815 CCCCACCAGGTCTACACAGATACCACTCTCACACAAGTTGCCGTCAAGGGCCACGCCCAC 874

Qy        385 TCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAG 444
              |||||  |||   |||||||||   ||| ||||||||||||||||||| ||||||||| |
Db        875 TCGGCCAACACCCACTGGTACCGCAAGGTCGACGGCGTCTGGAAGTTTGCCGGCCTCGAT 934

Qy        445 CCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGGATCTTTGAGGACGGACGGGAGACC 504
              ||| | |||||||||  ||| | ||| |||||  | | | ||||     ||| || ||
Db        935 CCCAAGATCCGCTGGTTCGAATACGATTTTGATAAGGTGTTTGCCAGCGGCCGCGACCAG 994

Qy        505 TTTGGCGACAA 515
              ||||||  | |
Db        995 TTTGGCACCGA 1005


RESULT 5
AY098662
LOCUS       AY098662                415 bp    DNA     linear   PLN 16-JAN-2003
DEFINITION  Ophiostoma piliferum isolate Cartapip scytalone dehydratase (SD)
            gene, partial cds.
ACCESSION   AY098662
VERSION     AY098662.1  GI:21238833
KEYWORDS    .
SOURCE      Ophiostoma piliferum
  ORGANISM  Ophiostoma piliferum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Inhibitors and genetic analysis of scytalone dehydratase confirm
            the presence of DHN-melanin pathway in sapstain fungi
  JOURNAL   Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE   2  (bases 1 to 415)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2002) Wood Science, University of British
            Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .415
                     /organism="Ophiostoma piliferum"
                     /mol_type="genomic DNA"
                     /isolate="Cartapip"
                     /db_xref="taxon:38032"
                     /country="USA"
     gene            <1. .>415
                     /gene="SD"
     mRNA            join(<1. .69,120. .>415)
                     /gene="SD"
                     /product="scytalone dehydratase"
     CDS             join(<1. .69,120. .>415)
                     /gene="SD"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAM34808.1"
                     /db_xref="GI:21238834"
                     /translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIG
                     MISDPSVLGNPLLRTQHFFGASRWERISDTEVVGHHQLRVPHQVYTDATLTQVAVKGH
                     AHSANTHWYRKVDGVWKFAG"
ORIGIN

  Query Match             37.2%;  Score 192;  DB 4;  Length 415;
  Best Local Similarity   78.0%;  Pred. No. 2.2e-37;
  Matches  231;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy        142 ATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTC 201
              || |||||||||||| |||||| |||||||||||||||| |||||||||| |||||| ||
Db        120 ATCGACTACCGCTCGTTCCTCAACAAGCTCTGGGAGGCCATGCCGGCCGACGAGTTCATC 179

Qy        202 GGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATC 261
              |||||| ||||           |||| ||| | ||    || ||||| ||||||||| ||
Db        180 GGCATGATCTCCGATCCCAGCGTGCTCGGCAATCCGCTGCTGCGCACCCAGCACTTCTTC 239

Qy        262 GGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGC 321
              |||| | ||||||||||||    | |||||   ||||||| ||||| ||||||||||||||
Db        240 GGCGCCTCGCGCTGGGAGCGCATCTCCGACACCGAGGTCGTCGGCCACCACCAGCTGCGC 299

Qy        322 GTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCC 381
              ||||| ||||||   ||||  ||  ||||| | |    ||||| || | ||||||||||||
Db        300 GTCCCCCACCAGGTCTACACCGATGCCACCCTCACACAGGTCGCCGTCAAGGGCCACGCC 359

Qy        382 CACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGG 437
              |||||||| |||   |||||||||   ||| ||||||||||||||||||| |||||
Db        360 CACTCGGCCAACACCCACTGGTACCGCAAGGTCGACGGCGTCTGGAAGTTTGCCGG 415


RESULT 6
AY214004
LOCUS       AY214004                1215 bp    DNA     linear   PLN 10-MAR-2004
DEFINITION  Ceratocystis resinifera syctalone dehydratase I (SD1) gene,
            complete cds.
ACCESSION   AY214004
VERSION     AY214004.1  GI:37787189
KEYWORDS    .
SOURCE      Ceratocystis resinifera
  ORGANISM  Ceratocystis resinifera
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Microascales; Microascales incertae sedis;
            Ceratocystis.
REFERENCE   1  (bases 1 to 1215)
  AUTHORS   Loppnau,P.A.
  TITLE     Canadian Populations and Melanin Biosynthesis Genes of Ceratocystis
            resinifera
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1215)
  AUTHORS   Loppnau,P.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JAN-2003) Wood Science, University of British
            Columbia, 4041-2424 Main Mall, Vancouver, BC V6T 1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .1215
                     /organism="Ceratocystis resinifera"
                     /mol_type="genomic DNA"
                     /isolate="EL3-21"
                     /specific_host="Pinus contorta"
                     /db_xref="taxon:95837"
                     /country="Canada: Alberta, Edson"
     gene            <233. .>934
                     /gene="SD1"
     mRNA            join(<233. .305,379. .476,545. .>934)
                     /gene="SD1"
                     /product="syctalone dehydratase I"
     CDS             join(233. .305,379. .476,545. .934)
                     /gene="SD1"
                     /codon_start=1
                     /product="syctalone dehydratase I"
                     /protein_id="AAO60167.1"
                     /db_xref="GI:37787190"
                     /translation="MVAGSSDSTQVTASTVNPKTISFEDYCGLNTALYEWADSYDSKD
                     WDRLRRTIAPTLRIDYRSFLDKLWEAMPAEDFIKMISDPNVLGDPLLKTQHFVGASRW
                     ERVSDDEVVGWHQLRVPHQRYTDATKTTVKVKGHAHSANKHWYKKVDGVWKFAGLYPE
                     IRWSEYDFDKVFASGREEFGDEDIDV"
     exon            233. .305
                     /gene="SD1"
                     /number=1
     exon            379. .476
                     /gene="SD1"
                     /number=2
     exon            545. .934
                     /gene="SD1"
                     /number=3
ORIGIN
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  Query Match           37.2%;  Score 191.8;  DB 4;  Length 1215;
  Best Local Similarity  69.8%;  Pred. No. 2.7e-37;
  Matches  259;  Conservative    0;  Mismatches  112;  Indels    0;  Gaps    0;

Qy        142 ATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTC 201
              || |||||||||||| ||||| || ||||| ||||| |||||||| |||||||| ||  |
Db        545 ATCGACTACCGCTCGTTCCTGGATAAGCTATGGGAAGCAATGCCTGCCGAGGACTTTATT 604

Qy        202 GGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATC 261
              |||  ||||   |    |  | || ||||||||    ||     || |||||||| ||
Db        605 AAGATGATCTCCGACCCCAACGTTCTCGGCGACCCTCTACTAAAGACCCAGCACTTCGTC 664

Qy        262 GGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGC 321
              ||||   ||||||||||    ||    || || || ||| | ||||  |||||||| ||
Db        665 GGCGCTTCGCGCTGGGAGCGTGTTAGTGACGATGAAGTCGTTGGCTGGCACCAGCTACGT 724

Qy        322 GTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCC 381
              || || |||||| | ||||  ||  | || | ||     ||||   | || |||||||||
Db        725 GTGCCCCACCAGCGCTACACTGATGCTACGAAGACCACCGTCAAGGTCAAAGGCCACGCC 784

Qy        382 CACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTC 441
              |||||  || |||   |||||||||||||| | || ||||| ||||| || ||||| |||
Db        785 CACTCAGCCAACAAGCACTGGTACAAGAAGGTAGATGGCGTGTGGAAATTTGCCGGTCTC 844

Qy        442 AAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGGATCTTTGAGGACGGACGGGAG 501
              | || || |||||||||    |||| ||| || |||| | | ||||    ||| || ||
Db        845 TATCCGGAGATCCGCTGGTCAGAGTACGATTTCGACAAGGTGTTTGCTAGCGGCCGTGAA 904

Qy        502 ACCTTTGGCGA 512
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Db        905 GAGTTTGGTGA 915
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RESULT 7
AY098664
LOCUS       AY098664                414 bp    DNA     linear   PLN 16-JAN-2003
DEFINITION  Ophiostoma piliferum isolate 201-1A scytalone dehydratase (SD)
            gene, partial cds.
ACCESSION   AY098664
VERSION     AY098664.1  GI:21238837
KEYWORDS    .
SOURCE      Ophiostoma piliferum
  ORGANISM  Ophiostoma piliferum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE   1  (bases 1 to 414)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Inhibitors and genetic analysis of scytalone dehydratase confirm
            the presence of DHN-melanin pathway in sapstain fungi
  JOURNAL   Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE   2  (bases 1 to 414)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2002) Wood Science, University of British
            Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .414
                     /organism="Ophiostoma piliferum"
                     /mol_type="genomic DNA"
                     /isolate="201-1A"
                     /db_xref="taxon:38032"
                     /country="Austria"
     gene            <1. .>414
                     /gene="SD"
     mRNA            join(<1. .69,120. .>414)
                     /gene="SD"
                     /product="scytalone dehydratase"
     CDS             join(<1. .69,120. .>414)
                     /gene="SD"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAM34810.1"
                     /db_xref="GI:21238838"
                     /translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSPLNKLWEAMPADEFIG
                     MISDPSVLGNPLLRTQHFFGASRWERISDTEVVGHHQLRVPHQVYTDATLSQVAVKGH
                     AHSANTHWYRKVDGVWKFA"
ORIGIN
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  Query Match           36.8%;  Score 190;  DB 4;  Length 414;
  Best Local Similarity  75.8%;  Pred. No. 7e-37;
  Matches  235;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;

Qy        127 GCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCG 186
              ||  ||   |  |  || |||||||||||| |||||| ||||||| ||||||| ||||||
Db        105 GCTGCTGACCGACAGATCGACTACCGCTCGTTCCTCAACAAGCTGTGGGAGGCCATGCCG 164

Qy        187 GCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGC 246
              ||||| |||||| |||||||| ||||   |      |||| ||| ||||    || |||
Db        165 GCCGACGAGTTCATCGGCATGATCTCCGACCCCAGCGTGCTCGGCAACCCGCTGCTGCGC 224

Qy        247 ACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGC 306
              || ||||||||| |||||| | ||||||||||    | |||||   ||||||| |||||
Db        225 ACCCAGCACTTCTTCGGCGCCTCGCGCTGGGAGCGCATCTCCGACACCGAGGTCGTCGGC 284

Qy        307 TACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACC 366
              |||||||||||||||||| ||||||   ||||  ||  | ||| |     ||||| ||
Db        285 CACCACCAGCTGCGCGTCCCCCACCAGGTCTACACCGATGCAACCCTCTCACAGGTCGCC 344

Qy        367 ATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGG 426
              | |||||||||||||||||| |||   |||||||||   ||| ||||||||||||||
Db        345 GTCAAGGGCCACGCCCACTCGGCCAACACCCACTGGTACCGCAAGGTCGACGGCGTCTGG 404

Qy        427 AAGTTCGCCG 436
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Db        405 AAGTTTGCCG 414
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RESULT 8
AY098663
LOCUS       AY098663                414 bp    DNA     linear   PLN 16-JAN-2003
DEFINITION  Ophiostoma piliferum isolate 198-2GF scytalone dehydratase (SD)
            gene, partial cds.
ACCESSION   AY098663
VERSION     AY098663.1  GI:21238835
KEYWORDS    .
SOURCE      Ophiostoma piliferum
  ORGANISM  Ophiostoma piliferum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE   1  (bases 1 to 414)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Inhibitors and genetic analysis of scytalone dehydratase confirm
            the presence of DHN-melanin pathway in sapstain fungi
  JOURNAL   Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE   2  (bases 1 to 414)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2002) Wood Science, University of British
            Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .414
                     /organism="Ophiostoma piliferum"
                     /mol_type="genomic DNA"
                     /isolate="198-2GF"
                     /db_xref="taxon:38032"
                     /country="United Kingdom"
     gene            <1. .>414
                     /gene="SD"
     mRNA            join(<1. .69,119. .>414)
                     /gene="SD"
                     /product="scytalone dehydratase"
     CDS             join(<1. .69,119. .>414)
                     /gene="SD"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAM34809.1"
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                     /db_xref="GI:21238836"
                     /translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIG
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                     AHSANTHWYRKVDGVWKFAG"
ORIGIN

  Query Match             36.7%;  Score 189.4;  DB 4;  Length 414;
  Best Local Similarity   75.6%;  Pred. No. 1e-36;
  Matches  235;  Conservative    0;  Mismatches   76;  Indels    0;  Gaps    0;

Qy        127 GCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCG 186
              ||  ||   |  |  || |||||||||||| |||||| ||||||| |||||||| ||||||
Db        104 GCTGCTGACCGACAGATCGACTACCGCTCGTTCCTCAACAAGCTGTGGGAGGCCATGCCG 163

Qy        187 GCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGC 246
              ||||| |||||| |||||||| ||||    |        |||| ||| ||||     || |||
Db        164 GCCGACGAGTTCATCGGCATGATCTCCGACCCCAGCGTGCTCGGCAACCCGCTGCTGCGC 223

Qy        247 ACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGC 306
              || ||||||||| |||||| | ||||||||||    | |||||   ||||||| |||||
Db        224 ACCCAGCACTTCTTCGGCGCCTCGCGCTGGGAGCGCATCTCCGACACCGAGGTCGTCGGC 283

Qy        307 TACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACC 366
              |||  |||||||||||||||| ||||||   ||||  ||  | |||  |      ||||| ||
Db        284 CACCGCCAGCTGCGCGTCCCCCACCAGGTCTACACCGATGCAACCCTCTCACAGGTCGCC 343

Qy        367 ATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGG 426
              | ||||||||||||||||||| |||    |||||||||   ||| ||||||||||||||
Db        344 GTCAAGGGCCACGCCCACTCGGCCAACACCCACTGGTACCGCAAGGTCGACGGCGTCTGG 403

Qy        427 AAGTTCGCCGG 437
              ||||| |||||
Db        404 AAGTTTGCCGG 414


RESULT 9
AY098658
LOCUS       AY098658                 433 bp    DNA     linear   PLN 16-JAN-2003
DEFINITION  Ophiostoma minus isolate 58-4 scytalone dehydratase (SD) gene,
            partial cds.
ACCESSION   AY098658
VERSION     AY098658.1  GI:21238825
KEYWORDS    .
SOURCE      Ophiostoma minus
  ORGANISM  Ophiostoma minus
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE   1  (bases 1 to 433)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Inhibitors and genetic analysis of scytalone dehydratase confirm
            the presence of DHN-melanin pathway in sapstain fungi
  JOURNAL   Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE   2  (bases 1 to 433)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2002) Wood Science, University of British
            Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .433
                     /organism="Ophiostoma minus"
                     /mol_type="genomic DNA"
                     /isolate="58-4"
                     /db_xref="taxon:150568"
                     /country="Canada"
     gene            <1. .>433
                     /gene="SD"
     mRNA            join(<1. .69,138. .>433)
                     /gene="SD"
                     /product="scytalone dehydratase"
     CDS             join(<1. .69,138. .>433)
                     /gene="SD"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAM34804.1"
                     /db_xref="GI:21238826"
                     /translation="EWADRYDSKDWVRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIS
                     MISDPSVLGNPLLRTQHFFGASRWERVSDTEVIGYHQLRVPHQVYTDASLSTVAVKGH
                     AHSANQHWYRKVDGVWKFAG"
ORIGIN

  Query Match             36.4%;  Score 187.8;  DB 4;  Length 433;
  Best Local Similarity   75.2%;  Pred. No. 2.5e-36;
  Matches  234;  Conservative    0;  Mismatches   77;  Indels    0;  Gaps    0;

Qy        127 GCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCG 186
              ||| |||      |  || |||||||||||| |||||  |||||||||||||||| ||||||
Db        123 GCGACTAACTGACAGATCGACTACCGCTCGTTCCTGAACAAGCTCTGGGAGGCCATGCCG 182

Qy        187 GCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGC 246
              || || |||||  || ||||| |||||  |        | || ||| |||||   || |||
Db        183 GCAGACGAGTTTATCAGCATGATCTCGGACCCCAGCGTCCTCGGCAACCCCCTGCTGCGC 242

Qy        247 ACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGC 306
              || ||||||||| | |||| | ||||||||||     || |||||    |||||||| |||
Db        243 ACACAGCACTTCTTTGGCGCCTCGCGCTGGGAACGCGTCTCCGACACTGAGGTCATTGGC 302

Qy        307 TACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACC 366
              ||||||||||||||||||| ||||||   || |  ||  || || ||  |   ||| ||
Db        303 TACCACCAGCTGCGCGTCCCCCACCAGGTTTATACTGATGCCTCCCTGTCGACCGTCGCC 362

Qy        367 ATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGG 426
              | |||||||||| |||||||| ||||  |||||||||   ||| ||||||||||||||
Db        363 GTCAAGGGCCACGCACACTCGGCCAACCAGCACTGGTACCGCAAGGTCGACGGCGTCTGG 422

Qy        427 AAGTTCGCCGG 437
              ||||||||||
Db        423 AAGTTCGCCGG 433


RESULT 10
AY098656
LOCUS       AY098656                 427 bp    DNA     linear   PLN 16-JAN-2003
DEFINITION  Ophiostoma piceae isolate AU1 scytalone dehydratase (SD) gene,
            partial cds.
ACCESSION   AY098656
VERSION     AY098656.1  GI:21238821
KEYWORDS    .
SOURCE      Ophiostoma piceae
  ORGANISM  Ophiostoma piceae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE   1  (bases 1 to 427)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Inhibitors and genetic analysis of scytalone dehydratase confirm
            the presence of DHN-melanin pathway in sapstain fungi
  JOURNAL   Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE   2  (bases 1 to 427)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2002) Wood Science, University of British
            Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .427
                     /organism="Ophiostoma piceae"
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                     /isolate="AU1"
                     /db_xref="taxon:61273"
                     /country="Canada"
     gene            <1. .>427
                     /gene="SD"
     mRNA            join(<1. .69,132. .>427)
                     /gene="SD"
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     CDS             join(<1. .69,132. .>427)
                     /gene="SD"
                     /codon_start=1
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                     /product="scytalone dehydratase"
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                     MISDPSVLGNPLLRTQHFFGASRWERISDTEVVGYHQLRVPHQVYTDTTLTQVAVKGH
                     AHSANTHWYRKVDGVWKFAG"
ORIGIN

  Query Match           36.0%;  Score 185.6;  DB 4;  Length 427;
  Best Local Similarity   76.7%;  Pred. No. 9e-36;
  Matches  227;  Conservative    0;  Mismatches   69;  Indels    0;  Gaps    0;

Qy        142 ATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTC 201
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Db        132 ATCGACTACCGCTCGTTCCTGAACAAGCTGTGGGAGGCCATGCCGGCCGAAGAGTTTATC 191

Qy        202 GGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATC 261
              |||||| ||||   |       | || ||| |||||   || ||||| || |||||| ||
Db        192 GGCATGATCTCCGACCCCAGCGTTCTCGGCAACCCCCTGCTGCGCACACAACACTTCTTC 251

Qy        262 GGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGC 321
              |||| | ||||||||||    | |||||   ||||||| | |||||||| |||||||||
Db        252 GGCGCCTCGCGCTGGGAGCGCATCTCCGACACCGAGGTCGTGGGCTACCATCAGCTGCGC 311

Qy        322 GTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCC 381
              ||||| ||||||   |||| || |||||  | |   ||  || | ||||||||||||
Db        312 GTCCCCCACCAGGTCTACACAGATACCACTCTCACACAAGTTGCCGTCAAGGGCCACGCC 371

Qy        382 CACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGG 437
              |||||||| |||   |||||||||   ||| ||||||||||||||||||||||||
Db        372 CACTCGGCCAACACCCACTGGTACCGCAAGGTCGACGGCGTCTGGAAGTTCGCCGG 427


RESULT 11
AY098657
LOCUS       AY098657                424 bp    DNA     linear   PLN 16-JAN-2003
DEFINITION  Ophiostoma floccosum isolate GR10 scytalone dehydratase (SD) gene,
            partial cds.
ACCESSION   AY098657
VERSION     AY098657.1  GI:21238823
KEYWORDS    .
SOURCE      Ophiostoma floccosum
  ORGANISM  Ophiostoma floccosum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE   1  (bases 1 to 424)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Inhibitors and genetic analysis of scytalone dehydratase confirm
            the presence of DHN-melanin pathway in sapstain fungi
  JOURNAL   Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE   2  (bases 1 to 424)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2002) Wood Science, University of British
            Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .424
                     /organism="Ophiostoma floccosum"
                     /mol_type="genomic DNA"
                     /isolate="GR10"
                     /db_xref="taxon:104300"
                     /country="United Kingdom"
     gene            <1. .>424
                     /gene="SD"
     mRNA            join(<1. .69,132. .>424)
                     /gene="SD"
                     /product="scytalone dehydratase"
     CDS             join(<1. .69,132. .>424)
                     /gene="SD"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAM34803.1"
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                     MISDPSVLGNPLLRTQHFFGASRWERISDTEVVGYHQLRVPHQVYTDTTLTQVAVKGH
                     AHSANTHWYRKVDGVWKFA"
ORIGIN

  Query Match           35.4%;  Score 182.6;  DB 4;  Length 424;
  Best Local Similarity   76.5%;  Pred. No. 5.1e-35;
  Matches  224;  Conservative    0;  Mismatches   69;  Indels    0;  Gaps    0;

Qy        142 ATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTC 201
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Db        132 ATCGACTACCGCTCGTTCCTGAACAAGCTGTGGGAGGCCATGCCGGCCGAAGAGTTTATC 191

Qy        202 GGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATC 261
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Db        192 GGCATGATCTCCGACCCCAGCGTTCTCGGCAACCCCCTGCTGCGCACACAACACTTCTTC 251

Qy        262 GGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGC 321
              |||| | ||||||||||    | |||||   ||||||| | |||||||| |||||||||
Db        252 GGCGCCTCGCGCTGGGAGCGCATCTCCGACACCGAGGTCGTGGGCTACCATCAGCTGCGC 311

Qy        322 GTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCC 381
              ||||| ||||||   |||| || |||||  | |   ||  || | ||||||||||||
Db        312 GTCCCCCACCAGGTCTACACAGATACCACTCTCACACAAGTTGCCGTCAAGGGCCACGCC 371

Qy        382 CACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGC 434
              |||||||| |||   |||||||||   ||| ||||||||||||||||||||||
Db        372 CACTCGGCCAACACCCACTGGTACCGCAAGGTCGACGGCGTCTGGAAGTTCGC 424


RESULT 12
AY098659
LOCUS       AY098659                428 bp    DNA     linear   PLN 16-JAN-2003
DEFINITION  Ophiostoma minus isolate OM3 scytalone dehydratase (SD) gene,
            partial cds.
ACCESSION   AY098659
VERSION     AY098659.1  GI:21238827
KEYWORDS    .
SOURCE      Ophiostoma minus
  ORGANISM  Ophiostoma minus
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE   1  (bases 1 to 428)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Inhibitors and genetic analysis of scytalone dehydratase confirm
            the presence of DHN-melanin pathway in sapstain fungi
  JOURNAL   Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE   2  (bases 1 to 428)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2002) Wood Science, University of British
            Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .428
                     /organism="Ophiostoma minus"
                     /mol_type="genomic DNA"
                     /isolate="OM3"
                     /db_xref="taxon:150568"
                     /country="United Kingdom"
     gene            <1. .>428
                     /gene="SD"
     mRNA            join(<1. .69,133. .>428)
                     /gene="SD"
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     CDS             join(<1. .69,133. .>428)
                     /gene="SD"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAM34805.1"
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                     AHSANQHWYRKVDGVWKFAG"
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ORIGIN

Query Match 35.3%; Score 182.4; DB 4; Length 428;
Best Local Similarity 76.0%; Pred. No. 5.7e-35;
Matches 225; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

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Qy        142 ATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTC 201
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Db        133 ATCGACTACCGCTCGTTTCTAAACAAGCTCTGGGAGGCCATGCCGGCAGACGAGTTTATC 192

Qy        202 GGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATC 261
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Db        193 AGCATGATCTCGGACCCCAGCGTCCTCGGCAACCCCCTGCTGCGCACACAGCACTCTTTT 252

Qy        262 GGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGC 321
              ||||  | |||||||||      ||  |||||    ||||||||  ||||||||||||||||||
Db        253 GGCGCCTCGCGCTGGGGACGCGTCTCCGACACCGAGGTCATTGGCTACCACCAGCTGCGC 312

Qy        322 GTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCC 381
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Db        313 GTCCCCCACCAGGTCTACACCGACGCCTCCCTGTCGACCGTGGCCGTCAAGGGCCACGCA 372

Qy        382 CACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGG 437
              ||||||||  ||||  |||||||||    |||  ||||||||||||||||||||||||
Db        373 CACTCGGCCAACCAGCACTGGTACCGCAAGGTCGACGGCGTCTGGAAGTTCGCCGG 428
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RESULT 13
AY098661
LOCUS AY098661 421 bp DNA linear PLN 16-JAN-2003
DEFINITION Ophiostoma piceae isolate W5 scytalone dehydratase (SD) gene, partial cds.
ACCESSION AY098661
VERSION AY098661.1 GI:21238831
KEYWORDS .
SOURCE Ophiostoma piceae
ORGANISM Ophiostoma piceae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE 1 (bases 1 to 421)
AUTHORS Fleet,C. and Breuil,C.
TITLE Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi
JOURNAL Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE 2 (bases 1 to 421)
AUTHORS Fleet,C. and Breuil,C.
TITLE Direct Submission
JOURNAL Submitted (22-APR-2002) Wood Science, University of British Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES Location/Qualifiers
source 1. .421
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/mol_type="genomic DNA"
/isolate="W5"
/db_xref="taxon:61273"
/country="Austria"
gene <1. .>421
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mRNA join(<1. .69,126. .>421)
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CDS join(<1. .69,126. .>421)
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ORIGIN

Query Match 34.7%; Score 179.2; DB 4; Length 421;
Best Local Similarity 75.3%; Pred. No. 3.7e-34;
Matches 223; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

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Db        126 ATCGATTACCGGTCGTTTCTGAACAAGCTCTGGGAGGCCATGCCGGCAGATGAGTTTATC 185

Qy        202 GGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATC 261
              ||||||  |||||  |     |  |  ||  |||  |||||    ||  |||||  ||  ||||||  |
Db        186 GGCATGATCTCGGACCCCAACGTCCTCGGCAACCCCCTGCTACGCACACAACACTTCTTT 245

Qy        262 GGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGC 321
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Db        246 GGCGCCTCACGCTGGGAACGCGTCTCCGATACGGAGGTCATTGGCTACCACCAGCTGCGC 305

Qy        322 GTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCC 381
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Db        306 GTCCCCCACCAGGTCTACACCGACGCCTCCCTGTCGACCGTTGCCGTCAAGGGCCACGCA 365

Qy        382 CACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGG 437
              ||||||||  ||||  |||||||||    |||  |  ||||||||||||||||||  |||||
Db        366 CACTCGGCCAACCAGCACTGGTACCGCAAGGTTGACGGCGTCTGGAAGTTTGCCGG 421
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RESULT 14
AY098660
LOCUS AY098660 423 bp DNA linear PLN 16-JAN-2003
DEFINITION Ophiostoma piceae isolate 187-1 scytalone dehydratase (SD) gene, partial cds.
ACCESSION AY098660
VERSION AY098660.1 GI:21238829
KEYWORDS .
SOURCE Ophiostoma piceae
ORGANISM Ophiostoma piceae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE 1 (bases 1 to 423)
AUTHORS Fleet,C. and Breuil,C.
TITLE Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi
JOURNAL Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE 2 (bases 1 to 423)
AUTHORS Fleet,C. and Breuil,C.
TITLE Direct Submission
JOURNAL Submitted (22-APR-2002) Wood Science, University of British Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES Location/Qualifiers
source 1. .423
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gene <1. .>423
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CDS join(<1. .69,128. .>423)
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/protein_id="AAM34806.1"
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AHSANQHWYRKVDGVWKFAG"

ORIGIN

Query Match 34.7%; Score 179.2; DB 4; Length 423;
Best Local Similarity 75.3%; Pred. No. 3.7e-34;
Matches 223; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

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Qy        142 ATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTC 201
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Db        128 ATCGATTACCGGTCGTTTCTGAACAAGCTCTGGGAGGCCATGCCGGCAGATGAGTTTATC 187

Qy        202 GGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATC 261
              |||||| |||||   |     |  | || ||| |||||   || || || || |||||| |
Db        188 GGCATGATCTCGGACCCCAACGTCCTCGGCAACCCCCTGCTACGGACACAACACTTCTTT 247

Qy        262 GGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGC 321
              |||| | ||||||||||    || |||||     ||||| || ||||||||||||||||||
Db        248 GGCGCCTCGCGCTGGGAACGCGTCTCCGATACGGAGGTTATTGGCTACCACCAGCTGCGC 307

Qy        322 GTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCC 381
              ||||| ||||||   ||||  ||| || || ||  |   ||  || | ||||||||||
Db        308 GTCCCCCACCAGGTCTACACCGACGCCTCCCTGTCGACCGTTGCCGTCAAGGGCCACGCA 367

Qy        382 CACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGG 437
              |||||||| ||||  |||||||||   ||| | ||||||||||||||||||||||
Db        368 CACTCGGCCAACCAGCACTGGTACCGCAAGGTTGACGGCGTCTGGAAGTTCGCCGG 423
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RESULT 15
AY098666
LOCUS AY098666 423 bp DNA linear PLN 16-JAN-2003
DEFINITION Ophiostoma setosum isolate NZFS3734 scytalone dehydratase (SD) gene, partial cds.
ACCESSION AY098666
VERSION AY098666.1 GI:21238841
KEYWORDS .
SOURCE Ophiostoma setosum
ORGANISM Ophiostoma setosum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE 1 (bases 1 to 423)
AUTHORS Fleet,C. and Breuil,C.
TITLE Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi
JOURNAL Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE 2 (bases 1 to 423)
AUTHORS Fleet,C. and Breuil,C.
TITLE Direct Submission
JOURNAL Submitted (22-APR-2002) Wood Science, University of British Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES Location/Qualifiers
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/organism="Ophiostoma setosum"
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/db_xref="taxon:107467"
/country="New Zealand"
gene <1. .>423
/gene="SD"
mRNA join(<1. .69,128. .>423)
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CDS join(<1. .69,128. .>423)
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/protein_id="AAM34812.1"
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ORIGIN

Query Match 34.7%; Score 179.2; DB 4; Length 423;
Best Local Similarity 75.3%; Pred. No. 3.7e-34;
Matches 223; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

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Qy        142 ATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTC 201
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Db        128 ATTGATTACCGCTCGTTCCTGAACAAGCTCTGGGAGGCCATGCCGGCAGATGAGTTTATC 187

Qy        202 GGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATC 261
              | |||| |||||  |       | || ||| ||||    || ||||| || |||||| |
Db        188 GTCATGATCTCGGACCCCAGCGTCCTCGGCAACCCGCTGCTGCGCACACAACACTTCTTT 247

Qy        262 GGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGC 321
              || | | ||||||||||||   || |||||     || ||||| || ||||||||||||||||
Db        248 GGTGCCTCGCGCTGGGAGCGCGTCTCCGACACTGAAGTCATTGGTTACCACCAGCTGCGC 307

Qy        322 GTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCC 381
              ||||| |||||   |||| ||  || || || ||  |   ||  || | ||||||||||
Db        308 GTCCCCCACCAGGTCTACACTGATGCCTCCCTGTCGACCGTTGCCGTCAAGGGCCACGCG 367

Qy        382 CACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGG 437
              |||||||| ||||  |||||||||   ||| |||||||||||||||||||||||
Db        368 CACTCGGCCAACCAGCACTGGTACCGCAAGGTCGACGGCGTCTGGAAGTTCGCCGG 423
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Job time : 2495 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: December 5, 2006, 01:27:41 ; Search time 52 Seconds
(without alignments)
289.524 Million cell updates/sec

Title: US-10-507-132-2
Perfect score: 942
Sequence: 1 MGSQVQKSDEITFSDYLGLM.....WGEFDFDRIFEDGRETFGDK 172

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	94.5	10.0	153	2	US-09-328-352-4170	Sequence 4170, Ap
2	84	8.9	338	2	US-09-543-681A-4649	Sequence 4649, Ap
3	84	8.9	349	2	US-09-625-634A-3	Sequence 3, Appli
4	81	8.6	349	2	US-09-625-634A-2	Sequence 2, Appli
5	77	8.2	700	2	US-09-252-991A-29072	Sequence 29072, A
6	76	8.1	602	2	US-09-248-796A-15811	Sequence 15811, A
7	74.5	7.9	437	2	US-09-477-135A-136	Sequence 136, App
8	74	7.9	768	2	US-09-489-039A-11131	Sequence 11131, A
9	72.5	7.7	388	1	US-08-282-197C-56	Sequence 56, Appl
10	72.5	7.7	518	2	US-09-489-039A-8407	Sequence 8407, Ap
11	72	7.6	396	2	US-09-328-352-7847	Sequence 7847, Ap
12	71.5	7.6	500	2	US-09-949-016-11697	Sequence 11697, A
13	71.5	7.6	613	2	US-09-149-727-5	Sequence 5, Appli
14	71.5	7.6	613	2	US-09-270-957-16	Sequence 16, Appl
15	71.5	7.6	651	2	US-09-715-858-2	Sequence 2, Appli
16	71.5	7.6	1207	2	US-10-098-600B-16	Sequence 16, Appl
17	71.5	7.6	1207	2	US-09-949-002-376	Sequence 376, App
18	71.5	7.6	1271	2	US-09-540-236-3740	Sequence 3740, Ap
19	71.5	7.6	1384	2	US-08-976-255-11	Sequence 11, Appl
20	71	7.5	251	2	US-09-248-796A-16943	Sequence 16943, A
21	71	7.5	728	2	US-09-543-681A-8132	Sequence 8132, Ap
22	70.5	7.5	110	1	US-08-194-290-9	Sequence 9, Appli
23	70.5	7.5	184	1	US-08-614-377A-9	Sequence 9, Appli
24	70.5	7.5	184	2	US-09-142-648B-9	Sequence 9, Appli
25	70.5	7.5	471	2	US-08-914-375C-70	Sequence 70, Appl
26	70.5	7.5	590	2	US-10-104-047-3415	Sequence 3415, Ap
27	70	7.4	176	2	US-09-543-681A-6922	Sequence 6922, Ap
28	70	7.4	243	2	US-09-252-991A-26765	Sequence 26765, A
29	69.5	7.4	146	2	US-09-270-767-33395	Sequence 33395, A
30	69.5	7.4	146	2	US-09-270-767-48612	Sequence 48612, A
31	69.5	7.4	166	2	US-09-328-352-7279	Sequence 7279, Ap
32	69.5	7.4	524	2	US-09-242-913B-15	Sequence 15, Appl
33	69.5	7.4	524	3	US-10-347-252-15	Sequence 15, Appl
34	69.5	7.4	653	2	US-09-171-937C-27	Sequence 27, Appl
35	69.5	7.4	779	2	US-09-171-937C-25	Sequence 25, Appl
36	69	7.3	224	2	US-09-134-000C-4000	Sequence 4000, Ap
37	69	7.3	614	2	US-09-328-352-4504	Sequence 4504, Ap
38	69	7.3	2154	1	US-08-841-349-4	Sequence 4, Appli
39	69	7.3	2154	2	US-09-431-184A-4	Sequence 4, Appli
40	69	7.3	2364	2	US-09-538-092-1243	Sequence 1243, Ap
41	68.5	7.3	331	2	US-09-107-433-4641	Sequence 4641, Ap
42	68.5	7.3	442	2	US-09-252-991A-31597	Sequence 31597, A
43	68.5	7.3	484	7	5171673-8	Patent No. 5171673
44	68.5	7.3	487	7	5171673-6	Patent No. 5171673
45	68.5	7.3	493	2	US-08-999-774A-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-328-352-4170
; Sequence 4170, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4170
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4170

Query Match 10.0%; Score 94.5; DB 2; Length 153;
Best Local Similarity 23.0%; Pred. No. 0.008;
Matches 31; Conservative 28; Mismatches 59; Indels 17; Gaps 6;

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Qy         15 DYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGMVSSKQ 74
              ||  ::  :  :   :| |:||   :::|  | :||  |  :    :  |: |  | :|
Db         13 DYHRILEVITRFQLVFDQKNWDAFDELLADQLEVDYLQFRGEPLCVVSCHEYKG--SRQQ 70

Qy         75 MLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHW 134
              |    || || :      :: :|:     |   :| |:        :   : ||   ::
Db         71 ALSH--LRLQHNLSNP-LIRIEQDQA----WLECNYQIYR------FSENDYFHSFGRYY 117

Qy        135 Y--KKIDGVWKFAGL 147
             :   |  |:||  |:
Db        118 FTLAKQQGIWKITGI 132
```

RESULT 2
US-09-543-681A-4649
; Sequence 4649, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344

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; SEQ ID NO 4649
;   LENGTH: 338
;   TYPE: PRT
;   ORGANISM: Proteus mirabilis
US-09-543-681A-4649

  Query Match             8.9%;  Score 84;  DB 2;  Length 338;
  Best Local Similarity   25.5%;  Pred. No. 0.38;
  Matches   39;  Conservative   18;  Mismatches   42;  Indels   54;  Gaps   10;

Qy         35 WDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPTLR-TQHFIGGTRWE 93
              ||: ::             |||::|  | : ||       || |  ||  :| :  | ||
Db         94 WDKAQR----------EDVLDKMFETAP-QSFV-------MLADLCLRGAKHTLQRTSWE 135

Qy         94 KVSEDEVIGYHQLR---------VPHQRYKDTTMKEVTMKGHAHSANLHWYKK--IDGVW 142
               :   |:|   :|:         |||    |    :  ||   :|  |  |    | :|
Db        136 GI---EII--ERLKAQGRNVIFMVPHGWAVDVPAMLLAAKGQKMAAMFHHQKDPVTDYLW 190

Qy        143 -------------KFAGLKPDIR------WGEF 156
                          : ||:|| |       || :
Db        191 NKARYHFGGRLHSREAGIKPFISTVRQGFWGYY 223


RESULT 3
US-09-625-634A-3
; Sequence 3, Application US/09625634A
; Patent No. 6653448
; GENERAL INFORMATION:
;  APPLICANT: Vernet, Corine
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Herrmann, John
;  TITLE OF INVENTION: WNT-7B-LIKE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
;  TITLE OF INVENTION:  SAME
;  FILE REFERENCE: Cura-244 (15966-744) US
;  CURRENT APPLICATION NUMBER: US/09/625,634A
;  CURRENT FILING DATE:  2000-07-26
;  PRIOR APPLICATION NUMBER: USSN 60/194,256
;  PRIOR FILING DATE: 2000-04-03
;  PRIOR APPLICATION NUMBER: USSN 60/192,838
;  PRIOR FILING DATE: 2000-03-29
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 349
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-09-625-634A-3

  Query Match             8.9%;  Score 84;  DB 2;  Length 349;
  Best Local Similarity   31.1%;  Pred. No. 0.4;
  Matches   32;  Conservative   11;  Mismatches   36;  Indels   24;  Gaps    7;

Qy         84 QHFIGGTRW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-------ANLH- 133
              ||      ||    : |  | |  :|||  :    |    :|  | ||:        ||
Db         74 QHQFRFGRWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSN 130

Qy        134 ---------WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                      :| : :| ||: |    |:|:|  || | | | ||
Db        131 CGCDREKQGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171


RESULT 4
US-09-625-634A-2
; Sequence 2, Application US/09625634A
; Patent No. 6653448
; GENERAL INFORMATION:
;  APPLICANT: Vernet, Corine
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Herrmann, John
;  TITLE OF INVENTION: WNT-7B-LIKE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
;  TITLE OF INVENTION:  SAME
;  FILE REFERENCE: Cura-244 (15966-744) US
;  CURRENT APPLICATION NUMBER: US/09/625,634A
;  CURRENT FILING DATE:  2000-07-26
;  PRIOR APPLICATION NUMBER: USSN 60/194,256
;  PRIOR FILING DATE: 2000-04-03
;  PRIOR APPLICATION NUMBER: USSN 60/192,838
;  PRIOR FILING DATE: 2000-03-29
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 349
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-625-634A-2

  Query Match             8.6%;  Score 81;  DB 2;  Length 349;
  Best Local Similarity   31.2%;  Pred. No. 0.88;
  Matches   30;  Conservative   11;  Mismatches   31;  Indels   24;  Gaps    7;

Qy         91 RW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-------ANLH-------- 133
              ||    : |  | |  :||| :    |    :|  | ||:        ||
Db         81 RWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSNCGCDREK 137

Qy        134 --WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                :| : :| ||: |    |:|:|  || | | | ||
Db        138 QGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171


RESULT 5
US-09-252-991A-29072
; Sequence 29072, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 29072
;   LENGTH: 700
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29072

  Query Match             8.2%;  Score 77;  DB 2;  Length 700;
  Best Local Similarity   28.1%;  Pred. No. 6.6;
  Matches   25;  Conservative   15;  Mismatches   35;  Indels   14;  Gaps    4;

Qy         59 EAMPAEEFVGM-VSSKQMLGDPTLRTQHFIGGTRW------EKVSEDEVIGYHQLRVPHQ 111
              |  |||: :|  |:   :|| |  |  | :  :        | | : | :|:| :   ||
Db        141 EDQPAEQRLGQRVAPGHILGYPEDRVAHRVQRSPQCRQAVAEVVEQGEDVGHHHIEEGHQ 200

Qy        112 RYK-----DTTMKEVTMKGH--AHSANLH 133
              |::     |: : |     |   | : ||
Db        201 RHRRQQEGDSALLEAVPDAHESIHRSVLH 229


RESULT 6
US-09-248-796A-15811
; Sequence 15811, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
;  APPLICANT: Keith Weinstock et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
;  TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 107196.132
;  CURRENT APPLICATION NUMBER: US/09/248,796A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER: US 60/074,725
```

```
;  PRIOR FILING DATE: 1998-02-13
;  PRIOR APPLICATION NUMBER: US 60/096,409
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15811
;   LENGTH: 602
;   TYPE: PRT
;   ORGANISM: Candida albicans
US-09-248-796A-15811

  Query Match             8.1%;  Score 76;  DB 2;  Length 602;
  Best Local Similarity   21.3%;  Pred. No. 7;
  Matches   36;  Conservative   24;  Mismatches   61;  Indels   48;  Gaps    6;

Qy          4 QVQKSDEITFSDYLGLMTCVYEWADSYDSKDW----DRLRKVIAPTLRIDYRSFLDKLWE 59
              | : | |||  :| |    | :   :    :|     |  :     :|  :   || |
Db        103 QEKSSVEITIENYEGHSPIVIKREFTAKESNWTVNNKRATESKIKDIRTKFNIQLDNLCH 162

Qy         60 AMPAE---EFVG------MVSSKQMLGDPTLRTQH-----------FIGGT------RWE 93
               :| |   || |       :: ::: |||  |   |           :|         |
Db        163 FLPQERVAEFAGLSPEKLLMETERTLGDGHLLIMHEDLIAKDNESQQLGNKIKDIEGRLA 222

Qy         94 KVSED-----------------EVIGYHQLRVPHQRYKDTTMKEVTMK 124
              |: ||                 | :  |:| :|: :|:|   :   :|
Db        223 KLHEDRSKLEEEARKLEEYDRKSEEVDNHRLLIPYAKYQDLKNQRTHLK 271


RESULT 7
US-09-477-135A-136
; Sequence 136, Application US/09477135A
; Patent No. 6572865
; GENERAL INFORMATION:
;  APPLICANT:  Nano, Francis
;  TITLE OF INVENTION:  Mycobacterium Tuberculosis DNA Sequences Encoding
;  TITLE OF INVENTION:  immunostimulatory Peptides
;  FILE REFERENCE:  52888
;  CURRENT APPLICATION NUMBER: US/09/477,135A
;  CURRENT FILING DATE:  2000-01-03
;  PRIOR APPLICATION NUMBER:  08990823
;  PRIOR FILING DATE:  1997-12-15
;  PRIOR APPLICATION NUMBER:  US 96/10375
;  PRIOR FILING DATE:  1996-06-14
;  PRIOR APPLICATION NUMBER:  60/000,254
;  PRIOR FILING DATE:  1995-06-15
;  NUMBER OF SEQ ID NOS:  169
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 136
;   LENGTH: 437
;   TYPE: PRT
;   ORGANISM: Mycobacterium tuberculosis
US-09-477-135A-136

  Query Match             7.9%;  Score 74.5;  DB 2;  Length 437;
  Best Local Similarity   20.5%;  Pred. No. 6.7;
  Matches   34;  Conservative   23;  Mismatches   48;  Indels   61;  Gaps    9;

Qy         58 WEAMPAEEFVGMVSSKQMLGD-----PTLRTQHFIGGTRWEKVSE-------------- 97
              | : | :      : ::::|      |||  :    |  :::|::
Db         43 WSSHPGQ---SSAAERELIGRFQDRFPTLSVKLIDAGKDYDEVAQKFNAALIGTDVPDVV 99

Qy         98 ------------------DEVIGYHQLRVPHQRYKDTTMKEVTMKG------HAHSANL 132
                               |:: |  |: |    | |: : :    |       :| |  |
Db        100 LLDDRWWFHFALSGVLTALDDLFG--QVGVDTTDYVDSLLADYEFNGRHYAVPYARSTPL 157

Qy        133 HWYKKIDGVWKFAGLKPD---IRWGEFD-----FDRIFEDGRETFG 170
               :| |    |: ||| ||     | |||       |:   ||   |
Db        158 FYYNK--AAWQQAGL-PDRGPQSWSEFDEWGPELQRVVGAGRSAHG 200


RESULT 8
US-09-489-039A-11131
; Sequence 11131, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 11131
;   LENGTH: 768
;   TYPE: PRT
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11131

  Query Match             7.9%;  Score 74;  DB 2;  Length 768;
  Best Local Similarity   20.6%;  Pred. No. 17;
  Matches   45;  Conservative   31;  Mismatches   66;  Indels   76;  Gaps   11;

Qy          8 SDEITFSDYLGLMTCVYEWADSYDS--KDWDRL-----RKVIA----------------P 44
              :|:   : : |  | :|| :|  :   :||: |     |: ::
Db        383 ADDFALASFDG--TSLYEHSDPREGYHQDWNTLIYNYGRREVSNYLVGNALYWIERFGID 440

Qy         45 TLRID------YRSFLDKLWEAMPAE----------EFVGMVSSKQMLGDPT-------L 81
                ||:|      || :  |  | :| |          ||  : :: ::||: |
Db        441 ALRVDAVASMIYRDYSRKAGEWIPNEYGGRENLEAIEF--LRNTNRILGEQTPGAVTMAE 498

Qy         82 RTQHFIGGTR------------WEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGH--- 126
              :  | | ||             |      : : | :|   |:||    |   :  :
Db        499 ESTDFAGVTRPPAGGGLGFWFKWNLGWMHDTLDYMKLDPVHRRYHHDKMTFGMLYNYTEN 558

Qy        127 -----AHSANLHWYKKI------DGVWKFAGLKPDIRW 153
                   :|   :|  | |      |   ||| |:    |
Db        559 FVLPLSHDEVVHGKKSILDRMPGDAWQKFANLRAYYGW 596


RESULT 9
US-08-282-197C-56
; Sequence 56, Application US/08282197C
; Patent No. 5871730
;  GENERAL INFORMATION:
;    APPLICANT:  Brzezinski, Ryszard
;    APPLICANT:  Dery, Claude V
;    APPLICANT:  Beaulieu, Carole
;    TITLE OF INVENTION:  Thermostable Xylanase DNA, Protein and
;    TITLE OF INVENTION:  Methods of Use
;    NUMBER OF SEQUENCES:  67
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;      STREET:  1100 New York Ave., NW
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/282,197C
;      FILING DATE:  29-JUL-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cimbala, Michele A
;      REGISTRATION NUMBER:  33,851
;      REFERENCE/DOCKET NUMBER:  1050.0410000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
```

```
;      LENGTH:  388 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
US-08-282-197C-56

  Query Match             7.7%;  Score 72.5;  DB 1;  Length 388;
  Best Local Similarity   21.9%;  Pred. No. 9.6;
  Matches   33;  Conservative   23;  Mismatches   68;  Indels   27;  Gaps    5;

Qy         31 DSKDWDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPTLRTQHFIGGT 90
              | | || : :|| |    |     :  |  :   |::          :   |     ||:
Db        176 DIKSWDVVNEVIEPN---DPGGMRNSPWYQITGTEYI----------EVAFRATREAGGS 222

Qy         91 RWEKVSEDEVIGYH-----QLRVPHQRYKDTTMKEVTMKGHAHSANLHWY-----KKIDG 140
                :    |    |:     :  : ::  |:   | | : |  |  ::  |     : |:
Db        223 DIKLYIND----YNTDDPVKRDILYELVKNLLEKGVPIDGVGHQTHIDIYNPPVERIIES 278

Qy        141 VWKFAGLKPDIRWGEFDFDRIFEDGRETFGD 171
              : |||||  |    | |      : |  :||
Db        279 IKKFAGLGLDNIITELDMSIYSWNDRSDYGD 309


RESULT 10
US-09-489-039A-8407
; Sequence 8407, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 8407
;   LENGTH: 518
;   TYPE: PRT
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8407

  Query Match             7.7%;  Score 72.5;  DB 2;  Length 518;
  Best Local Similarity   26.1%;  Pred. No. 14;
  Matches   36;  Conservative   16;  Mismatches   53;  Indels   33;  Gaps    6;

Qy         33 KDWDRLRKVIAPTLRI--DYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPTLRTQHFIGGT 90
              |: | | :     ||:    |: |::|   :| :  | | | :|  |   | |
Db        164 KETDALPEGERANLRVITQNRTALNQLTAVLPDDSKVIMSSLRQFSGTQPLYT------- 216

Qy         91 RWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDGVWKFAGLKP- 149
                : || |:  :|  | ::   |          |   | |       || |    | |
Db        217 ----LGEDGVLTNNQTHVKYRPNNDV--------GFYQSIN------ADGSWGNEKLSPG 258

Qy        150 ---DIRWGEFDFDRIFED 164
                 | |   :| |:| |
Db        259 YTVTIGWD--NFTRVFHD 274


RESULT 11
US-09-328-352-7847
; Sequence 7847, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
;  APPLICANT: Gary L. Breton et al.
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
;  TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC99-03PA
;  CURRENT APPLICATION NUMBER: US/09/328,352
;  CURRENT FILING DATE: 1999-06-04
;  NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7847
;   LENGTH: 396
;   TYPE: PRT
;   ORGANISM: Acinetobacter baumannii
US-09-328-352-7847

  Query Match             7.6%;  Score 72;  DB 2;  Length 396;
  Best Local Similarity   18.9%;  Pred. No. 11;
  Matches   35;  Conservative   27;  Mismatches   41;  Indels   82;  Gaps    8;

Qy          9 DEITFSDYLGLMTCVYEWADSYD----------SKDW---DRLRKVIAPTLRIDYRSFL 54
              ||: |  :   |   ::  :::|           |||   : | | : |  | :
Db         52 DELFFDKFDRAMKDYFDGIETFDIDELLKQVHKLPKDWFDLELLEKHLTPEQRAE----- 106

Qy         55 DKLWEAMPAEEFVGMVSSKQMLGDPTLRTQH--FIGGTR-------------------- 91
                | :|   || : |:  :       || ||    || |
Db        107 --LQKAGSLEELMKMLEER-------LREQHKKHQGGNRMVGTGGTSPFGAFGDHPEGVR 157

Qy         92 -------------WEK-----VSEDEVIGYHQLRVPHQRYK-------------DTTMKE 120
                          ||:     : :|:|:|  |:::  :| :              | |::|
Db        158 IGGPGRKRSAVKVWEQRKYQNLDDDQVLGTRQMQIALRRLRKFARQGAAEELDVDGTIRE 217

Qy        121 VTMKG 125
                :|
Db        218 TAKQG 222


RESULT 12
US-09-949-016-11697
; Sequence 11697, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11697
;   LENGTH: 500
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-11697

  Query Match             7.6%;  Score 71.5;  DB 2;  Length 500;
  Best Local Similarity   26.0%;  Pred. No. 18;
  Matches   34;  Conservative   19;  Mismatches   51;  Indels   27;  Gaps    6;

Qy         29 SYDSKDWDRLRKVIAPTLRIDY-----RSFLDK-----LWEAMPAEEFVGMVSSKQMLGD 78
              | : |: | |      : | |:     | | ::     |||: |  :      |   :  |
Db         43 SRECKELDGLW-----SFRADFSDNRRRGFEEQWYRRPLWESGPTVDMPVPSSFNDISQD 97

Qy         79 PTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKI 138
                ||  ||:|   :|:    |||       :| :  :|   :|   | |||  : |   :
Db         98 WRLR--HFVGWVWYER----EVI------LPERWTQDLRTRVVLRIGSAHSYAIVWVNGV 145

Qy        139 DGVWKFAGLKP 149
              | :    |  |
Db        146 DTLEHEGGYLP 156


RESULT 13
US-09-149-727-5
; Sequence 5, Application US/09149727
; Patent No. 6391547
; GENERAL INFORMATION:
```

```
;  APPLICANT: Jefferson, Richard A.
;  APPLICANT: Kilian, Andrzej
;  APPLICANT: Keese, Paul Konrad
;  TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND
;  TITLE OF INVENTION: USES THEREOF
;  FILE REFERENCE: 190106.405
;  CURRENT APPLICATION NUMBER: US/09/149,727
;  CURRENT FILING DATE: 1998-09-08
;  EARLIER APPLICATION NUMBER: US 60/058,263
;  EARLIER FILING DATE: 1997-09-09
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 613
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-149-727-5

  Query Match             7.6%;  Score 71.5;  DB 2;  Length 613;
  Best Local Similarity   26.0%;  Pred. No. 23;
  Matches   34;  Conservative   19;  Mismatches   51;  Indels   27;  Gaps    6;

Qy         29 SYDSKDWDRLRKVIAPTLRIDY-----RSFLDK-----LWEAMPAEEFVGMVSSKQMLGD 78
              | : |: | |      : | |:     | | ::     |||: |  :     |   :  |
Db         15 SRECKELDGLW-----SFRADFSDNRRRGFEEQWYRRPLWESGPTVDMPVPSSFNDISQD 69

Qy         79 PTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKI 138
               ||  ||:|   :|:    |||      :| :  :|   : |   | |||  : |   :
Db         70 WRLR--HFVGWVWYER----EVI------LPERWTQDLRTRVVLRIGSAHSYAIVWVNGV 117

Qy        139 DGVWKFAGLKP 149
              | :    |  |
Db        118 DTLEHEGGYLP 128


RESULT 14
US-09-270-957-16
; Sequence 16, Application US/09270957
; Patent No. 6641996
; GENERAL INFORMATION:
;  APPLICANT: Richard A. Jefferson and Jorge E. Mayer
;  TITLE OF INVENTION: MICROBIAL -GLUCURONIDASE GENES, GENE
;  TITLE OF INVENTION: PRODUCTS, AND USES THEREOF
;  FILE REFERENCE: 190106.405C1
;  CURRENT APPLICATION NUMBER: US/09/270,957
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 613
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-270-957-16

  Query Match             7.6%;  Score 71.5;  DB 2;  Length 613;
  Best Local Similarity   26.0%;  Pred. No. 23;
  Matches   34;  Conservative   19;  Mismatches   51;  Indels   27;  Gaps    6;

Qy         29 SYDSKDWDRLRKVIAPTLRIDY-----RSFLDK-----LWEAMPAEEFVGMVSSKQMLGD 78
              | : |: | |      : | |:     | | ::     |||: |  :     |   :  |
Db         15 SRECKELDGLW-----SFRADFSDNRRRGFEEQWYRRPLWESGPTVDMPVPSSFNDISQD 69

Qy         79 PTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKI 138
               ||  ||:|   :|:    |||      :| :  :|   : |   | |||  : |   :
Db         70 WRLR--HFVGWVWYER----EVI------LPERWTQDLRTRVVLRIGSAHSYAIVWVNGV 117

Qy        139 DGVWKFAGLKP 149
              | :    |  |
Db        118 DTLEHEGGYLP 128


RESULT 15
US-09-715-858-2
; Sequence 2, Application US/09715858
; Patent No. 6582692
; GENERAL INFORMATION:
;  APPLICANT:  Podsakoff, Gregory
;  APPLICANT:  Watson, Gordon
;  APPLICANT:  Couto, Linda B.
;  APPLICANT:  Yang, Bin
;  TITLE OF INVENTION:  RECOMBINANT ADENO-ASSOCIATED VIRUS VIRIONS FOR THE
;  TITLE OF INVENTION:  TREATMENT OF LYSOSOMAL DISORDERS
;  FILE REFERENCE:  0800-0021
;  CURRENT APPLICATION NUMBER: US/09/715,858
;  CURRENT FILING DATE:  2000-11-14
;  NUMBER OF SEQ ID NOS:  16
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 651
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-715-858-2

  Query Match             7.6%;  Score 71.5;  DB 2;  Length 651;
  Best Local Similarity   26.0%;  Pred. No. 25;
  Matches   34;  Conservative   19;  Mismatches   51;  Indels   27;  Gaps    6;

Qy         29 SYDSKDWDRLRKVIAPTLRIDY-----RSFLDK-----LWEAMPAEEFVGMVSSKQMLGD 78
              | : |: | |      : | |:     | | ::     |||: |  :     |   :  |
Db         35 SRECKELDGLW-----SFRADFSDNRRRGFEEQWYRRPLWESGPTVDMPVPSSFNDISQD 89

Qy         79 PTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKI 138
               ||  ||:|   :|:    |||      :| :  :|   : |   | |||  : |   :
Db         90 WRLR--HFVGWVWYER----EVI------LPERWTQDLRTRVVLRIGSAHSYAIVWVNGV 137

Qy        139 DGVWKFAGLKP 149
              | :    |  |
Db        138 DTLEHEGGYLP 148


Search completed: December  5, 2006, 01:29:07
Job time : 53 secs
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: December 5, 2006, 01:18:16 ; Search time 200 Seconds
(without alignments)
393.206 Million cell updates/sec

Title: US-10-507-132-2
Perfect score: 942
Sequence: 1 MGSQVQKSDEITFSDYLGLM.....WGEFDFDRIFEDGRETFGDK 172

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	942	100.0	172	7	ADC16591	Adc16591 Scytalone
2	938	99.6	172	7	ADC16593	Adc16593 Scytalone
3	94.5	10.0	153	6	ADA32883	Ada32883 Acinetoba
4	87	9.2	924	6	AAE38266	Aae38266 Rice dise
5	86.5	9.2	331	9	AEB40857	Aeb40857 L. pneumo
6	86.5	9.2	332	9	AEB37544	Aeb37544 L. pneumo
7	85	9.0	265	2	AAW98720	Aaw98720 H. pylori
8	84	8.9	338	7	ADF04364	Adf04364 Bacterial
9	84	8.9	349	4	AAE12983	Aae12983 Murine Wn
10	84	8.9	349	8	ADS31850	Ads31850 Mouse win
11	84	8.9	349	8	ADU86486	Adu86486 Mouse win
12	84	8.9	349	10	AED95375	Aed95375 Mouse Wnt
13	84	8.9	411	8	ADX93641	Adx93641 Plant ful
14	83	8.8	923	2	AAR61136	Aar61136 Plant bli
15	81	8.6	349	4	AAE12982	Aae12982 Human Wnt
16	81	8.6	349	6	ABU55890	Abu55890 Human WNT
17	81	8.6	349	6	AAE34044	Aae34044 WNT-7B pr
18	81	8.6	349	7	ADA27225	Ada27225 Human NOV
19	81	8.6	349	7	ADA27234	Ada27234 Human NOV
20	81	8.6	349	7	ADA27223	Ada27223 Human NOV
21	81	8.6	349	8	ADO08170	Ado08170 Human Wnt
22	81	8.6	349	8	ADO22234	Ado22234 Human WNT
23	81	8.6	349	8	ADU86448	Adu86448 Human win
24	81	8.6	349	9	ADV26391	Adv26391 Human Wnt
25	81	8.6	349	10	AED95373	Aed95373 Human Wnt
26	81	8.6	449	8	ADQ79686	Adq79686 Benzoate
27	79.5	8.4	1239	4	ABB58303	Abb58303 Drosophil
28	79	8.4	702	8	ADS45044	Ads45044 Bacterial
29	79	8.4	1066	5	ABP65862	Abp65862 Bifidobac
30	78.5	8.3	119	7	ADE31190	Ade31190 Human dia
31	78.5	8.3	485	5	AAE24847	Aae24847 Infectiou
32	77.5	8.2	371	5	ABR38848	Abr38848 A. niger
33	77.5	8.2	530	7	ADD46192	Add46192 Rat Prote
34	77	8.2	700	7	ABO80326	Abo80326 Pseudomon
35	76.5	8.1	834	7	ADC07804	Adc07804 Rice prot
36	76	8.1	227	6	ABU11390	Abu11390 Protein e
37	76	8.1	583	5	ABG69062	Abg69062 Amino aci
38	76	8.1	583	7	ADC68369	Adc68369 Lolium pe
39	76	8.1	583	9	AEB03072	Aeb03072 Fructan b
40	76	8.1	1073	5	ABP73320	Abp73320 Candida a
41	75.5	8.0	430	7	ADM05547	Adm05547 Human pro
42	75.5	8.0	430	9	AEC88477	Aec88477 Human cDN
43	75.5	8.0	591	8	ADN19131	Adn19131 Bacterial
44	75.5	8.0	36946	9	ADV97835	Adv97835 Murine pr
45	75	8.0	496	8	ABM82004	Abm82004 Tumour-as

ALIGNMENTS

RESULT 1
ADC16591
ID ADC16591 standard; protein; 172 AA.
XX
AC ADC16591;
XX
DT 18-DEC-2003 (first entry)
XX
DE Scytalone dehydrogenase #SEQ ID 2.
XX
KW Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor.
XX
OS Magnaporthe grisea.
XX
PN WO2003076628-A1.
XX
PD 18-SEP-2003.
XX
PF 24-FEB-2003; 2003WO-JP001980.
XX
PR 12-MAR-2002; 2002JP-00066955.
XX
PA (TSUB) KUMIAI CHEM IND CO LTD.
XX
PI Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;
XX
DR WPI; 2003-748394/70.
DR N-PSDB; ADC16590.
XX
PT Gene encoding for scytalone dehydrogenase (SCDH), useful for screening
PT for SCDH inhibitors and evaluating sensitivity to them.
XX
PS Claim 1; SEQ ID NO 2; 50pp; Japanese.
XX
CC The invention relates to a gene encoding scytalone dehydrogenase (SCDH),
CC that functions in the presence of an inhibitor, comprising an optionally
CC mutated, defined amino acid sequence given in the specification. Also
CC disclosed is a method for evaluating rice blast fungus (Pyricularia
CC oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase
CC inhibitors. The gene is useful for screening for new SCDH inhibitors and
CC evaluating sensitivity to them. The current sequence represents the
CC Scytalone dehydrogenase amino acid sequence.
XX
SQ Sequence 172 AA;

Query Match 100.0%; Score 942; DB 7; Length 172;

```
  Best Local Similarity   100.0%;  Pred. No. 1.2e-95;
  Matches  172;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60

Qy         61 MPAEEFVGMVSSKQMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MPAEEFVGMVSSKQMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE 120

Qy        121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172


RESULT 2
ADC16593
ID   ADC16593 standard; protein; 172 AA.
XX
AC   ADC16593;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Scytalone dehydrogenase #SEQ ID 4.
XX
KW   Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor.
XX
OS   Magnaporthe grisea.
XX
PN   WO2003076628-A1.
XX
PD   18-SEP-2003.
XX
PF   24-FEB-2003; 2003WO-JP001980.
XX
PR   12-MAR-2002; 2002JP-00066955.
XX
PA   (TSUB ) KUMIAI CHEM IND CO LTD.
XX
PI   Kaku K,  Watanabe S,  Kawai K,  Shimizu T,  Nagayama K;
XX
DR   WPI; 2003-748394/70.
DR   N-PSDB; ADC16592.
XX
PT   Gene encoding for scytalone dehydrogenase (SCDH), useful for screening
PT   for SCDH inhibitors and evaluating sensitivity to them.
XX
PS   Claim 7; SEQ ID NO 4; 50pp; Japanese.
XX
CC   The invention relates to a gene encoding scytalone dehydrogenase (SCDH),
CC   that functions in the presence of an inhibitor, comprising an optionally
CC   mutated, defined amino acid sequence given in the specification. Also
CC   disclosed is a method for evaluating rice blast fungus (Pyricularia
CC   oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase
CC   inhibitors. The gene is useful for screening for new SCDH inhibitors and
CC   evaluating sensitivity to them. The current sequence represents the
CC   Scytalone dehydrogenase amino acid sequence.
XX
SQ   Sequence 172 AA;

  Query Match             99.6%;  Score 938;  DB 7;  Length 172;
  Best Local Similarity   99.4%;  Pred. No. 3.3e-95;
  Matches  171;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60

Qy         61 MPAEEFVGMVSSKQMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE 120
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MPAEEFVGMVSSKQVLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE 120

Qy        121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172


RESULT 3
ADA32883
ID   ADA32883 standard; protein; 153 AA.
XX
AC   ADA32883;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Acinetobacter baumannii protein #44.
XX
KW   Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
KW   plant biocontrol agent.
XX
OS   Acinetobacter baumannii.
XX
PN   US6562958-B1.
XX
PD   13-MAY-2003.
XX
PF   04-JUN-1999;   99US-00328352.
XX
PR   09-JUN-1998;   98US-0088701P.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
XX
PI   Breton G,  Bush D;
XX
DR   WPI; 2003-576092/54.
DR   N-PSDB; ADA28757.
XX
PT   New Acinetobacter baumanii proteins and nucleic acids, useful as reagents
PT   for diagnosing a bacterial disease, as components of antibacterial
PT   vaccines, as targets for antibacterial drugs, or as biocontrol agents for
PT   plants.
XX
PS   Example; SEQ ID NO 4170; 328pp; English.
XX
CC   The invention relates to isolated Acinetobacter baumannii nucleic acids.
CC   The A. baumannii nucleic acids and polypeptides are useful as reagents
CC   for diagnosing a bacterial disease, as components of antibacterial
CC   vaccines, as targets for antibacterial drugs, to detect the presence of
CC   A. baumannii and other Acinetobacter species in a sample, in screening
CC   compounds for the ability to interfere with the A. baumannii life cycle
CC   or to inhibit A. baumannii infection, and as biocontrol agents for
CC   plants. The present sequence represents the amino acid sequence of an A.
CC   baumannii protein.
XX
SQ   Sequence 153 AA;

  Query Match             10.0%;  Score 94.5;  DB 6;  Length 153;
  Best Local Similarity   23.0%;  Pred. No. 0.062;
  Matches   31;  Conservative   28;  Mismatches   59;  Indels   17;  Gaps    6;

Qy         15 DYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGMVSSKQ 74
              ||  ::  :  :   :| |:||   :::|  | :||  |  :    :   |: |  | :|
Db         13 DYHRILEVITRFQLVFDQKNWDAFDELLADQLEVDYLQFRGEPLCVVSCHEYKG--SRQQ 70

Qy         75 MLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHW 134
                |    || || :       :: :|:       |   :| |:       :   : ||   ::
Db         71 ALSH--LRLQHNLSNP-LIRIEQDQA----WLECNYQIYR------FSENDYFHSFGRYY 117

Qy        135 Y--KKIDGVWKFAGL 147
              :   |  |:||  |:
Db        118 FTLAKQQGIWKITGI 132


RESULT 4
AAE38266
```

ID AAE38266 standard; protein; 924 AA.
XX
AC AAE38266;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice disease resistance protein, LOX1.
XX
KW Rice; abiotic stress tolerance; pathogen resistance; disease resistance;
KW grain quality; nutritional content; plant yield; LOX1; plant.
XX
OS Oryza sativa.
XX
PN WO2003048319-A2.
XX
PD 12-JUN-2003.
XX
PF 27-NOV-2002; 2002WO-US038359.
XX
PR 30-NOV-2001; 2001US-0334501P.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Sainz MB, Salmeron J, Weislo L;
XX
DR WPI; 2003-505288/47.
DR N-PSDB; AAD57634.
XX
PT New nucleic acid from Oryza sativa, useful for altering abiotic stress
PT tolerance, pathogen or disease resistance or the grain quality,
PT nutritional content or yield in a plant.
XX
PS Claim 1; Page 133-137; 223pp; English.
XX
CC The invention relates to nucleic acid molecules from rice encoding
CC proteins for abiotic stress tolerance, enhanced pathogen or disease
CC resistance and altered nutritional quality. The sequences of the
CC invention are useful for altering abiotic stress tolerance, pathogen or
CC disease resistance or the grain quality, nutritional content or yield in
CC a plant. The present sequence is rice disease resistance protein, LOX1
XX
SQ Sequence 924 AA;

Query Match 9.2%; Score 87; DB 6; Length 924;
Best Local Similarity 23.0%; Pred. No. 4.7;
Matches 34; Conservative 16; Mismatches 44; Indels 54; Gaps 7;

```
Qy          55 DKLW----EAMPAEEFVGMVSSKQMLGDPTLRTQHFI-----------GGTRWEKV--- 95
               ||||    ||:||:    :|       |||   :| :           |   |: :
Db         654 DKLWRFDTEALPAD----LVRRGMAEEDPT--AEHGLKLAIEDYPFANDGLLIWDAIKTW 707

Qy          96 ----------SEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDG----- 140
                       | | |  :|:            ||  |||    :  |: |:|
Db         708 VQAYVARFYPDADSVAGDEELQ--------AFWTEVRTKGHGDKKDAPWWPKLDSPESLA 759

Qy         141 ------VWKFAGLKPDIRWGEFDFDRIF 162
                    ||  |     : :|::||   |
Db         760 HTLTTIVWVAAAHHAAVNFGQYDFGGYF 787
```

RESULT 5
AEB40857
ID AEB40857 standard; protein; 331 AA.
XX
AC AEB40857;
XX
DT 08-SEP-2005 (first entry)
XX
DE L. pneumophila protein SEQ ID NO 5189.
XX
KW detection; infection; Antibacterial; Vaccine.
XX
OS Legionella pneumophila.
XX
PN WO2005049642-A2.
XX
PD 02-JUN-2005.
XX
PF 23-SEP-2004; 2004WO-IB003578.
XX
PR 21-NOV-2003; 2003FR-00013687.
XX
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;
PI Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;
PI Jarraud S;
XX
DR WPI; 2005-388305/40.
XX
PT New genome of Legionella pneumophila Paris strain and derived
PT polypeptides, useful for detection or identification of the strain and
PT for treatment and prevention of infections.
XX
PS Claim 3; SEQ ID NO 5189; 660pp; English.
XX
CC The invention relates to an isolated or purified nucleotide sequences (I)
CC from Legionella pneumophila Paris strain. (I), and their related
CC sequences or fragments, are useful as primers and probes for detection
CC and amplification, including differentiation between the Paris and
CC Philadelphia strains of Legionella pneumophila and to prepare recombinant
CC (hybrid) polypeptides (II). (II) are also useful for preparation of
CC specific antibodies (Ab), also used for detection/identification of
CC Legionella, and some (I), specifically those involved in synthesis of
CC surface proteins, are targets for identification of inhibitors. (II), or
CC vectors that contain (I), are useful as vaccines and immunogenic
CC compositions, for treatment and prevention of infections by L.
CC pneumophila. The present squence represents the amino acid sequence of a
CC L. pneumophila protein.
XX
SQ Sequence 331 AA;

Query Match 9.2%; Score 86.5; DB 9; Length 331;
Best Local Similarity 22.8%; Pred. No. 1.3;
Matches 26; Conservative 20; Mismatches 51; Indels 17; Gaps 2;

```
Qy          74 QMLGDPTLRTQHFIGGTR-------WEKVSEDEVIGYHQLRVPHQRYK----------DT 116
               |:|||    :  :|         |:::::   :|   :|:||| |:          :
Db          13 QILGDGACHSGSELGNALKISRSAVWKQINQLNDLGIPIIRIPHQGYQLEKPLILLDSNE 72

Qy         117 TMKEVTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFG 170
                 |::  || :   ||| :  ||   ::    |     |     :   ||  ||
Db          73 ITKQLHSKGFSQPFNLHLFTSIDSTNRYLKDLPSSSAVEICCTEMQTQGRGRFG 126
```

RESULT 6
AEB37544
ID AEB37544 standard; protein; 332 AA.
XX
AC AEB37544;
XX
DT 08-SEP-2005 (first entry)
XX
DE L. pneumophila protein SEQ ID NO 1876.
XX
KW detection; infection; Antibacterial; Vaccine.
XX
OS Legionella pneumophila.
XX
PN WO2005049642-A2.
XX
PD 02-JUN-2005.
XX

PF 23-SEP-2004; 2004WO-IB003578.
XX
PR 21-NOV-2003; 2003FR-00013687.
XX
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;
PI Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;
PI Jarraud S;
XX
DR WPI; 2005-388305/40.
XX
PT New genome of Legionella pneumophila Paris strain and derived
PT polypeptides, useful for detection or identification of the strain and
PT for treatment and prevention of infections.
XX
PS Claim 3; SEQ ID NO 1876; 660pp; English.
XX
CC The invention relates to an isolated or purified nucleotide sequences (I)
CC from Legionella pneumophila Paris strain. (I), and their related
CC sequences or fragments, are useful as primers and probes for detection
CC and amplification, including differentiation between the Paris and
CC Philadelphia strains of Legionella pneumophila and to prepare recombinant
CC (hybrid) polypeptides (II). (II) are also useful for preparation of
CC specific antibodies (Ab), also used for detection/identification of
CC Legionella, and some (I), specifically those involved in synthesis of
CC surface proteins, are targets for identification of inhibitors. (II), or
CC vectors that contain (I), are useful as vaccines and immunogenic
CC compositions, for treatment and prevention of infections by L.
CC pneumophila. The present squence represents the amino acid sequence of a
CC L. pneumophila protein.
XX
SQ Sequence 332 AA;

Query Match 9.2%; Score 86.5; DB 9; Length 332;
Best Local Similarity 22.8%; Pred. No. 1.3;
Matches 26; Conservative 20; Mismatches 51; Indels 17; Gaps 2;

```
Qy         74 QMLGDPTLRTQHFIGGTR-------WEKVSEDEVIGYHQLRVPHQRYK----------DT 116
              |:|||    :   :|          |:::::   :|   :|:||| |:          :
Db         14 QILGDGACHSGSELGNALKISRSAVWKQINQLNDLGIPIIRIPHQGYQLEKPLILLDSNE 73

Qy        117 TMKEVTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFG 170
                |::  || :   ||| :  ||  ::    |     |     :   ||  ||
Db         74 ITKQLHSKGFSQPFNLHLFTSIDSTNRYLKDLPSSSAVEICCTEMQTQGRGRFG 127
```

RESULT 7
AAW98720
ID AAW98720 standard; protein; 265 AA.
XX
AC AAW98720;
XX
DT 31-MAR-1999 (first entry)
XX
DE H. pylori GHPO 811 protein.
XX
KW GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis;
KW peptic ulcer disease.
XX
OS Helicobacter pylori.
XX
PN WO9843478-A1.
XX
PD 08-OCT-1998.
XX
PF 01-APR-1998; 98WO-US006371.
XX
PR 01-APR-1997; 97US-00833457.
PR 24-JUN-1997; 97US-00881227.
PR 29-JUL-1997; 97US-00902615.
XX
PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Kleanthous H, Al-Garawi A, Miller C, Tomb J, Oomen RP;
XX
DR WPI; 1998-542293/46.
DR N-PSDB; AAX14439.
XX
PT New isolated Helicobacter polynucleotides - used to develop products for
PT the diagnosis, prevention and treatment of Helicobacter infections and
PT gastrointestinal diseases.
XX
PS Claim 8; Page 1521-1522; 2054pp; English.
XX
CC This sequence represents a Helicobacter pylori GHPO protein of the
CC invention. The polypeptides can be used for preventing or treating
CC Helicobacter infections, and gastroduodenal diseases associated with
CC these infections, including acute, chronic, and atrophic gastritis, and
CC peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be
CC used for the production of antibodies. The products can also be used for
CC detection and diagnosis
XX
SQ Sequence 265 AA;

Query Match 9.0%; Score 85; DB 2; Length 265;
Best Local Similarity 22.4%; Pred. No. 1.5;
Matches 39; Conservative 28; Mismatches 57; Indels 50; Gaps 7;

```
Qy         13 FSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKL--WEAMPAEEFVGMV 70
              |  ::|       ::||  ::   |:: |: |   :|  ||| :   |    | : :|:|
Db        102 FYQFVG-------FSDSCKNRRRXRVKCVLLPNESVDSLSFLYRSANWSEREAYDMLGIV 154

Qy         71 SSK----------QMLGDPTLRTQHFIGG--TRWEKVSE------DEVIGYHQ------ 105
                |            :| | ||:    |    :| :| :       ||:|  |
Db        155 FDKHPYLKRLIMPHDWVGHPLLRSYPLKGDEFAQWYEVDKIFGKEYREVVGKEQRDSARV 214

Qy        106 --------LRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDGVWKFAGLKPDI 151
                    :: ::: |   :|||  |        | :|||  |     : | |
Db        215 DEKDTFNFAKIGYEQGKGEELKEVEEK--------HAFKKIPFVKDLHKIAPTI 260
```

RESULT 8
ADF04364
ID ADF04364 standard; protein; 338 AA.
XX
AC ADF04364;
XX
DT 12-FEB-2004 (first entry)
XX
DE Bacterial polypeptide #477.
XX
KW Proteus mirabilis infection; bacterial infection; antibacterial;
KW immunostimulant.
XX
OS Proteus mirabilis.
XX
PN US6605709-B1.
XX
PD 12-AUG-2003.
XX
PF 05-APR-2000; 2000US-00543681.
XX
PR 09-APR-1999; 99US-0128706P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Breton GL;
XX
DR WPI; 2003-895291/82.
DR N-PSDB; ADF00192.
XX

PT New Proteus mirabilis polypeptides and polynucleotides, useful as
PT reagents for diagnosis of bacterial disease, as components of
PT antibacterial vaccines, as targets for antibacterial drugs, or as
PT biocontrol agents for plants.
XX
PS Disclosure; SEQ ID NO 4649; 870pp; English.
XX
CC The invention relates to new Proteus mirabilis polypeptides and
CC polynucleotides. The invention also relates to antibodies against the
CC polypeptides, methods for producing the polypeptides, a method of
CC generating vaccines for immunising an individual against P. mirabilis, a
CC method for evaluating a compound for the ability to bind a P. mirabilis
CC polypeptide and a method for screening test compounds for anti-bacterial
CC activity. The polypeptides and polynucleotides are useful as molecular
CC targets for diagnosing, preventing and treating pathological conditions
CC resulting from bacterial infection, as reagents for diagnosis of
CC bacterial diseases, as components of antibacterial vaccines, as targets
CC for antibacterial drugs or as bio-control agents for plants. This
CC sequence represents a Proteus mirabilis polypeptide of the invention.
XX
SQ Sequence 338 AA;

Query Match 8.9%; Score 84; DB 7; Length 338;
Best Local Similarity 25.5%; Pred. No. 2.6;
Matches 39; Conservative 18; Mismatches 42; Indels 54; Gaps 10;

```
Qy         35 WDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPTLR-TQHFIGGTRWE 93
              ||: ::             |||::|  | : ||       || |  ||  :| :  | ||
Db         94 WDKAQR----------EDVLDKMFETAP-QSFV-------MLADLCLRGAKHTLQRTSWE 135

Qy         94 KVSEDEVIGYHQLR---------VPHQRYKDTTMKEVTMKGHAHSANLHWYKK--IDGVW 142
               :   |:|   :|:          |||    |     :  ||   :|  |  |    | :|
Db        136 GI---EII--ERLKAQGRNVIFMVPHGWAVDVPAMLLAAKGQKMAAMFHHQKDPVTDYLW 190

Qy        143 -------------KFAGLKPDIR------WGEF 156
                          : ||:|| |       || :
Db        191 NKARYHFGGRLHSREAGIKPFISTVRQGFWGYY 223
```

RESULT 9
AAE12983
ID AAE12983 standard; protein; 349 AA.
XX
AC AAE12983;
XX
DT 28-JAN-2002 (first entry)
XX
DE Murine Wnt-7B protein.
XX
KW Mouse; Wnt-7B-like protein; gene therapy; hypotensive; neoplasia; cancer;
KW tranquillizer; inflammatory disorder; arthritis; haematopoiesis; allergy;
KW immune disorder; autoimmune disease; thyroiditis; restenosis; thrombosis;
KW neurological disease; Alzheimer's disease; cardiovascular disorder; burn;
KW diabetes mellitus; periodontal disease; haemorrhage; multiple sclerosis;
KW rheumatoid arthritis; thrombocytopaenia; skin disorder; atherosclerosis;
KW lung fibrosis; skeletal disorder; platelet disorder; cell proliferation;
KW transplant rejection; acquired immune deficiency syndrome; AIDS; wound;
KW connective tissue disease; drug screening; ulcer; liver fibrosis.
XX
OS Mus musculus.
XX
PN WO200174856-A2.
XX
PD 11-OCT-2001.
XX
PF 03-APR-2001; 2001WO-US010679.
XX
PR 03-APR-2000; 2000US-0194256P.
PR 26-JUL-2000; 2000US-00625634.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Vernet CAM, Rastelli L, Herrmann JL;
XX
DR WPI; 2001-626382/72.
XX
PT New Wnt-7B-like polypeptides and polynucleotides for diagnosing,
PT preventing and treating broad range of pathological states such as
PT cancer, hematopoietic, inflammatory, skin, skeletal disorders and
PT atherosclerosis.
XX
PS Claim 15; Fig 2B; 115pp; English.
XX
CC The invention relates to human Wnt-7B-like protein and its cDNA molecule.
CC Human Wnt-7B-like proteins and their nucleic acids are useful for
CC treating and preventing Wnt-7B-like-associated disorders such as
CC neoplasia, cancer, e.g., colorectal carcinoma, prostate cancer, immune
CC disorder, autoimmune diseases, such as connective tissue disease,
CC multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis,
CC acquired immune deficiency syndrome (AIDS), transplant rejection,
CC allergy, infection, inflammatory disorder, arthritis, haematopoietic
CC disorder, skin disorder (keloid), restenosis, neurological disease,
CC Alzheimer's disease, trauma, wound, spinal cord injury, skeletal disorder
CC and cardiovascular disorders such as diabetes mellitus, atherosclerosis,
CC cerebral thrombosis or haemorrhage, and other diseases, including
CC hypertension, hypothyroidism, myeloid or lymphoid cell deficiencies and
CC various platelet disorders such as thrombocytopaenia. Wnt-7B-like protein
CC is also useful for cell proliferation, tissue repair and in the treatment
CC of burns, incisions and ulcers, periodontal disease and treatment of lung
CC or liver fibrosis. Wnt-7B-like protein plays an important role in
CC autocrine stimulation of tumour growth, chemoresistance, radiotherapy
CC resistance and also for screening drugs. Wnt-7B-like nucleic acids are
CC useful in gene therapy. The present sequence is murine Wnt-7B protein
CC related to the invention
XX
SQ Sequence 349 AA;

Query Match 8.9%; Score 84; DB 4; Length 349;
Best Local Similarity 31.1%; Pred. No. 2.7;
Matches 32; Conservative 11; Mismatches 36; Indels 24; Gaps 7;

```
Qy         84 QHFIGGTRW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-------ANLH- 133
              ||     ||    : |  | |  :|||  :    |    :|  | ||:         ||
Db         74 QHQFRFGRWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSN 130

Qy        134 ---------WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                      :| : :| ||: |   |:|:|  || | | | ||
Db        131 CGCDREKQGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171
```

RESULT 10
ADS31850
ID ADS31850 standard; protein; 349 AA.
XX
AC ADS31850;
XX
DT 30-DEC-2004 (first entry)
XX
DE Mouse wingless Wnt7b.
XX
KW vulnerary; cell therapy; cartilage formation;
KW fibroblast growth factor 18; FGF-18; sonic hedgehog; Shh; beta-catenin;
KW Wnt; tissue repair; tissue reconstructon; airway; trachea; bronchi; lung;
KW larynx; mouse; Wnt7b.
XX
OS Mus musculus.
XX
PN WO2004087055-A2.
XX
PD 14-OCT-2004.
XX
PF 26-MAR-2004; 2004WO-US009264.
XX
PR 27-MAR-2003; 2003US-0458224P.
XX
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

```
XX
PI   Whitsett JA;
XX
DR   WPI; 2004-729163/71.
DR   N-PSDB; ADS31849.
XX
PT   New pharmaceutical composition comprising a cartilage formation inducing
PT   protein, e.g., fibroblast growth factor (FGF)-18, sonic hedgehog (Shh),
PT   beta-catenin or Wnt proteins, useful in repairing tissues in a conducting
PT   airway.
XX
PS   Disclosure; SEQ ID NO 14; 94pp; English.
XX
CC   The invention describes a new pharmaceutical composition comprises at
CC   least one cartilage formation inducing protein consisting of fibroblast
CC   growth factor (FGF)-18, sonic hedgehog (Shh), beta-catenin or Wnt
CC   proteins to induce cartilage formation. Also described are: inducing
CC   cartilage formation in an affected area of a patient requiring such
CC   treatment; an expression vector comprising at least one nucleotide
CC   sequence encoding at least one cartilage formation inducing protein
CC   consisting of FGF-18, Shh, beta-catenin or Wnt proteins; expressing FGF-
CC   18 protein in a cell in vitro; treating a patient in need of cartilage
CC   formation in an affected area of the patient; a cell culture comprising
CC   cells, in a medium capable of sustaining cell growth, having an
CC   expression vector comprising at least one nucleotide sequence encoding at
CC   least one cartilage formation inducing protein consisting of FGF-18, Shh,
CC   beta-catenin or Wnt proteins; and preparing a cell culture comprising
CC   cells capable of inducing cartilage formation in vitro in a medium
CC   capable of sustaining cell growth. The pharmaceutical composition is
CC   useful in inducing cartilage formation for repairing and reconstructing
CC   various tissues in a conducting airway, e.g., trachea, bronchi, lung or
CC   larynx of a patient. This is the amino acid sequence of mouse Wnt7b.
CC   Note: The sequence listing of this specification was not finished upon
CC   filing resulting in the loss of SEQ ID NO 1 and the N-terminal end of SEQ
CC   ID NO 2.
XX
SQ   Sequence 349 AA;

  Query Match             8.9%;  Score 84;  DB 8;  Length 349;
  Best Local Similarity   31.1%;  Pred. No. 2.7;
  Matches   32;  Conservative   11;  Mismatches   36;  Indels   24;  Gaps    7;

Qy         84 QHFIGGTRW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-------ANLH- 133
              ||      ||    : |  | |  :|||  :    |    :|  | ||:          ||
Db         74 QHQFRFGRWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSN 130

Qy        134 ---------WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                      :| : :| ||: |   |:|:|  || | | | ||
Db        131 CGCDREKQGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171


RESULT 11
ADU86486
ID   ADU86486 standard; protein; 349 AA.
XX
AC   ADU86486;
XX
DT   24-FEB-2005  (first entry)
XX
DE   Mouse wingless-type protein, Wnt7B.
XX
KW   Wnt; wingless-type protein; neurogenesis; spinal cord injury; injury;
KW   parkinsons disease; antiparkinsonian; neurological disease;
KW   motor neurone disease; neuroprotective; paralysis.
XX
OS   Mus musculus.
XX
PN   WO2004103394-A2.
XX
PD   02-DEC-2004.
XX
PF   17-MAY-2004; 2004WO-US015264.
XX
PR   15-MAY-2003; 2003US-0470913P.
XX
PA   (UYCH-) UNIV CHICAGO.
XX
PI   Zou Y;
XX
DR   WPI; 2004-834171/82.
DR   N-PSDB; ADU86485.
XX
PT   Modulating growth of a neuron for treating spinal cord disorder or
PT   paralysis comprises contacting the neuron with a Wnt, a Wnt-like
PT   substance, and/or a chemical compound affecting a Wnt signaling pathway.
XX
PS   Disclosure; SEQ ID NO 60; 248pp; English.
XX
CC   The invention relates to modulating growth of a neuron comprises
CC   contacting the neuron with a Wnt (wingless-type protein), a Wnt-like
CC   substance, and/or a chemical compound affecting a Wnt signaling pathway.
CC   Also included are a method for identifying a substance that modulates
CC   growth of a neuron, a pharmaceutical composition for modulating growth of
CC   a neuron in a mammal (comprising a Wnt, a Wnt-like substance, or a
CC   chemical compound affecting a Wnt signaling pathway and a pharmaceutical
CC   preparation suitable for delivery to the mammal) and a method of
CC   inhibiting growth of a neuron in a subject. The neuron is a neuron in a
CC   spinal cord that has been damaged by traumatic spinal cord injury.
CC   Inhibiting growth of a neuron in a subject comprises providing a
CC   composition (comprising a secreted frizzled-related protein (sFRP), sFRP-
CC   like substance, Ryk or Ryk-like substance and a pharmaceutical
CC   preparation suitable for delivery to the subject and administering the
CC   composition to the subject. sFRP and Ryk are both proteins that bind to
CC   block the activity of Wnt. The method is useful for modulating growth of
CC   a neuron for preparing a composition for treating spinal cord disorder,
CC   paralysis, Parkinson's disease and motor neurone disease. The present
CC   sequence represents a Wnt protein from human or mouse.
XX
SQ   Sequence 349 AA;

  Query Match             8.9%;  Score 84;  DB 8;  Length 349;
  Best Local Similarity   31.1%;  Pred. No. 2.7;
  Matches   32;  Conservative   11;  Mismatches   36;  Indels   24;  Gaps    7;

Qy         84 QHFIGGTRW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-------ANLH- 133
              ||      ||    : |  | |  :|||  :    |    :|  | ||:          ||
Db         74 QHQFRFGRWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSN 130

Qy        134 ---------WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                      :| : :| ||: |   |:|:|  || | | | ||
Db        131 CGCDREKQGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171


RESULT 12
AED95375
ID   AED95375 standard; protein; 349 AA.
XX
AC   AED95375;
XX
DT   26-JAN-2006  (first entry)
XX
DE   Mouse Wnt7B protein SEQ ID NO:46.
XX
KW   cell proliferation; cell regeneration; Wnt signaling pathway; cardiant;
KW   antiarteriosclerotic; vasotropic; cytostatic; myocardial infarction;
KW   atherosclerosis; coronary artery disease; myocardial disease;
KW   cardiac failure; heart disease; cancer; Wnt7B.
XX
OS   Mus musculus.
XX
PN   US2005261189-A1.
XX
PD   24-NOV-2005.
XX
PF   18-APR-2005; 2005US-00108528.
XX
```

PR 16-APR-2004; 2004US-0563137P.
PR 02-AUG-2004; 2004US-0598368P.
XX
PA (HYDR-) HYDRA BIOSCIENCES INC.
XX
PI Larsen G, Marvin M, Li DY, Wang E, Chen CMA, Shamah SM;
XX
DR WPI; 2006-008454/01.
DR N-PSDB; AED95374.
DR GENBANK; NM_009528.
XX
PT Promoting neonatal or adult cardiac cell proliferation or regeneration,
PT by contacting a cell with a composition comprising an agent that acts at
PT the cell surface to promote signaling via the canonical Wnt signaling
PT pathway.
XX
PS Disclosure; SEQ ID NO 46; 203pp; English.
XX
CC The invention relates to a method for promoting neonatal or adult cardiac
CC cell proliferation and/or regeneration. The method comprises contacting
CC the cell with a composition comprising an agent that acts at the cell
CC surface to promote signaling via the canonical Wnt signaling pathway,
CC where the cell is contacted with an amount of the composition to promote
CC neonatal or adult cardiac cell proliferation and/or regeneration. Also
CC described: (1) treating a condition having cardiac cell injury or death;
CC (2) treating a developmental disorder of cardiac cells; and (3) a
CC modified polypeptide comprising a Wnt-related polypeptide or bioactive
CC fragment, appended with one or more moieties to produce a modified Wnt-
CC related polypeptide or bioactive fragment, where the modified Wnt-related
CC polypeptide or bioactive fragment promotes Wnt signaling via the
CC canonical Wnt signaling pathway. The Wnt polypeptide or bioactive
CC fragment is useful in the manufacture of a medicament for promoting
CC cardiac cell proliferation and/or regeneration, where the Wnt
CC polypeptide, or bioactive fragment promotes Wnt signaling via the
CC canonical Wnt signaling pathway, and where the Wnt polypeptide or
CC bioactive fragment is modified with one or more moieties to produce a
CC modified Wnt polypeptide or bioactive fragment. The method is useful for
CC promoting neonatal or adult cardiac cell proliferation and/or
CC regeneration. The Wnt polypeptide is also useful for treating cardiac
CC cell injury or death, e.g. myocardial infarction, atherosclerosis,
CC coronary artery disease, obstructive vascular disease, dilated
CC cardiomyopathy, heart failure, myocardial necrosis, valvular heart
CC disease, non-compaction of the ventricular myocardium, hypertrophic
CC cardiomyopathy, cancer or cancer-related conditions such as structural
CC defects resulting from cancer or cancer treatments. The present sequence
CC represents mouse Wnt7B, which is used in the exemplification of the
CC present invention. Mouse Wnt7B is located on chromosome 15.
XX
SQ Sequence 349 AA;

Query Match 8.9%; Score 84; DB 10; Length 349;
Best Local Similarity 31.1%; Pred. No. 2.7;
Matches 32; Conservative 11; Mismatches 36; Indels 24; Gaps 7;

```
Qy          84 QHFIGGTRW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-------ANLH- 133
               ||     ||    : |  | |  :|||  :    |    :|  | ||:         ||
Db          74 QHQFRFGRWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSN 130

Qy         134 ---------WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                       :| : :| ||: |   |:|:|  || | | | ||
Db         131 CGCDREKQGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171
```

RESULT 13
ADX93641
ID ADX93641 standard; protein; 411 AA.
XX
AC ADX93641;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polypeptide seqid 56305.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
DR WPI; 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 56305; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 411 AA;

Query Match 8.9%; Score 84; DB 8; Length 411;
Best Local Similarity 25.2%; Pred. No. 3.4;
Matches 35; Conservative 17; Mismatches 31; Indels 56; Gaps 10;

```
Qy          26 WADSYDSKDW-DRLRKVIAPTLRIDYRSF--------LDK-----LW-EAMPAEEFVGMV 70
               | | :||  | | : : | | ||:  : |         ||:     ||  |:| :  | |
Db         171 WKDVFDSASWEDLIVRYIIPKLRLALQDFQINPANQKLDQFNWVMLWTSAIPVQLMVHM- 229

Qy          71 SSKQMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSA 130
                        |    |   ::|::|       || |  |:  : :
Db         230 ----------LEVDFF---SKWQQVL------YHWLCSPNPDFNEI-------------- 256

Qy         131 NLHWYKKIDGVWKFAGLKP 149
                 ::|||     ||  || |
```

```
Db        257 -MNWYKG----WK--GLFP 268
```

RESULT 14
AAR61136
ID AAR61136 standard; protein; 923 AA.
XX
AC AAR61136;
XX
DT 18-MAY-1995 (first entry)
XX
DE Plant blight-specific resistance lipoxygenase.
XX
KW Plant blight specific resistance lipoxygenase; chloroplast; resistant;
KW blight; gene expression; recombinant production.
XX
OS Oryza sativa.
XX
PN JP06225774-A.
XX
PD 16-AUG-1994.
XX
PF 16-JUN-1992; 92JP-00180552.
XX
PR 16-JUN-1992; 92JP-00180552.
XX
PA (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
XX
DR WPI; 1994-298802/37.
DR N-PSDB; AAQ68842.
XX
PT Plant blight resistance-specific lipoxygenase gene - useful for
PT expression of proteins in the chloroplast.
XX
PS Claim 2; Page 5-11; 13pp; Japanese.
XX
CC The cDNA encoding the blight resistance-specific lipoxygenase (See
CC AAQ68842) is useful for the elucidation of the mechanism of blight
CC resistance in plants and makes possible the expression of various
CC proteins in the chloroplast. The cDNA may also be expressed in bacterial,
CC animal or plant cells to recombinantly produce the blight resistance-
CC specific lipoxygenase
XX
SQ Sequence 923 AA;

```
  Query Match             8.8%;  Score 83;  DB 2;  Length 923;
  Best Local Similarity   23.3%;  Pred. No. 13;
  Matches   34;  Conservative   16;  Mismatches   46;  Indels   50;  Gaps    7;

Qy         55 DKLW----EAMPAEEFVGMVSSKQMLGDPT------LRTQHF----IGGTRWEKV----- 95
              ||||    ||:||:    :|       |||      |  : :     |   |: :
Db        653 DKLWRFDTEALPAD----LVRRGMAEEDPTAEQGLKLAIEDYPFANDGLLIWDAIKTWVQ 708

Qy         96 --------SEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDG------- 140
                      | | |  :|:            ||  |||    :  |: |:|
Db        709 AYVARFYPDADSVAGDEELQ--------AFWTEVRTKGHGDKKDAPWWPKLDSPESLAHT 760

Qy        141 ----VWKFAGLKPDIRWGEFDFDRIF 162
                  ||  |     : :|::||   |
Db        761 LTNIVWVAAAHHAAVNFGQYDFGGYF 786
```

RESULT 15
AAE12982
ID AAE12982 standard; protein; 349 AA.
XX
AC AAE12982;
XX
DT 28-JAN-2002 (first entry)
XX
DE Human Wnt-7B-like protein from clone 29518614.0.61.
XX
KW Human; Wnt-7B-like protein; gene therapy; hypotensive; neoplasia; cancer;
KW tranquillizer; inflammatory disorder; arthritis; haematopoiesis; allergy;
KW immune disorder; autoimmune disease; thyroiditis; restenosis; thrombosis;
KW neurological disease; Alzheimer's disease; cardiovascular disorder; burn;
KW diabetes mellitus; periodontal disease; haemorrhage; multiple sclerosis;
KW rheumatoid arthritis; thrombocytopaenia; skin disorder; atherosclerosis;
KW lung fibrosis; skeletal disorder; platelet disorder; cell proliferation;
KW transplant rejection; acquired immune deficiency syndrome; AIDS; wound;
KW connective tissue disease; drug screening; ulcer; liver fibrosis.
XX
OS Homo sapiens.
XX
PN WO200174856-A2.
XX
PD 11-OCT-2001.
XX
PF 03-APR-2001; 2001WO-US010679.
XX
PR 03-APR-2000; 2000US-0194256P.
PR 26-JUL-2000; 2000US-00625634.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Vernet CAM, Rastelli L, Herrmann JL;
XX
DR WPI; 2001-626382/72.
DR N-PSDB; AAD20986.
XX
PT New Wnt-7B-like polypeptides and polynucleotides for diagnosing,
PT preventing and treating broad range of pathological states such as
PT cancer, hematopoietic, inflammatory, skin, skeletal disorders and
PT atherosclerosis.
XX
PS Claim 12; Fig 2A; 115pp; English.
XX
CC The invention relates to human Wnt-7B-like protein and its cDNA molecule.
CC Human Wnt-7B-like proteins and their nucleic acids are useful for
CC treating and preventing Wnt-7B-like-associated disorders such as
CC neoplasia, cancer, e.g., colorectal carcinoma, prostate cancer, immune
CC disorder, autoimmune diseases, such as connective tissue disease,
CC multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis,
CC acquired immune deficiency syndrome (AIDS), transplant rejection,
CC allergy, infection, inflammatory disorder, arthritis, haematopoietic
CC disorder, skin disorder (keloid), restenosis, neurological disease,
CC Alzheimer's disease, trauma, wound, spinal cord injury, skeletal disorder
CC and cardiovascular disorders such as diabetes mellitus, atherosclerosis,
CC cerebral thrombosis or haemorrhage, and other diseases, including
CC hypertension, hypothyroidism, myeloid or lymphoid cell deficiencies and
CC various platelet disorders such as thrombocytopaenia. Wnt-7B-like protein
CC is also useful for cell proliferation, tissue repair and in the treatment
CC of burns, incisions and ulcers, periodontal disease and treatment of lung
CC or liver fibrosis. Wnt-7B-like protein plays an important role in
CC autocrine stimulation of tumour growth, chemoresistance, radiotherapy
CC resistance and also for screening drugs. Wnt-7B-like nucleic acids are
CC useful in gene therapy. The present sequence is human Wnt-7B-like protein
CC which is obtained from clone 29518614.0.61
XX
SQ Sequence 349 AA;

```
  Query Match             8.6%;  Score 81;  DB 4;  Length 349;
  Best Local Similarity   31.2%;  Pred. No. 5.8;
  Matches   30;  Conservative   11;  Mismatches   31;  Indels   24;  Gaps    7;

Qy         91 RW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-------ANLH-------- 133
              ||    :  |  | |  :|||  :    |    :|  | ||:        ||
Db         81 RWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSNCGCDREK 137

Qy        134 --WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                :| : :| ||: |    |:|:|  || | | | ||
Db        138 QGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171
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Search completed: December 5, 2006, 01:22:15
Job time : 202 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: December 5, 2006, 01:19:01 ; Search time 302 Seconds
(without alignments)
526.830 Million cell updates/sec

Title: US-10-507-132-2
Perfect score: 942
Sequence: 1 MGSQVQKSDEITFSDYLGLM.....WGEFDFDRIFEDGRETFGDK 172

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	938	99.6	172	1	SCYD_MAGGR	P56221 magnaporthe
2	698	74.1	186	2	Q6XRI1_9PEZI	Q6xri1 ceratocysti
3	686	72.8	188	1	SCYD_GLOLA	Q00455 glomerella
4	686	72.8	216	2	Q9C426_OPHFL	Q9c426 ophiostoma
5	657	69.7	185	2	Q7Z8L5_9PLEO	Q7z8l5 bipolaris o
6	627.5	66.6	174	2	Q7SBE1_NEUCR	Q7sbe1 neurospora
7	550	58.4	122	2	Q8NJI6_9PEZI	Q8nji6 ophiostoma
8	548.5	58.2	150	2	Q2WEI4_SORMA	Q2wei4 sordaria ma
9	544	57.7	121	2	Q8NJI5_OPHFL	Q8nji5 ophiostoma
10	542	57.5	122	2	Q8NJI7_9PEZI	Q8nji7 ceratocysti
11	540	57.3	121	2	Q8NJI8_9PEZI	Q8nji8 ceratocysti
12	537	57.0	122	2	Q8NIE1_9PEZI	Q8nie1 ophiostoma
13	537	57.0	122	2	Q8NJI2_OPHPI	Q8nji2 ophiostoma
14	532	56.5	121	2	Q8NJI0_OPHPI	Q8nji0 ophiostoma
15	530	56.3	122	2	Q8NJI1_OPHPI	Q8nji1 ophiostoma
16	528	56.1	122	2	Q8NJH8_9PEZI	Q8njh8 ophiostoma
17	526	55.8	168	1	SCYD_ASPFU	O14434 aspergillus
18	522	55.4	122	2	Q8NJI4_9PEZI	Q8nji4 ophiostoma
19	516	54.8	122	2	Q8NJI3_9PEZI	Q8nji3 ophiostoma
20	503	53.4	121	2	Q8NJH9_9PEZI	Q8njh9 ophiostoma
21	427	45.3	161	2	Q4I8I1_GIBZE	Q4i8i1 gibberella
22	332	35.2	1201	2	Q5BH35_EMENI	Q5bh35 aspergillus
23	99.5	10.6	605	2	Q8ZSD9_ANASP	Q8zsd9 anabaena sp
24	92	9.8	185	2	Q5YQ84_NOCFA	Q5yq84 nocardia fa
25	91	9.7	168	2	Q9RB47_9CLOT	Q9rb47 clostridium
26	90	9.6	318	2	Q7TDF4_9VIRU	Q7tdf4 halovirus h
27	89.5	9.5	583	2	Q6BVC7_DEBHA	Q6bvc7 debaryomyce
28	88.5	9.4	530	2	Q2UUC3_ASPOR	Q2uuc3 aspergillus
29	88	9.3	166	1	BAIE_EUBSP	P19412 eubacterium
30	87.5	9.3	333	2	Q5WYB7_LEGPL	Q5wyb7 legionella
31	87	9.2	211	2	Q3IE87_PSEHT	Q3ie87 pseudoalter
32	87	9.2	286	2	Q3G8U4_9FIRM	Q3g8u4 syntrophomo
33	87	9.2	924	1	LOXC1_ORYSA	P38419 oryza sativ
34	87	9.2	941	1	LOXC2_ORYSA	Q84yk8 oryza sativ
35	87	9.2	1277	2	Q2UED8_ASPOR	Q2ued8 aspergillus
36	86.5	9.2	331	2	Q5X6W7_LEGPA	Q5x6w7 legionella
37	86.5	9.2	331	2	Q5ZXE8_LEGPH	Q5zxe8 legionella
38	86	9.1	201	2	Q2IS89_RHOPA	Q2is89 rhodopseudo
39	84.5	9.0	380	2	O26444_METTH	O26444 methanobact
40	84	8.9	349	1	WNT7B_MOUSE	P28047 mus musculu
41	84	8.9	349	2	Q5NSW6_RAT	Q5nsw6 rattus norv
42	84	8.9	353	2	Q6NZR1_MOUSE	Q6nzr1 mus musculu
43	84	8.9	441	2	Q4IDL7_GIBZE	Q4idl7 gibberella
44	84	8.9	1058	2	Q4X125_ASPFU	Q4x125 aspergillus
45	83.5	8.9	468	2	Q7R5D9_GIALA	Q7r5d9 giardia lam

ALIGNMENTS

RESULT 1
SCYD_MAGGR
ID SCYD_MAGGR STANDARD; PRT; 172 AA.
AC P56221;
DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT 15-JUL-1998, sequence version 1.
DT 07-FEB-2006, entry version 34.
DE Scytalone dehydratase (EC 4.2.1.94).
GN Name=Sdh1;
OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
OX NCBI_TaxID=148305;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=98233280; PubMed=9571787;
RA Motoyama T., Imanishi K., Yamaguchi I.;
RT "cDNA cloning, expression, and mutagenesis of scytalone dehydratase
RT needed for pathogenicity of the rice blast fungus, Pyricularia
RT oryzae.";
RL Biosci. Biotechnol. Biochem. 62:564-566(1998).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=95171111; PubMed=7866745;
RA Lundqvist T., Rice J., Hodge C.N., Basarab G.S., Pierce J.,
RA Lindqvist Y.;
RT "Crystal structure of scytalone dehydratase -- a disease determinant
RT of the rice pathogen, Magnaporthe grisea.";
RL Structure 2:937-944(1994).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX MEDLINE=98332516; PubMed=9665698; DOI=10.1021/bi980321b;
RA Nakasako M., Motoyama T., Kurahashi Y., Yamaguchi I.;
RT "Cryogenic X-ray crystal structure analysis for the complex of
RT scytalone dehydratase of a rice blast fungus and its tight-binding
RT inhibitor, carpropamid: the structural basis of tight-binding
RT inhibition.";
RL Biochemistry 37:9931-9939(1998).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).
RX MEDLINE=99119201; PubMed=9922139; DOI=10.1021/bi981848r;
RA Chen J.M., Xu S.L., Wawrzak Z., Basarab G.S., Jordan D.B.;
RT "Structure-based design of potent inhibitors of scytalone dehydratase:
RT displacement of a water molecule from the active site.";
RL Biochemistry 37:17735-17744(1998).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS).
RX MEDLINE=99310043; PubMed=10382670;
RX DOI=10.1002/(SICI)1097-0134(19990601)35:4<425::AID-PROT6>3.3.CO;2-T;
RA Wawrzak Z., Sandalova T., Steffens J.J., Basarab G.S., Lundqvist T.,
RA Lindqvist Y., Jordan D.B.;
RT "High-resolution structures of scytalone dehydratase-inhibitor
RT complexes crystallized at physiological pH.";
RL Proteins 35:425-439(1999).

```
CC   -!- FUNCTION: Catalyzes two steps in melanin biosynthesis. From
CC       scytalone they are two dehydration steps and one reduction step to
CC       yield melanin.
CC   -!- CATALYTIC ACTIVITY: Scytalone = 1,3,8-trihydroxynaphthalene +
CC       H(2)O.
CC   -!- PATHWAY: Fungal melanin biosynthesis; first step.
CC   -!- SUBUNIT: Homotrimer. Each subunit contains an active site, located
CC       in the central part of the hydrophobic core of the monomer, which
CC       functions independently.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB004741; BAA34046.1; -; mRNA.
DR   PDB; 1IDP; X-ray; A/B/C=1-172.
DR   PDB; 1STD; X-ray; @=1-172.
DR   PDB; 2STD; X-ray; @=1-172.
DR   PDB; 3STD; X-ray; A/B/C=10-172.
DR   PDB; 4STD; X-ray; A/B/C=10-172.
DR   PDB; 5STD; X-ray; A/B/C=10-172.
DR   PDB; 6STD; X-ray; A/B/C=10-172.
DR   PDB; 7STD; X-ray; A/B/C=10-172.
DR   LinkHub; P56221; -.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
KW   3D-structure; Lyase; Melanin biosynthesis.
FT   CHAIN         1    172       Scytalone dehydratase.
FT                                /FTId=PRO_0000097639.
FT   HELIX        13     32
FT   TURN         33     33
FT   HELIX        35     39
FT   TURN         40     41
FT   STRAND       42     49
FT   HELIX        51     54
FT   STRAND       55     55
FT   STRAND       57     62
FT   HELIX        63     71
FT   STRAND       72     72
FT   TURN         73     76
FT   TURN         79     80
FT   STRAND       81     83
FT   STRAND       86     96
FT   TURN         97     98
FT   STRAND       99    115
FT   TURN        116    117
FT   STRAND      121    138
FT   TURN        139    140
FT   STRAND      141    155
SQ   SEQUENCE   172 AA;  20250 MW;  2FA56296D5EE00DC CRC64;

  Query Match             99.6%;  Score 938;  DB 1;  Length 172;
  Best Local Similarity   99.4%;  Pred. No. 3e-77;
  Matches  171;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60

Qy         61 MPAEEFVGMVSSKQMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE 120
              |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MPAEEFVGMVSSKQVLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE 120

Qy        121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172


RESULT 2
Q6XR11_9PEZI
ID   Q6XR11_9PEZI   PRELIMINARY;   PRT;   186 AA.
AC   Q6XR11;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Syctalone dehydratase I.
GN   Name=SD1;
OS   Ceratocystis resinifera.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Hypocreomycetidae; Microascales; Microascales incertae sedis;
OC   Ceratocystis.
OX   NCBI_TaxID=95837;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Loppnau P.A.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY214004; AAO60167.1; -; Genomic_DNA.
DR   SMR; Q6XR11; 21-182.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
SQ   SEQUENCE   186 AA;  21516 MW;  FD947DBB2534005F CRC64;

  Query Match             74.1%;  Score 698;  DB 2;  Length 186;
  Best Local Similarity   72.8%;  Pred. No. 2.4e-55;
  Matches  118;  Conservative   21;  Mismatches   23;  Indels    0;  Gaps    0;

Qy         11 ITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGMV 70
              |:| || || | :|||||||||||||||: |||||||||||||||||||||||:|: |:
Db         21 ISFEDYCGLNTALYEWADSYDSKDWDRLRRTIAPTLRIDYRSFLDKLWEAMPAEDFIKMI 80

Qy         71 SSKQMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSA 130
                 :|||| |:||||:| :|||:||:|||:|:|||||||||| | |   | :|||||||
Db         81 SDPNVLGDPLLKTQHFVGASRWERVSDDEVVGWHQLRVPHQRYTDATKTTVKVKGHAHSA 140

Qy        131 NLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172
              | |||||:|||||||| |:||| |:|||::|  ||| |||:
Db        141 NKHWYKKVDGVWKFAGLYPEIRWSEYDFDKVFASGREEFGDE 182


RESULT 3
SCYD_GLOLA
ID   SCYD_GLOLA     STANDARD;      PRT;   188 AA.
AC   Q00455;
DT   15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1996, sequence version 1.
DT   07-FEB-2006, entry version 28.
DE   Scytalone dehydratase (EC 4.2.1.94).
GN   Name=SCD1;
OS   Glomerella lagenarium (Anthracnose fungus) (Colletotrichum
OS   lagenarium).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
OC   mitosporic Phyllachoraceae; Colletotrichum.
OX   NCBI_TaxID=5462;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC   STRAIN=104-T;
RX   MEDLINE=97111971; PubMed=8953707;
RA   Kubo Y., Takano Y., Endo N., Yasuda N., Tajima S., Furusawa I.;
RT   "Cloning and structural analysis of the melanin biosynthesis gene SCD1
RT   encoding scytalone dehydratase in Colletotrichum lagenarium.";
RL   Appl. Environ. Microbiol. 62:4340-4344(1996).
CC   -!- FUNCTION: Catalyzes two steps in melanin biosynthesis. From
CC       scytalone they are two dehydration steps and one reduction step to
CC       yield melanin.
CC   -!- CATALYTIC ACTIVITY: Scytalone = 1,3,8-trihydroxynaphthalene +
CC       H(2)O.
CC   -!- PATHWAY: Fungal melanin biosynthesis; first step.
CC   -!- SUBUNIT: Homotrimer. Each subunit contains an active site, located
```

```
CC       in the central part of the hydrophobic core of the monomer, which
CC       functions independently (By similarity).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; D86079; BAA13009.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
DR   SMR; Q00455; 6-167.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
KW   Lyase; Melanin biosynthesis.
FT   CHAIN         1    188       Scytalone dehydratase.
FT                                /FTId=PRO_0000097638.
SQ   SEQUENCE   188 AA;  21687 MW;  A58F3EB940321EFA CRC64;

  Query Match             72.8%;  Score 686;  DB 1;  Length 188;
  Best Local Similarity   71.9%;  Pred. No. 3e-54;
  Matches  115;  Conservative   24;  Mismatches   21;  Indels    0;  Gaps    0;

Qy         11 ITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGMV 70
              ||| |||||   ::||||||||||||||||| ||| ||||||||||:|||||||||: |:
Db          8 ITFEDYLGLNAALFEWADSYDSKDWDRLRKCIAPELRIDYRSFLDKIWEAMPAEEFIAMI 67

Qy         71 SSKQMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSA 130
              | | :||:| |:|||||||:||||||: ||||:||||||||:| | :  || :||||||
Db         68 SDKSVLGNPLLKTQHFIGGSRWEKVSDTEVIGHHQLRVPHQKYTDASRTEVAVKGHAHSY 127

Qy        131 NLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFG 170
              |:|||:|::|||||||| |:||| |:||| :| |||:::|
Db        128 NMHWYRKVNGVWKFAGLNPEIRWSEYDFDAVFADGRDSYG 167


RESULT 4
Q9C426_OPHFL
ID   Q9C426_OPHFL   PRELIMINARY;   PRT;   216 AA.
AC   Q9C426;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   Scytalone dehydratase.
GN   Name=OSD1;
OS   Ophiostoma floccosum.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX   NCBI_TaxID=104300;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=387N;
RX   MEDLINE=21473268; PubMed=11589570; DOI=10.1007/s004380100534;
RA   Wang H.L., Kim S.H., Breuil C.;
RT   "A scytalone dehydratase gene from Ophiostoma floccosum restores the
RT   melanization and pathogenicity phenotypes of a melanin-deficient
RT   Colletotrichum lagenarium mutant.";
RL   Mol. Genet. Genomics 266:126-132(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=387N;
RA   Wang H., Breuil C.;
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC   ---------------------------------------------------------------------
DR   EMBL; AF316575; AAK11296.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
DR   SMR; Q9C426; 22-182.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
SQ   SEQUENCE   216 AA;  24167 MW;  D349BF7F4DDF3D4D CRC64;

  Query Match             72.8%;  Score 686;  DB 2;  Length 216;
  Best Local Similarity   71.4%;  Pred. No. 3.5e-54;
  Matches  115;  Conservative   23;  Mismatches   23;  Indels    0;  Gaps    0;

Qy         10 EITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGM 69
              :|:| ||:|| :  ||||||||||||||||| ||||||||||||:||||||||||:||
Db         22 DISFEDYMGLCSAAYEWADSYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPAEEFIGM 81

Qy         70 VSSKQMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS 129
              :|   :||:| |||||| | :|||::|: ||:||||||||| | |||: :| :||||||
Db         82 ISDPSVLGNPLLRTQHFFGASRWERISDTEVVGYHQLRVPHQVYTDTTLTQVAVKGHAHS 141

Qy        130 ANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFG 170
              || |||:|:||||||| | ||| |:|||::|  ||: ||
Db        142 ANTHWYRKVDGVWKFAGLDPKIRWFEYDFDKVFASGRDQFG 182


RESULT 5
Q7Z8L5_9PLEO
ID   Q7Z8L5_9PLEO   PRELIMINARY;   PRT;   185 AA.
AC   Q7Z8L5;
DT   01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2003, sequence version 1.
DT   07-FEB-2006, entry version 9.
DE   Scytalone dehydratase.
GN   Name=BSCD1;
OS   Bipolaris oryzae.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC   Pleosporales; Pleosporaceae; mitosporic Cochliobolus; Bipolaris.
OX   NCBI_TaxID=33195;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=D9/F6-69;
RX   PubMed=14716498; DOI=10.1007/s00294-003-0477-1;
RA   Kihara J., Moriwaki A., Ueno M., Tokunaga T., Arase S., Honda Y.;
RT   "Cloning, functional analysis and expression of a scytalone
RT   dehydratase gene ( SCD1) involved in melanin biosynthesis of the
RT   phytopathogenic fungus Bipolaris oryzae.";
RL   Curr. Genet. 45:197-204(2004).
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CC   ---------------------------------------------------------------------
DR   EMBL; AB100172; BAC79365.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
DR   SMR; Q7Z8L5; 10-168.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
SQ   SEQUENCE   185 AA;  21285 MW;  EB9937DB661D5DCB CRC64;

  Query Match             69.7%;  Score 657;  DB 2;  Length 185;
  Best Local Similarity   67.5%;  Pred. No. 1.3e-51;
  Matches  112;  Conservative   22;  Mismatches   32;  Indels    0;  Gaps    0;

Qy          6 QKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEAMPAEE 65
              :|  : || : :|  :  ||||||||||||:|||| :||||:|||||||||:||||||:|
Db          4 KKELQPTFEEVMGCQSACYEWADSYDSKDWERLRKCVAPTLKIDYRSFLDKIWEAMPADE 63

Qy         66 FVGMVSSKQMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKG 125
              || | |   :||:| |:||||||||||||: :|||: |||||||||||| | :   | :||
Db         64 FVAMASDPAVLGNPLLKTQHFIGGTRWEKTAEDEITGYHQLRVPHQRYTDESRATVAVKG 123

Qy        126 HAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGD 171
              |||| | |||||||| |||||| ||||| |:|||::| :|||  |:
Db        124 HAHSFNTHWYKKIDGEWKFAGLNPDIRWYEYDFDKVFAEGREQLGE 169


RESULT 6
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Q7SBE1_NEUCR
ID   Q7SBE1_NEUCR   PRELIMINARY;   PRT;   174 AA.
AC   Q7SBE1;
DT   15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT   15-DEC-2003, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Hypothetical protein.
GN   ORFNames=NCU07823.1;
OS   Neurospora crassa.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX   NCBI_TaxID=5141;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=74-OR23-1A / FGSC 987;
RX   MEDLINE=22598136; PubMed=12712197; DOI=10.1038/nature01554;
RA   Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA   Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA   Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA   Qui D., Ianakiev P., Bell-Pedersen D., Nelson M.A.,
RA   Werner-Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L.,
RA   Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C.,
RA   Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
RA   Stange-Thomann N., Barrett R., Gnerre S., Kamal M., Kamvysselis M.,
RA   Mauceli E., Bielke C., Rudd S., Frishman D., Krystofova S.,
RA   Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C.,
RA   Macino G., Catcheside D.E.A., Li W., Pratt R.J., Osmani S.A.,
RA   DeSouza C.P.C., Glass N.L., Orbach M.J., Berglund J.A., Voelker R.,
RA   Yarden O., Plamann M., Seiler S., Dunlap J.C., Radford A., Aramayo R.,
RA   Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA   Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.W.;
RT   "The genome sequence of the filamentous fungus Neurospora crassa.";
RL   Nature 422:859-868(2003).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
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CC   ---------------------------------------------------------------------
DR   EMBL; AABX01000169; EAA33708.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
DR   SMR; Q7SBE1; 11-171.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   174 AA;  20156 MW;  9CD5927C2302FE9A CRC64;

  Query Match             66.6%;  Score 627.5;  DB 2;  Length 174;
  Best Local Similarity   65.1%;  Pred. No. 5.8e-49;
  Matches  112;  Conservative   25;  Mismatches   34;  Indels    1;  Gaps    1;

Qy          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60
              | :       ||| :|||     :|||||||:||:||||| |||||||||||||:|||||
Db          1 MANAANPEKRITFEEYLGCTEACFEWADSYDTKDFDRLRKCIAPTLRIDYRSFLNKLWEA 60

Qy         61 MPAEEFVGMVSSKQMLGDPTLRTQHFIGG-TRWEKVSEDEVIGYHQLRVPHQRYKDTTMK 119
              ||||||: ||| |:::|:| |||||||: | ::|||||: |:||||||||| | |::
Db         61 MPAEEFIKMVSDKKVIGNPLLRTQHFMSGISKWEKVSDTEIIGYHQLRVPHQVYTDSSCT 120

Qy        120 EVTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGD 171
              :| : ||||| | |:||||:|||||||| ||||| | |||::| ||||  |:
Db        121 KVAVTGHAHSHNTHYYKKINGVWKFAGLNPDIRWTEGDFDKVFADGREELGE 172


RESULT 7
Q8NJI6_9PEZI
ID   Q8NJI6_9PEZI   PRELIMINARY;   PRT;   122 AA.
AC   Q8NJI6;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Scytalone dehydratase (Fragment).
OS   Ophiostoma piceae.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX   NCBI_TaxID=61273;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fleet C., Breuil C.;
RT   "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT   presence of DHN-melanin pathway in sapstain fungi.";
RL   Mycol. Res. 106:1331-1339(2002).
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CC   ---------------------------------------------------------------------
DR   EMBL; AY098656; AAM34802.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
DR   SMR; Q8NJI6; 1-122.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
FT   NON_TER       1      1
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  14291 MW;  50E940509D85F8A4 CRC64;

  Query Match             58.4%;  Score 550;  DB 2;  Length 122;
  Best Local Similarity   76.2%;  Pred. No. 4.4e-42;
  Matches   93;  Conservative   15;  Mismatches   14;  Indels    0;  Gaps    0;

Qy         25 EWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPTLRTQ 84
              |||| |||||||||| |||||||||||:|||||||||:||:|   :||:| ||||
Db          1 EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPAEEFIGMISDPSVLGNPLLRTQ 60

Qy         85 HFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDGVWKF 144
              || | :|||::|: ||:|||||||||| | |||: :| :|||||||| |||:|:||||||
Db         61 HFFGASRWERISDTEVVGYHQLRVPHQVYTDTTLTQVAVKGHAHSANTHWYRKVDGVWKF 120

Qy        145 AG 146
              ||
Db        121 AG 122


RESULT 8
Q2WEI4_SORMA
ID   Q2WEI4_SORMA   PRELIMINARY;   PRT;   150 AA.
AC   Q2WEI4;
DT   10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT   10-JAN-2006, sequence version 1.
DT   07-FEB-2006, entry version 3.
DE   Scytalone dehydrogenase homologue (Fragment).
GN   Name=smu7823;
OS   Sordaria macrospora.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Sordariales; Sordariaceae; Sordaria.
OX   NCBI_TaxID=5147;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=S48977; TISSUE=Mycelium;
RA   Nowrousian M., Wuertz C., Poeggeler S., Kueck U.;
RT   "Why sequencing of Sordaria macrospora will lead to an improved
RT   annotation of the Neurospora crassa genome.";
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ575152; CAE00795.1; -; Genomic_DNA.
FT   NON_TER     150    150
SQ   SEQUENCE   150 AA;  17348 MW;  CB9B307F47C1D5A7 CRC64;
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  Query Match             58.2%;  Score 548.5;  DB 2;  Length 150;
  Best Local Similarity   65.3%;  Pred. No. 7.7e-42;
  Matches   98;  Conservative   21;  Mismatches   30;  Indels    1;  Gaps    1;

Qy          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60
              | :       ||| :|||     :||||||||||:|||||  ||||||:||||||:|||||
Db          1 MANAANPKTRITFBEYLGCTEACFEWADSYDSKDFDRLRKCIAPTLRVDYRSFLNKLWEA 60

Qy         61 MPAEEFVGMVSSKQMLGDPTLRTQHFIGG-TRWEKVSEDEVIGYHQLRVPHQRYKDTTMK 119
              ||||||: ||| |:::|:| |||||||: | ::|||||: |:||||||||||| | | :
Db         61 MPAEEFIQMVSDKKVIGNPLLRTQHFMSGISKWEKVSDTEIIGYHQLRVPHQVYTDKSCT 120

Qy        120 EVTMKGHAHSANLHWYKKIDGVWKFAGLKP 149
              :| : ||||| | |:|||:|||||||||| |
Db        121 KVAVTGHAHSHNTHYYKKVDGVWKFAGLNP 150


RESULT 9
Q8NJI5_OPHFL
ID   Q8NJI5_OPHFL   PRELIMINARY;   PRT;   121 AA.
AC   Q8NJI5;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Scytalone dehydratase (Fragment).
OS   Ophiostoma floccosum.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX   NCBI_TaxID=104300;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fleet C., Breuil C.;
RT   "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT   presence of DHN-melanin pathway in sapstain fungi.";
RL   Mycol. Res. 106:1331-1339(2002).
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CC   ---------------------------------------------------------------------
DR   EMBL; AY098657; AAM34803.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
DR   SMR; Q8NJI5; 1-121.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
FT   NON_TER       1      1
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  14234 MW;  1940509D85F8A42A CRC64;

  Query Match             57.7%;  Score 544;  DB 2;  Length 121;
  Best Local Similarity   76.0%;  Pred. No. 1.5e-41;
  Matches   92;  Conservative   15;  Mismatches   14;  Indels    0;  Gaps    0;

Qy         25 EWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPTLRTQ 84
              |||| |||||||||| ||||||||||||:||||||||||:||:|   :||:| ||||
Db          1 EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPAEEFIGMISDPSVLGNPLLRTQ 60

Qy         85 HFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDGVWKF 144
              || | :|||::|: ||:|||||||||| | |||: :| :|||||||| |||:|:||||||
Db         61 HFFGASRWERISDTEVVGYHQLRVPHQVYTDTTLTQVAVKGHAHSANTHWYRKVDGVWKF 120

Qy        145 A 145
              |
Db        121 A 121


RESULT 10
Q8NJI7_9PEZI
ID   Q8NJI7_9PEZI   PRELIMINARY;   PRT;   122 AA.
AC   Q8NJI7;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Scytalone dehydratase (Fragment).
OS   Ceratocystis resinifera.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Hypocreomycetidae; Microascales; Microascales incertae sedis;
OC   Ceratocystis.
OX   NCBI_TaxID=95837;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fleet C., Breuil C.;
RT   "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT   presence of DHN-melanin pathway in sapstain fungi.";
RL   Mycol. Res. 106:1331-1339(2002).
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CC   ---------------------------------------------------------------------
DR   EMBL; AY098655; AAM34801.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
DR   SMR; Q8NJI7; 1-122.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
FT   NON_TER       1      1
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  14376 MW;  D807589723063C91 CRC64;

  Query Match             57.5%;  Score 542;  DB 2;  Length 122;
  Best Local Similarity   75.4%;  Pred. No. 2.4e-41;
  Matches   92;  Conservative   14;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         25 EWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPTLRTQ 84
              |||| ||||||||| : |||||||||||||||||||||:|: |:|   :|||| |:||
Db          1 EWADRYDSKDWDRLXRTIAPTLRIDYRSFLDKLWEAMPAEDFIKMISDPNVLGDPLLKTQ 60

Qy         85 HFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDGVWKF 144
              ||:| :|||:||:|||:|:|||||||||| | |   | :|||||||| |||||:||||||
Db         61 HFVGASRWERVSDDEVVGWHQLRVPHQRYTDATKTTVKVKGHAHSANKHWYKKVDGVWKF 120

Qy        145 AG 146
              ||
Db        121 AG 122


RESULT 11
Q8NJI8_9PEZI
ID   Q8NJI8_9PEZI   PRELIMINARY;   PRT;   121 AA.
AC   Q8NJI8;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Scytalone dehydratase (Fragment).
OS   Ceratocystis pinicola.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Hypocreomycetidae; Microascales; Microascales incertae sedis;
OC   Ceratocystis.
OX   NCBI_TaxID=72031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fleet C., Breuil C.;
RT   "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT   presence of DHN-melanin pathway in sapstain fungi.";
RL   Mycol. Res. 106:1331-1339(2002).
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CC   ---------------------------------------------------------------------
DR   EMBL; AY098654; AAM34800.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
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DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
FT   NON_TER       1      1
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  14394 MW;  C183FA038FCF5820 CRC64;

  Query Match             57.3%;  Score 540;  DB 2;  Length 121;
  Best Local Similarity   76.0%;  Pred. No. 3.6e-41;
  Matches   92;  Conservative   14;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          25 EWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPTLRTQ 84
               |||| |||||||||||: |||||||||||||||||||||||:|: |:|   :|||| |:||
Db           1 EWADWYDSKDWDRLRRTIAPTLRIDYRSFLDKLWEAMPAEDFIKMISDPNVLGDPLLKTQ 60

Qy          85 HFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDGVWKF 144
               ||:| :|||:||:|||:|:|||||||||| | |    | :|||||||| |||||:||||||
Db          61 HFVGASRWERVSDDEVVGWHQLRVPHQRYTDATKTTVKVKGHAHSANKHWYKKVDGVWKF 120

Qy         145 A 145
               |
Db         121 A 121


RESULT 12
Q8NIE1_9PEZI
ID   Q8NIE1_9PEZI   PRELIMINARY;   PRT;   122 AA.
AC   Q8NIE1;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Scytalone dehydratase (Fragment).
OS   Ophiostoma piceae.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX   NCBI_TaxID=61273;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fleet C., Breuil C.;
RT   "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT   presence of DHN-melanin pathway in sapstain fungi.";
RL   Mycol. Res. 106:1331-1339(2002).
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CC   ---------------------------------------------------------------------
DR   EMBL; AY098660; AAM34806.1; -; Genomic_DNA.
DR   EMBL; AY098661; AAM34807.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
DR   SMR; Q8NIE1; 1-122.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
FT   NON_TER       1      1
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  14246 MW;  A17A6DD02BD9CB0A CRC64;

  Query Match             57.0%;  Score 537;  DB 2;  Length 122;
  Best Local Similarity   75.4%;  Pred. No. 6.8e-41;
  Matches   92;  Conservative   14;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          25 EWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPTLRTQ 84
               |||| |||||||||||:|||||||||:||::|:|   :||:| ||||
Db           1 EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIGMISDPNVLGNPLLRTQ 60

Qy          85 HFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDGVWKF 144
               || | :|||:||: |||||||||||| | | ::  | :|||||||| |||:|:||||||
Db          61 HFFGASRWERVSDTEVIGYHQLRVPHQVYTDASLSTVAVKGHAHSANQHWYRKVDGVWKF 120

Qy         145 AG 146
               ||
Db         121 AG 122


RESULT 13
Q8NJI2_OPHPI
ID   Q8NJI2_OPHPI   PRELIMINARY;   PRT;   122 AA.
AC   Q8NJI2;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Scytalone dehydratase (Fragment).
OS   Ophiostoma piliferum.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX   NCBI_TaxID=38032;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fleet C., Breuil C.;
RT   "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT   presence of DHN-melanin pathway in sapstain fungi.";
RL   Mycol. Res. 106:1331-1339(2002).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY098662; AAM34808.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
DR   SMR; Q8NJI2; 1-122.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
FT   NON_TER       1      1
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  14221 MW;  7A99419E73E0735E CRC64;

  Query Match             57.0%;  Score 537;  DB 2;  Length 122;
  Best Local Similarity   73.8%;  Pred. No. 6.8e-41;
  Matches   90;  Conservative   17;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          25 EWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPTLRTQ 84
               |||| |||||||||||| ||||||||||||:||||||||:||:||:|   :||:| ||||
Db           1 EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIGMISDPSVLGNPLLRTQ 60

Qy          85 HFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDGVWKF 144
               || | :|||::|: ||:|:|||||||| | | |: :| :|||||||| |||:|:||||||
Db          61 HFFGASRWERISDTEVVGHHQLRVPHQVYTDATLTQVAVKGHAHSANTHWYRKVDGVWKF 120

Qy         145 AG 146
               ||
Db         121 AG 122


RESULT 14
Q8NJI0_OPHPI
ID   Q8NJI0_OPHPI   PRELIMINARY;   PRT;   121 AA.
AC   Q8NJI0;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Scytalone dehydratase (Fragment).
OS   Ophiostoma piliferum.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX   NCBI_TaxID=38032;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fleet C., Breuil C.;
RT   "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT   presence of DHN-melanin pathway in sapstain fungi.";
```

```
RL   Mycol. Res. 106:1331-1339(2002).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY098664; AAM34810.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
DR   SMR; Q8NJI0; 1-121.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
FT   NON_TER       1      1
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  14150 MW;  1941990397735E1F CRC64;

  Query Match             56.5%;  Score 532;  DB 2;  Length 121;
  Best Local Similarity   73.6%;  Pred. No. 1.9e-40;
  Matches   89;  Conservative   17;  Mismatches   15;  Indels    0;  Gaps    0;

Qy         25 EWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPTLRTQ 84
              |||| |||||||||| |||||||||||||:||||||||:||:||:|   :||:| ||||
Db          1 EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIGMISDPSVLGNPLLRTQ 60

Qy         85 HFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDGVWKF 144
              || | :|||::|: ||:|:|||||||| | | |: :| :|||||||| |||:|:||||||
Db         61 HFFGASRWERISDTEVVGHHQLRVPHQVYTDATLSQVAVKGHAHSANTHWYRKVDGVWKF 120

Qy        145 A 145
              |
Db        121 A 121


RESULT 15
Q8NJI1_OPHPI
ID   Q8NJI1_OPHPI   PRELIMINARY;   PRT;   122 AA.
AC   Q8NJI1;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Scytalone dehydratase (Fragment).
OS   Ophiostoma piliferum.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX   NCBI_TaxID=38032;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fleet C., Breuil C.;
RT   "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT   presence of DHN-melanin pathway in sapstain fungi.";
RL   Mycol. Res. 106:1331-1339(2002).
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AY098663; AAM34809.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
DR   SMR; Q8NJI1; 1-122.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
FT   NON_TER       1      1
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  14226 MW;  7A995CA5F045735E CRC64;

  Query Match             56.3%;  Score 530;  DB 2;  Length 122;
  Best Local Similarity   73.0%;  Pred. No. 2.9e-40;
  Matches   89;  Conservative   17;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         25 EWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPTLRTQ 84
              |||| |||||||||| |||||||||||||:||||||||:||:||:|   :||:| ||||
Db          1 EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIGMISDPSVLGNPLLRTQ 60

Qy         85 HFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDGVWKF 144
              || | :|||::|: ||:|:|||||||| | | |: :| :|||||||| |||:|:||||||
Db         61 HFFGASRWERISDTEVVGHRQLRVPHQVYTDATLSQVAVKGHAHSANTHWYRKVDGVWKF 120

Qy        145 AG 146
              ||
Db        121 AG 122


Search completed: December  5, 2006, 01:27:22
Job time : 304 secs
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: December 5, 2006, 01:22:36 ; Search time 40 Seconds
(without alignments)
413.732 Million cell updates/sec

Title: US-10-507-132-2
Perfect score: 942
Sequence: 1 MGSQVQKSDEITFSDYLGLM.....WGEFDFDRIFEDGRETFGDK 172

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	932	98.9	172	2	JE0130	scytalone dehydrat
2	99.5	10.6	605	2	AI2535	hypothetical prote
3	88	9.3	166	2	D37844	baiE 19.5K protein
4	84.5	9.0	380	1	C69144	UDP-galactopyranos
5	84	8.9	349	2	H36470	Wnt-7b protein - m
6	83	8.8	266	2	F64677	NADH2 dehydrogenas
7	83	8.8	923	2	A53054	lipoxygenase (EC 1
8	80	8.5	388	2	S57526	cellulase - Fibrob
9	79.5	8.4	614	2	T01121	probable beta-gluc
10	79.5	8.4	1239	1	A32579	neuroglian - fruit
11	79	8.4	265	2	D71838	nadh oxidoreductas
12	79	8.4	469	2	B96947	beta-glucosidase [
13	79	8.4	702	2	A75630	ribonucleoside-dip
14	78.5	8.3	380	2	I47176	chymosin (EC 3.4.2
15	77.5	8.2	299	2	T40437	phosphoribosylamid
16	77.5	8.2	356	2	G64997	isochorismate synt
17	77.5	8.2	816	2	S54518	probable membrane
18	77	8.2	274	2	T51714	probable formamido
19	77	8.2	479	2	T26951	hypothetical prote
20	76.5	8.1	325	2	G84362	hypothetical prote
21	76.5	8.1	356	2	A91023	isochorismate hydr
22	76.5	8.1	356	2	B85867	hypothetical prote
23	76	8.1	1150	2	T41260	hypothetical prote
24	75.5	8.0	315	2	JQ1250	coat protein - chr
25	75.5	8.0	591	2	S56202	probable glycerone
26	75	8.0	497	2	T27012	hypothetical prote
27	75	8.0	514	2	B64055	periplasmic oligop
28	75	8.0	1405	2	T40607	probable dna-direc
29	74.5	7.9	162	2	H69896	hypothetical prote
30	74.5	7.9	259	2	E69811	hypothetical prote
31	74.5	7.9	436	2	D70693	probable ugpB lipo
32	74.5	7.9	667	2	AE2943	oxidoreductase Atu
33	74.5	7.9	667	2	E98339	probable oxidoredu
34	74	7.9	442	2	I50110	Wnt10a protein - z
35	74	7.9	26926	1	I38344	titin, cardiac mus
36	73.5	7.8	143	2	AB1701	hypothetical prote
37	73.5	7.8	313	2	H69984	conserved hypothet
38	73.5	7.8	482	2	S15748	nitrogenase (EC 1.
39	73.5	7.8	589	2	T42244	probable polypepti
40	73.5	7.8	763	2	S23457	polysulfide reduct
41	73.5	7.8	817	2	D86217	protein T27G7.8 [i
42	73.5	7.8	4859	2	S74173	ryanodine receptor
43	73	7.7	153	2	S53544	hypothetical prote
44	73	7.7	430	1	UYPVF1	nonstructural prot
45	72.5	7.7	97	2	A34291	pollen allergen Lo

ALIGNMENTS

RESULT 1
JE0130
scytalone dehydratase (EC 4.2.1.94) - Pyricularia oryzae
C;Species: Pyricularia oryzae
C;Date: 03-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 31-Dec-2004
C;Accession: JE0130
R;Motoyama, T.; Imanishi, K.; Yamaguchi, I.
Biosci. Biotechnol. Biochem. 62, 564-566, 1998
A;Title: cDNA cloning, expression, and mutagenesis of scytalone dehydratase needed for pa
A;Reference number: JE0130; MUID:98233280; PMID:9571787
A;Accession: JE0130
A;Molecule type: mRNA
A;Residues: 1-172 <MOT>
A;Cross-references: UNIPARC:UPI0000179D1F; DDBJ:AB004701
C;Comment: The C-terminal protein of this enzyme is important in catalysis or/and structu
C;Superfamily: scytalone dehydratase
C;Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 98.9%; Score 932; DB 2; Length 172;
Best Local Similarity 98.8%; Pred. No. 3.9e-79;
Matches 170; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60

Qy         61 MPAEEFVGMVSSKQMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE 120
              |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MPAEEFVGMVSSKQVLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE 120

Qy        121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFADK 172
```

RESULT 2
AI2535
hypothetical protein alr7572 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120bet
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AI2535
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AI2535
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-605 <KUR>
A;Cross-references: UNIPROT:Q8ZSD9; UNIPARC:UPI00000CCD88; GB:AP003602; PIDN:BAB77215.1;

```
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr7572
A;Genome: plasmid

  Query Match             10.6%;  Score 99.5;  DB 2;  Length 605;
  Best Local Similarity   24.6%;  Pred. No. 0.24;
  Matches   32;  Conservative   27;  Mismatches   52;  Indels   19;  Gaps    6;

Qy         16 YLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGMVSSKQM 75
              |  :: |   | |  :|| | ||:: :   |  | |   ::|   :|:  :  :: :
Db        205 YEEILAC---WKDGPNSKGWKRLKEYLIYDLE-DTRLIANRL---VPSYYYEALIVPEMN 257

Qy         76 LGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMK------GHAHS 129
              |   ||       ||:||:: |    ||     ||::||       ::       |:|
Db        258 LQQLTLAG----NGTKWERIFEHHYPGYKP--KPHRKYKFQGGMAYSIPGLYRRVGYADI 311

Qy        130 ANLHWYKKID 139
              :::| :  :|
Db        312 SSMHPWAMLD 321


RESULT 3
D37844
baiE 19.5K protein - Eubacterium sp.
C;Species: Eubacterium sp.
C;Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 22-Oct-1999
C;Accession: D37844
R;Mallonee, D.H.; White, W.B.; Hylemon, P.B.
J. Bacteriol. 172, 7011-7019, 1990
A;Title: Cloning and sequencing of a bile acid-inducible operon from Eubacterium sp. str
A;Reference number: A37844; MUID:91072253; PMID:2254270
A;Accession: D37844
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-166 <MAL>
A;Cross-references: UNIPARC:UPI0000126771; GB:U57489; GB:M36292; NID:g1381562; PIDN:AAC4

  Query Match              9.3%;  Score 88;  DB 2;  Length 166;
  Best Local Similarity   25.5%;  Pred. No. 0.58;
  Matches   37;  Conservative   15;  Mismatches   53;  Indels   40;  Gaps    7;

Qy         31 DSKDWDRLRKVIAPTLRIDY----------RSFLDKLWEAMPAEEFVGMVSSKQMLGDPT 80
              | | || |   ::| :    |          :   | |  :|| ||      |  |    |
Db         35 DGKMWDELETTLSPNIVTSYSNGKLVFHSPKEVTDYLKSSMPKEEI-----SMHMGHTPE 89

Qy         81 LRTQHFIGGT-RWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKID 139
              :        | ||    || :|           : |   |:| : | |   :   |:|||
Db         90 ITIDSETTATGRW--YLEDRLI-----------FTDGKYKDVGINGGAFYTDK--YEKID 134

Qy        140 GVWKFAGLKPDIRWGEFDFDRIFED 164
              | |             |  : ||:|:
Db        135 GQWYIL---------ETGYVRIYEE 150


RESULT 4
C69144
UDP-galactopyranose mutase - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: C69144
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: C69144
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-380 <MTH>
A;Cross-references: UNIPROT:O26444; UNIPARC:UPI0000066482; GB:AE000819; GB:AE000666; NID
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH344
C;Superfamily: Methanobacterium thermoautotrophicum UDP-galactopyranose mutase

  Query Match              9.0%;  Score 84.5;  DB 1;  Length 380;
  Best Local Similarity   22.3%;  Pred. No. 3.4;
  Matches   39;  Conservative   28;  Mismatches   51;  Indels   57;  Gaps    9;

Qy         29 SYDSKDWDRLRKVIAP--------TLRIDYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPT 80
              :|  | |    : : |          |  | | | |: ::|:| : :  ||  ::||  |
Db        155 NYTRKQWGLKPEEMDPEVTGRVPVVLSRDDRYFTDR-YQAVPRDGYTAMV--ERMLDHPC 211

Qy         81 LRTQ---------------HFIGGTRWEKV----SEDEVIGYHQLRVPHQRYKDTTMKE 120
              ::                 ||:|     ||       ||: ||    :|::
Db        212 IKLMLNTSHHEVLELRDGQIHFMGSEFRGKVIFTGKIDELFGYRYGELPYR--------- 262

Qy        121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFE-------DGRET 168
               ::     ||:  |:::: |       |:    ::|| || |       | | |
Db        263 -SLDLQFESADTEWFQEVATV-----NYPN----DYDFTRITEFKHLHPTDSRRT 307


RESULT 5
H36470
Wnt-7b protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 09-Jul-2004
C;Accession: H36470
R;Gavin, B.J.; McMahon, J.A.; McMahon, A.P.
Genes Dev. 4, 2319-2332, 1990
A;Title: Expression of multiple novel Wnt-1/int-1-related genes during fetal and adult mo
A;Reference number: A36470; MUID:91122634; PMID:2279700
A;Accession: H36470
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-349 <GAV>
A;Cross-references: UNIPROT:P28047; UNIPARC:UPI0000021EC1; GB:M89802; NID:g202411; PIDN:A
C;Superfamily: int-1 transforming protein

  Query Match              8.9%;  Score 84;  DB 2;  Length 349;
  Best Local Similarity   31.1%;  Pred. No. 3.4;
  Matches   32;  Conservative   11;  Mismatches   36;  Indels   24;  Gaps    7;

Qy         84 QHFIGGTRW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-------ANLH- 133
              ||     ||    : |  | |  :|||  :    |    :|  | ||:          ||
Db         74 QHQFRFGRWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSN 130

Qy        134 ---------WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                      :| : :| ||: |   |:|:|  || | | | ||
Db        131 CGCDREKQGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171


RESULT 6
F64677
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain NQO5 - Helicobacter pylori (strain 26
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 31-Dec-2004
C;Accession: F64677
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.M
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: F64677
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-266 <TOM>
A;Cross-references: UNIPROT:O25852; UNIPARC:UPI00000D31A4; GB:AE000631; GB:AE000511; NID:
C;Genetics:
A;Start codon: GTG
C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 30kD/NdhJ/NuoC
C;Keywords: electron transfer; membrane-associated complex; NAD; oxidoreductase
```

Query Match 8.8%; Score 83; DB 2; Length 266;
Best Local Similarity 22.4%; Pred. No. 3;
Matches 39; Conservative 28; Mismatches 57; Indels 50; Gaps 7;

```
Qy         13 FSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKL--WEAMPAEEFVGMV 70
Db        103 FYQFVG-------FSDSCKNRRRVRVKCVLLPNESVDSLSFLYRSANWSEREAYDMLGIV 155

Qy         71 SSK----------QMLGDPTLRTQHFIGG--TRWEKVSE------DEVIGYHQ------ 105
Db        156 FDKHPYLKRLIMPHDWVGHPLLRSYPLKGDEFAQWYEVDKIFGKEYREVVGKEQRDSARV 215

Qy        106 ---------LRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDGVWKFAGLKPDI 151
Db        216 DEKDTFNFAKIGYEQGKGEELKEVEEK--------HAFKKIPFVKDLHKIAPTI 261
```

RESULT 7
A53054
lipoxygenase (EC 1.13.11.12) L-2 - rice
C;Species: Oryza sativa (rice)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 12-Mar-1999
C;Accession: A53054
R;Peng, Y.L.; Shirano, Y.; Ohta, H.; Hibino, T.; Tanaka, K.; Shibata, D.
J. Biol. Chem. 269, 3755-3761, 1994
A;Title: A novel lipoxygenase from rice. Primary structure and specific expression upon
A;Reference number: A53054; MUID:94148883; PMID:7508918
A;Accession: A53054
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-923 <PEN>
A;Cross-references: UNIPARC:UPI000017524C
A;Experimental source: cv. Aichiasahi, blast fungus-infected leaves
A;Note: sequence extracted from NCBI backbone (NCBIN:143808, NCBIP:143809)
A;Note: GB:D14000; NID:g468491
C;Superfamily: lipoxygenase
C;Keywords: oxidoreductase

Query Match 8.8%; Score 83; DB 2; Length 923;
Best Local Similarity 23.3%; Pred. No. 14;
Matches 34; Conservative 16; Mismatches 46; Indels 50; Gaps 7;

```
Qy         55 DKLW----EAMPAEEFVGMVSSKQMLGDPT------LRTQHF----IGGTRWEKV----- 95
Db        653 DKLWRFDTEALPAD----LVRRGMAEEDPTAEQGLKLAIEDYPFANDGLLIWDAIKTWVQ 708

Qy         96 --------SEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDG------- 140
Db        709 AYVARFYPDADSVAGDEELQ--------AFWTEVRTKGHGDKKDAPWWPKLDSPESLAHT 760

Qy        141 ----VWKFAGLKPDIRWGEFDFDRIF 162
Db        761 LTNIVWVAAAHHAAVNFGQYDFGGYF 786
```

RESULT 8
S57526
cellulase - Fibrobacter succinogenes
C;Species: Fibrobacter succinogenes
C;Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S57526
R;Ozcan, N.; Cunningham, C.; Harris, W.J.
submitted to the EMBL Data Library, June 1995
A;Description: Cloning of a cellulase gene from the rumen anaerobe fibrobacter succinoge
A;Reference number: S57526
A;Accession: S57526
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-388 <OZC>
A;Cross-references: UNIPROT:Q47929; UNIPARC:UPI00000B5944; EMBL:X88561; NID:g887439; PID
C;Superfamily: Fibrobacter succinogenes cellulase

Query Match 8.5%; Score 80; DB 2; Length 388;
Best Local Similarity 23.4%; Pred. No. 9;
Matches 34; Conservative 23; Mismatches 54; Indels 34; Gaps 7;

```
Qy         31 DSKDWDRLRKVIAPTLRIDYRSFLDK----LW--EAMPAEE-FVGMVSSKQMLGDPTLRT 83
Db          4 DNNDWSGVTYSLGEGKFIDLSKVRDKGGLYFWIKGKLGGEKLYVGILDNQ----GHDIKS 59

Qy         84 QHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDGVWK 143
Db         60 QTKVGLNDWIKVSKD----WQLAKIPLKRFTD--------KGKAWDAN----------K 96

Qy        144 FAGLKPDIRWGEFDFDRIFEDGRET 168
Db         97 SAEVAKDIKWTRFRKSASLSDWAKT 121
```

RESULT 9
T01121
probable beta-glucosidase At2g32860 [imported] - Arabidopsis thaliana
N;Alternate names: thioglucosidase homolog T21L14.20
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01121; D84738
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
submitted to the EMBL Data Library, December 1997
A;Description: Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence.
A;Reference number: Z14209
A;Accession: T01121
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-614 <ROU>
A;Cross-references: UNIPROT:O48779; UNIPARC:UPI000009CB18; EMBL:AC003033; NID:g2702261; P
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84738
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-614 <STO>
A;Cross-references: UNIPARC:UPI000009CB18; GB:AE002093; NID:g2702276; PIDN:AAB91979.1; GS
C;Genetics:
A;Gene: At2g32860; T21L14.20
A;Map position: 2
A;Introns: 113/3; 137/1; 156/3; 182/1; 208/1; 237/2; 324/1; 362/2; 435/1; 481/1; 517/2
C;Superfamily: Agrobacterium beta-glucosidase

Query Match 8.4%; Score 79.5; DB 2; Length 614;
Best Local Similarity 23.2%; Pred. No. 17;
Matches 57; Conservative 29; Mismatches 61; Indels 99; Gaps 15;

```
Qy          6 QKSDE----------ITFSDYLGLMTCVYEWADSYD-------------SKDWDRLRKVI 42
Db         29 QPSDEDLGTIIGPHQTSFDDEIGIVIGPHATVDDEDIDMDMGTTVGPQTNLNDDDLGTII 88

Qy         43 APTLRIDYRSFLDKLWEAMPAEEFVG-MVSSKQMLGDPTLRTQHFIGGTRW--------E 93
Db         89 GPEFEIHKQDF--------PADFIFGTSVSAYQVEG---AKKGSGRGLTSWDEFTHMFPE 137

Qy         94 KVSE----DEVIGYHQLRVPHQRYKD--TTMKEVTMKGHAHSANLHWYKKI--------- 138
Db        138 KVQQNGDGDEGVDF------YTRYKDDIKLMKELNTNGFRFS--ISWTRILPYGTIKKGV 189

Qy        139 --DGVWKF----------AGLKP-------------DIRWGEFDFDRIFEDGRE------ 167
Db        190 NEEGV-KFYNDLINELLANGIQPSVTLFHWESPLALEMEYGGFLNERIVEDFREFANFCF 248

Qy        168 -TFGDK 172
```

```
Db        249 KEPGDR 254


RESULT 10
A32579
neuroglian - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A32579
R;Bieber, A.J.; Snow, P.M.; Hortsch, M.; Patel, N.H.; Jacobs, J.R.; Traquina, Z.R.; Schi
Cell 59, 447-460, 1989
A;Title: Drosophila neuroglian: a member of the immunoglobulin superfamily with extensiv
A;Reference number: A32579; MUID:90030418; PMID:2805067
A;Accession: A32579
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1239 <BIE>
A;Cross-references: UNIPROT:P20241; UNIPARC:UPI00001743A0; GB:M28231; NID:g157998; PIDN:
A;Note: the authors translated the codon TAT for residue 1234 as Thr and AAA for residue
C;Genetics:
A;Gene: FlyBase:Nrg
A;Cross-references: FlyBase:FBgn0002968
C;Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat homology; i
C;Keywords: alternative splicing; cell adhesion; duplication; membrane protein
F;353-412/Domain: immunoglobulin homology <IMM1>
F;446-502/Domain: immunoglobulin homology <IMM2>
F;535-596/Domain: immunoglobulin homology <IMM3>

  Query Match             8.4%;  Score 79.5;  DB 1;  Length 1239;
  Best Local Similarity   27.6%;  Pred. No. 41;
  Matches   32;  Conservative   20;  Mismatches   51;  Indels   13;  Gaps    4;

Qy         34 DWDRLRKVIA--PTL---RIDYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPTLRTQHFI- 87
              ||  :   |||  ||     |   :  |:    : ||| ||     :  |  ||  |   |
Db        769 DWRQNNIVIADQPTFVKYLIKVVAINDRGESNVAAEEVVGYSGEDRPLDAPTNFTMRQIT 828

Qy         88 ----GGTRWEKVSEDEVIGY---HQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYK 136
                  |   |  |||: | |:   ::::   :   :  ::|: :||  |:| :  :|
Db        829 SSTSGYMAWTPVSEESVRGHFKGYKIQTWTENEGEEGLREIHVKGDTHNALVTQFK 884


RESULT 11
D71838
nadh oxidoreductase I - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 31-Dec-2004
C;Accession: D71838
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: D71838
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-265 <ARN>
A;Cross-references: UNIPROT:Q9ZJW5; UNIPARC:UPI00000D3707; GB:AE001545; GB:AE001439; NID
A;Experimental source: strain J99
C;Genetics:
A;Gene: nuoC
C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 30kD/NdhJ/NuoC

  Query Match             8.4%;  Score 79;  DB 2;  Length 265;
  Best Local Similarity   21.8%;  Pred. No. 7;
  Matches   38;  Conservative   28;  Mismatches   58;  Indels   50;  Gaps    7;

Qy         13 FSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKL--WEAMPAEEFVGMV 70
                 |  ::|       ::||  ::   |:: |: |   :|  ||| :   |     | : :|:|
Db        102 FYQFVG-------FSDSCKNRRRVRVKCVLLPNESVDSLSFLYRSANWSEREAYDMLGIV 154

Qy         71 SSK----------QMLGDPTLRTQHFIGG--TRWEKVSE------DEVIGYHQ------ 105
                 |            :| | ||:    |    :| :| :       ||:|  |
Db        155 FDKHPYLKRLIMPHDWVGHPLLRSYPLKGDEFAQWYEVDKIFGKEYREVVGKEQRDSARV 214

Qy        106 --------LRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDGVWKFAGLKPDI 151
                     :: ::: |   :||  |       | :|||  |     : | |
Db        215 DEKDTFNFAKIGYEQGKGEELKETEEK--------HAFKKIPFVKDLHKIAPTI 260


RESULT 12
B96947
beta-glucosidase [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: B96947
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: B96947
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-469 <KUR>
A;Cross-references: UNIPROT:Q97M15; UNIPARC:UPI00000C9E54; GB:AE001437; PIDN:AAK78365.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0385
C;Superfamily: Agrobacterium beta-glucosidase

  Query Match             8.4%;  Score 79;  DB 2;  Length 469;
  Best Local Similarity   19.2%;  Pred. No. 14;
  Matches   25;  Conservative   28;  Mismatches   39;  Indels   38;  Gaps    6;

Qy         45 TLRIDYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPTLR-TQHFIGGTRWEKVSEDEVIGY 103
              |:::| :::    ||  |    :|:   |:  ||  :  |:: :|    : : |||::
Db        334 TVKMDDKTYTKWGWEISPESLILGLEKLKEQYGDIKIYITENGLGDQ--DPIIEDEILDM 391

Qy        104 HQLRV--PHQR-YKDTTMKEVTMKG-------------------------HAHS----- 129
               :::    | |  |:   : : :||                        | |:
Db        392 PRIKFIEAHLRAIKEAISRGINLKGYYAWSVIDLLSWLNGYKKQYGFIYVDHKHNLDRKK 451

Qy        130 -ANLHWYKKI 138
                : :||||:
Db        452 KLSFYWYKKV 461


RESULT 13
A75630
ribonucleoside-diphosphate reductase, alpha chain - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: A75630
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; H
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mak
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: A75630
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-702 <WHI>
A;Cross-references: UNIPROT:Q9RZL7; UNIPARC:UPI00000D3B5A; GB:AE001826; NID:g6460827; PII
A;Experimental source: strain R1
C;Genetics:
A;Gene: DRB0108
A;Map position: megaplasmid
A;Genome: plasmid
A;Note: plasmid MP1
C;Superfamily: Salmonella typhimurium ribonucleoside-diphosphate reductase

  Query Match             8.4%;  Score 79;  DB 2;  Length 702;
  Best Local Similarity   25.4%;  Pred. No. 23;
  Matches   32;  Conservative   21;  Mismatches   45;  Indels   28;  Gaps    8;
```

```
Qy          58 WEAMPAEEFVGMVSSKQMLGDPTLRTQHFIGGTR---WEKVSEDEVIGYHQLR------V 108
Db           3 WRTHPMERWIEL--NNKVLAGNVVDTQHDTDALQAYFQEKVNPNTVF-FHDLREKIRYLT 59

Qy         109 PH--------QRYKDTTMKEVTMKGHAHSANLHWYKKIDGVWKF----AGLKPD-IRWGE 155
Db          60 EHGLWDARLFERYSSEDVRQVFEKAYGYKFR---FKAFMGAYKFYSEYAGMTPDRSRWLE 116

Qy         156 FDFDRI 161
Db         117 RYEDRL 122
```

RESULT 14
I47176
chymosin (EC 3.4.23.4) precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-Oct-2004
C;Accession: I47176
R;Foltmann, B.; Jensen, A.L.; Loenblad, P.; Smidt, E.; Axelsen, N.H.
Comp. Biochem. Physiol. A 68, 9-13, 1981
A;Title: A Developmental Analysis of the Production of Chymosin and Pepsin in Pigs.
A;Reference number: I47176
A;Accession: I47176
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-380 <FOL>
A;Cross-references: UNIPROT:Q28950; UNIPARC:UPI0000088E4A; EMBL:U14406; NID:g540096; PID
C;Superfamily: Pepsin
C;Keywords: aspartic proteinase; hydrolase

Query Match 8.3%; Score 78.5; DB 2; Length 380;
Best Local Similarity 24.6%; Pred. No. 12;
Matches 43; Conservative 21; Mismatches 62; Indels 49; Gaps 8;

```
Qy           3 SQVQKSDEITFSDYLGLMTCVY-EWADSYDSKDWDRL--RKVIAPTLRIDYRSFLDKLWE 59
Db         163 STQEPSDIFTYSEFDGILGLGYPELASEYTVPVFDNMMHRHLVAQDLFAVYMSRNDE--- 219

Qy          60 AMPAEEFVGMVSSKQMLG--DPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTT 117
Db         220 -----------GSMLTLGAIDPS----YYTGSLHW------------VPVTMQLYWQFT 251

Qy         118 MKEVTMKGHAHSANLHWYKKID-GVWKFAGLKPDI------------RWGEFDFD 159
Db         252 VDSVTINGVVVACNGGCQAILDTGTSMLAGPSSDILNIQMAIGATESQYGEFDID 306
```

RESULT 15
T40437
phosphoribosylamidoimidazole-succinocarboxamide synthase - fission yeast (Schizosaccharo
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40437
R;Lyne, M.H.; Rajandream, M.A.; Barrell, B.G.; Chillingworth, T.; Churcher, C.M.
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21929
A;Accession: T40437
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-299 <LYN>
A;Cross-references: UNIPROT:Q9UUB4; UNIPARC:UPI0000132AAE; EMBL:AL109822; PIDN:CAB52612.
A;Experimental source: strain 972h-; cosmid c409
C;Genetics:
A;Gene: SPDB:SPBC409.10
A;Map position: 2
C;Superfamily: phosphoribosylaminoimidazolesuccinocarboxamide synthase

Query Match 8.2%; Score 77.5; DB 2; Length 299;
Best Local Similarity 24.4%; Pred. No. 11;
Matches 30; Conservative 13; Mismatches 41; Indels 39; Gaps 5;

```
Qy          35 WDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPTLRTQHFIGGTRWEK 94
Db          83 WEELPPVITKHEELKDRSMLVKKYKILPIEAIV----------------RGYITGSAWKE 126

Qy          95 VSEDEVIGYHQLRVPHQRYKDTTMKEV-----------TMKGHAHSANLHWYKKIDGVWK 143
Db         127 YQKQGTV--HGLNVP------TGMKEAEAFPEPLFTPSTKAAEGHDENIH----PDEVSK 174

Qy         144 FAG 146
Db         175 IVG 177
```

Search completed: December 5, 2006, 01:28:09
Job time : 42 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: December 5, 2006, 01:41:31 ; Search time 45 Seconds
(without alignments)
340.946 Million cell updates/sec

Title: US-10-507-132-2
Perfect score: 942
Sequence: 1 MGSQVQKSDEITFSDYLGLM.....WGEFDFDRIFEDGRETFGDK 172

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 351643 seqs, 89200972 residues

Total number of hits satisfying chosen parameters: 351643

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	942	100.0	172	6	US-10-507-132-2	Sequence 2, Appli
2	938	99.6	172	6	US-10-507-132-4	Sequence 4, Appli
3	87	9.2	941	6	US-10-449-902-44748	Sequence 44748, A
4	80.5	8.5	444	7	US-11-174-307B-3704	Sequence 3704, Ap
5	79.5	8.4	614	7	US-11-056-355B-70678	Sequence 70678, A
6	79.5	8.4	615	7	US-11-056-355B-78750	Sequence 78750, A
7	77	8.2	375	7	US-11-056-355B-65439	Sequence 65439, A
8	77	8.2	436	6	US-10-449-902-30829	Sequence 30829, A
9	77	8.2	436	6	US-10-449-902-50460	Sequence 50460, A
10	77	8.2	844	6	US-10-449-902-52228	Sequence 52228, A
11	76.5	8.1	596	6	US-10-449-902-47097	Sequence 47097, A
12	76.5	8.1	827	6	US-10-449-902-41550	Sequence 41550, A
13	76	8.1	537	6	US-10-953-349-24962	Sequence 24962, A
14	76	8.1	634	6	US-10-953-349-24961	Sequence 24961, A
15	76	8.1	664	6	US-10-953-349-24960	Sequence 24960, A
16	75.5	8.0	430	7	US-11-293-697-4232	Sequence 4232, Ap
17	75	8.0	497	7	US-11-282-262-9	Sequence 9, Appli
18	74.5	7.9	359	6	US-10-953-349-22948	Sequence 22948, A
19	74.5	7.9	393	6	US-10-953-349-22947	Sequence 22947, A
20	73.5	7.8	564	7	US-11-056-355B-76449	Sequence 76449, A
21	73.5	7.8	615	7	US-11-056-355B-76448	Sequence 76448, A
22	73.5	7.8	763	7	US-11-330-403-8316	Sequence 8316, Ap
23	73.5	7.8	809	7	US-11-056-355B-76447	Sequence 76447, A
24	73	7.7	319	6	US-10-805-394-5612	Sequence 5612, Ap
25	73	7.7	484	6	US-10-449-902-35955	Sequence 35955, A
26	72.5	7.7	464	7	US-11-330-403-16935	Sequence 16935, A
27	72	7.6	215	6	US-10-805-394-5489	Sequence 5489, Ap
28	72	7.6	546	7	US-11-056-355B-70680	Sequence 70680, A
29	72	7.6	547	7	US-11-056-355B-78752	Sequence 78752, A
30	72	7.6	548	7	US-11-056-355B-70679	Sequence 70679, A
31	72	7.6	549	7	US-11-056-355B-78751	Sequence 78751, A
32	72	7.6	973	7	US-11-330-403-9960	Sequence 9960, Ap
33	71.5	7.6	651	6	US-10-511-937-2401	Sequence 2401, Ap
34	71.5	7.6	651	7	US-11-329-941-2	Sequence 2, Appli
35	71	7.5	565	7	US-11-357-421-206	Sequence 206, App
36	71	7.5	1169	6	US-10-449-902-41184	Sequence 41184, A
37	71	7.5	1254	7	US-11-366-965-1028	Sequence 1028, Ap
38	70.5	7.5	818	6	US-10-449-902-51784	Sequence 51784, A
39	70	7.4	239	7	US-11-056-355B-19951	Sequence 19951, A
40	70	7.4	325	6	US-10-449-902-50076	Sequence 50076, A
41	70	7.4	327	7	US-11-056-355B-19950	Sequence 19950, A
42	70	7.4	391	7	US-11-056-355B-19949	Sequence 19949, A
43	70	7.4	415	6	US-10-449-902-36376	Sequence 36376, A
44	70	7.4	785	6	US-10-449-902-47774	Sequence 47774, A
45	70	7.4	785	6	US-10-449-902-52542	Sequence 52542, A

ALIGNMENTS

RESULT 1
US-10-507-132-2
; Sequence 2, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
; APPLICANT: Koichiro KAKU et al.
; TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
; TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
; FILE REFERENCE: 1254-0258PUS1
; CURRENT APPLICATION NUMBER: US/10/507,132
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: JP 2002-66955
; PRIOR FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Pyricularia oryzae
US-10-507-132-2

Query Match 100.0%; Score 942; DB 6; Length 172;
Best Local Similarity 100.0%; Pred. No. 5.1e-84;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60

Qy         61 MPAEEFVGMVSSKQMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MPAEEFVGMVSSKQMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE 120

Qy        121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172
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RESULT 2
US-10-507-132-4
; Sequence 4, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
; APPLICANT: Koichiro KAKU et al.
; TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
; TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
; FILE REFERENCE: 1254-0258PUS1
; CURRENT APPLICATION NUMBER: US/10/507,132

```
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: JP 2002-66955
;  PRIOR FILING DATE: 2002-03-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 172
;   TYPE: PRT
;   ORGANISM: Pyricularia oryzae
US-10-507-132-4

  Query Match             99.6%;  Score 938;  DB 6;  Length 172;
  Best Local Similarity   99.4%;  Pred. No. 1.2e-83;
  Matches  171;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60

Qy         61 MPAEEFVGMVSSKQMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE 120
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db         61 MPAEEFVGMVSSKQVLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE 120

Qy        121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172


RESULT 3
US-10-449-902-44748
; Sequence 44748, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44748
;   LENGTH: 941
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-44748

  Query Match             9.2%;  Score 87;  DB 6;  Length 941;
  Best Local Similarity   23.0%;  Pred. No. 3.9;
  Matches   34;  Conservative   16;  Mismatches   44;  Indels   54;  Gaps    7;

Qy         55 DKLW----EAMPAEEFVGMVSSKQMLGDPTLRTQHFI-----------GGTRWEKV--- 95
              ||||    ||:||:    :|       |||   :| :           |   |: :
Db        671 DKLWRFDMEALPAD----LVRRGMAEEDPT--AEHGLRLAIEDYPFANDGLLIWDAIKTW 724

Qy         96 ----------SEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDG----- 140
                       | | |  :|:            ||  |||    :  |: |:|
Db        725 VQAYVARFYPDADSVAGDEELQ--------AFWTEVRTKGHGDKKDAPWWPKLDSPESLA 776

Qy        141 ------VWKFAGLKPDIRWGEFDFDRIF 162
                   ||  |     : :|::||   |
Db        777 HTLTTIVWVAAAHHAAVNFGQYDFGGYF 804


RESULT 4
US-11-174-307B-3704
; Sequence 3704, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai
;  APPLICANT:  BROVER, Vyacheslav
;  TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
;  TITLE OF INVENTION:  USEFUL FOR MODIFYING PLANT CHARACTERISTICS
;  FILE REFERENCE: 2750-1601PUS2
;  CURRENT APPLICATION NUMBER: US/11/174,307B
;  CURRENT FILING DATE:  2005-06-30
;  PRIOR APPLICATION NUMBER: 60/583,671
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,781
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,651
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 3704
;   LENGTH: 444
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: PFam Name: HSP70; PFam Description: Hsp70 protein
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 19813; NR Description: luminal binding protein
;   OTHER INFORMATION: (BiP) [Nicotiana tabacum] >gi|100340|pir||S21880 dnaK-type
;   OTHER INFORMATION: molecular chaperone blp5 precursor - common tobacco
;   OTHER INFORMATION: >gi|729623|sp|Q03685|BIP5_TOBAC Luminal binding homolog 5) (GRP
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 19811; NR Description: luminal binding protein
;   OTHER INFORMATION: (BiP) [Nicotiana tabacum] >gi|100339|pir||S21879 dnaK-type
;   OTHER INFORMATION: molecular chaperone blp4 precursor - common tobacco
;   OTHER INFORMATION: >gi|729620|sp|Q03684|BIP4_TOBAC Luminal binding homolog 4) (GRP
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 1346172; NR Description: Luminal binding protein
;   OTHER INFORMATION: precursor (BiP) (78 kDa glucose-regulated protein homolog) (GRP 78
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 13398537; NR Description: BiP-isoform D [Glycine max]
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 2642238; NR Description: endoplasmic reticulum
;   OTHER INFORMATION: HSC70-cognate binding protein precursor [Glycine max]
;   OTHER INFORMATION: >gi|11277127|pir||T46574 dnaK-type molecular chaperone BiP
US-11-174-307B-3704

  Query Match             8.5%;  Score 80.5;  DB 7;  Length 444;
  Best Local Similarity   23.6%;  Pred. No. 6.7;
  Matches   35;  Conservative   25;  Mismatches   45;  Indels   43;  Gaps    7;

Qy         54 LDKLWEAMPAEEFVG------MVSSKQMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLR 107
              | || |:  || ::|      :|:  |   ||          :|:  :   |: |    |
Db        159 LAKLRES--AEAYLGRAIQEAIVTVPQQYNDP----------SRYSMLRAAELAGLRVTR 206

Qy        108 V------------PHQRYKDT-TMKEVTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWG 154
              :            |:: :|   :  : : |     |:: ||  :|||::| |   |  :|
Db        207 MIDEPTAAAVAHGLHRKLRDEGNVLVLHVGGGTSDASVMWY--VDGVFEFMGADEDPFFG 264

Qy        155 EFDFDRIFED----------GRETFGDK 172
                 |||:   |          |::   ||
Db        265 GQDFDQRIVDHFVELIRKKHGKDLSNDK 292


RESULT 5
```

```
US-11-056-355B-70678
; Sequence 70678, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 70678
;   LENGTH: 614
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(614)
;   OTHER INFORMATION: Ceres Seq. ID no. 2717494
US-11-056-355B-70678

  Query Match             8.4%;  Score 79.5;  DB 7;  Length 614;
  Best Local Similarity   23.2%;  Pred. No. 12;
  Matches   57;  Conservative   29;  Mismatches   61;  Indels   99;  Gaps   15;

Qy          6 QKSDE----------ITFSDYLGLMTCVYEWADSYD------------SKDWDRLRKVI 42
              | |||           :| | :|::   :  |  |              : : | |  :|
Db         29 QPSDEDLGTIIGPHQTSFDDEIGIVIGPHATVDDEDIDMDMGTTVGPQTNLNDDDLGTII 88

Qy         43 APTLRIDYRSFLDKLWEAMPAEEFVG-MVSSKQMLGDPTLRTQHFIGGTRW--------E 93
               |   |  : |        ||:   |  ||: |: |    :     | | |        |
Db         89 GPEFEIHKQDF--------PADFIFGTSVSAYQVEG---AKKGSGRGLTSWDEFTHMFPE 137

Qy         94 KVSE----DEVIGYHQLRVPHQRYKD--TTMKEVTMKGHAHSANLHWYKKI--------- 138
              || :    || : :      : ||||    |||:   |   | : | : :
Db        138 KVQQNGDGDEGVDF------YTRYKDDIKLMKELNTNGFRFS--ISWTRILPYGTIKKGV 189

Qy        139 --DGVWKF----------AGLKP-------------DIRWGEFDFDRIFEDGRE------ 167
                :|| ||          |::|              :: :| |  :|| || ||
Db        190 NEEGV-KFYNDLINELLANGIQPSVTLFHWESPLALEMEYGGFLNERIVEDFREFANFCF 248

Qy        168 -TFGDK 172
                |||:
Db        249 KEFGDR 254


RESULT 6
US-11-056-355B-78750
; Sequence 78750, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 78750
;   LENGTH: 615
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(615)
;   OTHER INFORMATION: Ceres Seq. ID no. 12644996
US-11-056-355B-78750

  Query Match             8.4%;  Score 79.5;  DB 7;  Length 615;
  Best Local Similarity   23.2%;  Pred. No. 12;
  Matches   57;  Conservative   29;  Mismatches   61;  Indels   99;  Gaps   15;

Qy          6 QKSDE----------ITFSDYLGLMTCVYEWADSYD------------SKDWDRLRKVI 42
              | |||           :| | :|::   :  |  |              : : | |  :|
Db         29 QPSDEDLGTIIGPHQTSFDDEIGIVIGPHATVDDEDIDMDMGTTVGPQTNLNDDDLGTII 88

Qy         43 APTLRIDYRSFLDKLWEAMPAEEFVG-MVSSKQMLGDPTLRTQHFIGGTRW--------E 93
               |   |  : |        ||:   |  ||: |: |    :     | | |        |
Db         89 GPEFEIHKQDF--------PADFIFGTSVSAYQVEG---AKKGSGRGLTSWDEFTHMFPE 137

Qy         94 KVSE----DEVIGYHQLRVPHQRYKD--TTMKEVTMKGHAHSANLHWYKKI--------- 138
              || :    || : :      : ||||    |||:   |   | : | : :
Db        138 KVQQNGDGDEGVDF------YTRYKDDIKLMKELNTNGFRFS--ISWTRILPYGTIKKGV 189

Qy        139 --DGVWKF----------AGLKP-------------DIRWGEFDFDRIFEDGRE------ 167
                :|| ||          |::|              :: :| |  :|| || ||
Db        190 NEEGV-KFYNDLINELLANGIQPSVTLFHWESPLALEMEYGGFLNERIVEDFREFANFCF 248

Qy        168 -TFGDK 172
                |||:
Db        249 KEFGDR 254


RESULT 7
US-11-056-355B-65439
; Sequence 65439, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 65439
;   LENGTH: 375
;   TYPE: prt
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(375)
;   OTHER INFORMATION: Ceres Seq. ID no. 15225494
US-11-056-355B-65439

  Query Match             8.2%;  Score 77;  DB 7;  Length 375;
  Best Local Similarity   22.2%;  Pred. No. 12;
  Matches   38;  Conservative   28;  Mismatches   67;  Indels   38;  Gaps   10;

Qy         25 EWADSYDSKDWDRLRKVIAPTLRIDYR-SFLDKLWEAMP--AEEFV--------GMVSSK 73
              :|||    :|      | :   |:  ||  :: : |   |   : |          :  |
Db        174 KWADGKKFED-----KFVDTLLKYGYRGQYMSENWLKQPLFIQSFAPSSLVHVSNLTDSP 228

Qy         74 Q--MLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTM----------KEV 121
              :  :: | |:|||     : ||  |:| :       |    :||| :          ::
Db        229 KIFLIDDTTVRTQD-TNQSYWEITSDDYLAYISNYVVGLGPWKDTIVPVAKNYLLEPTDL 287

Qy        122 TMKGHAHSANLHWYK-KIDGVWKFAGLKPDIRWGEFDF-------DRIFED 164
              : |||:  :| |  : :  :        |  : ||||        | :| |
Db        288 VARAHAHNLQVHPYTYRNENQFLHFDFHQD-PYAEFDFWINTMGVDGLFTD 337


RESULT 8
US-10-449-902-30829
; Sequence 30829, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30829
;   LENGTH: 436
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-30829

  Query Match             8.2%;  Score 77;  DB 6;  Length 436;
  Best Local Similarity   32.1%;  Pred. No. 14;
  Matches   25;  Conservative   15;  Mismatches   22;  Indels   16;  Gaps    4;

Qy         33 KDWDRLRKVI--APTLRI------DYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPTLRTQ 84
              |: | |: |:   | :||       ||| |:|::| |||  | ||:  :::       :|
Db        243 KNLDFLKTVMDRLPGVRIAFIGDGPYRSELEKMFEGMPA-VFTGMMQGEEL-------SQ 294

Qy         85 HFIGGTRWEKVSEDEVIG 102
               :  |  :   || | :|
Db        295 AYASGDVFVMPSESETLG 312


RESULT 9
US-10-449-902-50460
; Sequence 50460, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50460
;   LENGTH: 436
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-50460

  Query Match             8.2%;  Score 77;  DB 6;  Length 436;
  Best Local Similarity   32.1%;  Pred. No. 14;
  Matches   25;  Conservative   15;  Mismatches   22;  Indels   16;  Gaps    4;

Qy         33 KDWDRLRKVI--APTLRI------DYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPTLRTQ 84
              |: | |: |:   | :||       ||| |:|::| |||  | ||:  :::       :|
Db        243 KNLDFLKTVMDRLPGVRIAFIGDGPYRSELEKMFEGMPA-VFTGMMQGEEL-------SQ 294

Qy         85 HFIGGTRWEKVSEDEVIG 102
               :  |  :   || | :|
Db        295 AYASGDVFVMPSESETLG 312


RESULT 10
US-10-449-902-52228
; Sequence 52228, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52228
;   LENGTH: 844
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-52228

  Query Match             8.2%;  Score 77;  DB 6;  Length 844;
  Best Local Similarity   23.0%;  Pred. No. 32;
  Matches   32;  Conservative   19;  Mismatches   32;  Indels   56;  Gaps   10;

Qy         26 WADSYDSKDW-DRLRKVIAPTLRIDYRSF--------LDK-----LW-EAMPAEEFVGMV 70
              | | :|:  | | : : | | |::  : |         ||:     :|  |:|    | |
Db        599 WKDVFDAASWEDLIVRYIVPKLKMALQEFQINPANQKLDQFNWVMIWASAIPVHHMVHM- 657

Qy         71 SSKQMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSA 130
                        |    |   ::|::|       || |  |:  : :
Db        658 ----------LEVDFF---SKWQQVL------YHWLCSPNPDFNEI-------------- 684

Qy        131 NLHWYKKIDGVWKFAGLKP 149
               ::|||     ||  || |
Db        685 -MNWYKG----WK--GLFP 696


RESULT 11
US-10-449-902-47097
; Sequence 47097, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47097
;   LENGTH: 596
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-47097

  Query Match             8.1%;  Score 76.5;  DB 6;  Length 596;
  Best Local Similarity   22.5%;  Pred. No. 23;
  Matches   36;  Conservative   21;  Mismatches   50;  Indels   53;  Gaps    9;

Qy         26 WADSY--DSKDWDRLRKVIAPTLRIDYRSFLDKLWE--------AMPAEEFVGMVSSKQM 75
              |  |   |  :|  |   : ||   |     :  |           |:||  : |: :||:
Db         85 WGHSVSGDLLNWAALDTALDPTSPFD----ANGCWSGSATILPGALPAILYTGIDASKEQ 140
```

```
Qy          76 L---------GDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGH 126
               :           || ||         ||| : : ||      ||  :::| :
Db         141 VQNVAFAKNPSDPLLR--------EWEKPAYNPVIAL-PADVPGDKFRDPSTA------- 184

Qy         127 AHSANLHWYKKIDGVWKFA------GLKPDIRWGEFDFDR 160
                     |  : ||:|: |      |:   : :   || |
Db         185 -------WLGR-DGLWRVAVSAEVDGVASTLVYRSKDFVR 216


RESULT 12
US-10-449-902-41550
; Sequence 41550, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41550
;   LENGTH: 827
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-449-902-41550

  Query Match             8.1%;  Score 76.5;  DB 6;  Length 827;
  Best Local Similarity   27.8%;  Pred. No. 35;
  Matches   25;  Conservative    9;  Mismatches   27;  Indels   29;  Gaps    4;

Qy           4 QVQKSD-------EITFSDYLGLMTCVYE----------WADSYDSKDW---------DR 37
               |::|||       ||   :     | ::          | | |     |
Db         690 QLEKSDNCIWLGVEILMGESATTKTDIFAYGIVLWELLFWGDPYPDHTWMSQLEVDIKAG 749

Qy          38 LRKVIAPTLR---IDYRSFLDKLWEAMPAE 64
               || || |  |    :|   ::| |||:|||
Db         750 LRPVIPPDSRQIFPEYIILMEKCWEALPAE 779


RESULT 13
US-10-953-349-24962
; Sequence 24962, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24962
;   LENGTH: 537
;   TYPE: PRT
;   ORGANISM: Glycine max
US-10-953-349-24962

  Query Match             8.1%;  Score 76;  DB 6;  Length 537;
  Best Local Similarity   20.3%;  Pred. No. 23;
  Matches   28;  Conservative   23;  Mismatches   43;  Indels   44;  Gaps    7;

Qy          56 KLW----EAMPAEEFVGMVSSKQMLGDPTLRTQHFIGGTR--------------WEKVS 96
               |||    |::||:    ::     : ||::       | :               |  :
Db         269 KLWRFDMESLPAD----LIRRGMAVDDPSMPC-----GVKLVIDDYPYAADGLLIWSAIK 319

Qy          97 E-DEVIGYHQLRVPHQRYKDTTM----KEVTMKGHAHSANLHWYKKIDG---------- 140
               |  |    |    |:    |  :    :|: :|||:   |  |: |:|
Db         320 EWVESYVAHFYSDPNSVTSDVELQAWWREIKLKGHSDKKNEPWWPKLDTKEDLSGILTTM 379

Qy         141 VWKFAGLKPDIRWGEFDF 158
               :|  :|    | :|:: |
Db         380 IWIASGQHAAINFGQYPF 397


RESULT 14
US-10-953-349-24961
; Sequence 24961, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24961
;   LENGTH: 634
;   TYPE: PRT
;   ORGANISM: Glycine max
US-10-953-349-24961

  Query Match             8.1%;  Score 76;  DB 6;  Length 634;
  Best Local Similarity   20.3%;  Pred. No. 28;
  Matches   28;  Conservative   23;  Mismatches   43;  Indels   44;  Gaps    7;

Qy          56 KLW----EAMPAEEFVGMVSSKQMLGDPTLRTQHFIGGTR--------------WEKVS 96
               |||    |::||:    ::     : ||::       | :               |  :
Db         366 KLWRFDMESLPAD----LIRRGMAVDDPSMPC-----GVKLVIDDYPYAADGLLIWSAIK 416

Qy          97 E-DEVIGYHQLRVPHQRYKDTTM----KEVTMKGHAHSANLHWYKKIDG---------- 140
               |  |    |    |:    |  :    :|: :|||:   |  |: |:|
Db         417 EWVESYVAHFYSDPNSVTSDVELQAWWREIKLKGHSDKKNEPWWPKLDTKEDLSGILTTM 476

Qy         141 VWKFAGLKPDIRWGEFDF 158
               :|  :|    | :|:: |
Db         477 IWIASGQHAAINFGQYPF 494


RESULT 15
US-10-953-349-24960
; Sequence 24960, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24960
;   LENGTH: 664
;   TYPE: PRT
;   ORGANISM: Glycine max
US-10-953-349-24960

  Query Match             8.1%;  Score 76;  DB 6;  Length 664;
  Best Local Similarity   20.3%;  Pred. No. 30;
  Matches   28;  Conservative   23;  Mismatches   43;  Indels   44;  Gaps    7;

Qy          56 KLW----EAMPAEEFVGMVSSKQMLGDPTLRTQHFIGGTR--------------WEKVS 96
               |||    |::||:    ::     : ||::       | :               |  :
Db         396 KLWRFDMESLPAD----LIRRGMAVDDPSMPC-----GVKLVIDDYPYAADGLLIWSAIK 446
```

```
Qy          97 E-DEVIGYHQLRVPHQRYKDTTM----KEVTMKGHAHSANLHWYKKIDG---------- 140
               |  |    |    |:    |  :    :|: :|||:   |  |: |:|
Db         447 EWVESYVAHFYSDPNSVTSDVELQAWWREIKLKGHSDKKNEPWWPKLDTKEDLSGILTTM 506

Qy         141 VWKFAGLKPDIRWGEFDF 158
               :|  :|    | :|:: |
Db         507 IWIASGQHAAINFGQYPF 524
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Search completed: December 5, 2006, 01:45:21
Job time : 46 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: December 5, 2006, 01:39:46 ; Search time 187 Seconds
(without alignments)
426.059 Million cell updates/sec

Title: US-10-507-132-2
Perfect score: 942
Sequence: 1 MGSQVQKSDEITFSDYLGLM.....WGEFDFDRIFEDGRETFGDK 172

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	87	9.2	924	5	US-10-491-733-22	Sequence 22, Appl
2	85	9.0	265	3	US-09-882-227-306	Sequence 306, App
3	84	8.9	349	5	US-10-847-972-60	Sequence 60, Appl
4	84	8.9	349	6	US-11-108-528-46	Sequence 46, Appl
5	84	8.9	411	4	US-10-425-114-56305	Sequence 56305, A
6	84	8.9	411	4	US-10-425-115-213325	Sequence 213325,
7	81	8.6	349	4	US-10-285-976-21	Sequence 21, Appl
8	81	8.6	349	4	US-10-364-888-2	Sequence 2, Appli
9	81	8.6	349	4	US-10-364-888-6	Sequence 6, Appli
10	81	8.6	349	4	US-10-364-888-8	Sequence 8, Appli
11	81	8.6	349	5	US-10-678-639-20	Sequence 20, Appl
12	81	8.6	349	5	US-10-847-972-22	Sequence 22, Appl
13	81	8.6	349	6	US-11-108-528-44	Sequence 44, Appl
14	79.5	8.4	614	6	US-11-096-568A-28399	Sequence 28399, A
15	79.5	8.4	1239	6	US-11-097-143-1701	Sequence 1701, Ap
16	79	8.4	266	4	US-10-335-977-6427	Sequence 6427, Ap
17	79	8.4	702	4	US-10-369-493-23474	Sequence 23474, A
18	78.5	8.3	374	4	US-10-156-761-7674	Sequence 7674, Ap
19	78	8.3	424	4	US-10-424-599-282063	Sequence 282063,
20	78	8.3	861	6	US-11-087-099-1420	Sequence 1420, Ap
21	78	8.3	861	6	US-11-188-298-12347	Sequence 12347, A
22	78	8.3	2195	4	US-10-437-963-181567	Sequence 181567,
23	77.5	8.2	371	5	US-10-469-204-150	Sequence 150, App
24	77.5	8.2	598	4	US-10-437-963-142051	Sequence 142051,
25	77	8.2	375	6	US-11-096-568A-13512	Sequence 13512, A
26	77	8.2	436	4	US-10-437-963-178354	Sequence 178354,
27	77	8.2	844	4	US-10-437-963-132118	Sequence 132118,
28	76.5	8.1	834	5	US-10-481-032A-70	Sequence 70, Appl
29	76	8.1	227	4	US-10-314-657-51	Sequence 51, Appl
30	76	8.1	227	5	US-10-473-193-51	Sequence 51, Appl
31	76	8.1	583	4	US-10-289-757-79	Sequence 79, Appl
32	76	8.1	583	5	US-10-955-745-79	Sequence 79, Appl
33	76	8.1	1073	4	US-10-032-585-7157	Sequence 7157, Ap
34	75.5	8.0	430	4	US-10-108-260A-4232	Sequence 4232, Ap
35	75.5	8.0	591	4	US-10-369-493-1784	Sequence 1784, Ap
36	75.5	8.0	36946	5	US-10-840-512-155	Sequence 155, App
37	75	8.0	463	4	US-10-437-963-154890	Sequence 154890,
38	75	8.0	497	4	US-10-179-766-9	Sequence 9, Appli
39	75	8.0	767	6	US-11-188-298-12759	Sequence 12759, A
40	75	8.0	798	4	US-10-696-616-20	Sequence 20, Appl
41	75	8.0	1397	4	US-10-369-493-2413	Sequence 2413, Ap
42	74.5	7.9	348	4	US-10-437-963-136067	Sequence 136067,
43	74.5	7.9	436	4	US-10-282-122A-62311	Sequence 62311, A
44	74.5	7.9	436	4	US-10-282-122A-64780	Sequence 64780, A
45	74.5	7.9	437	3	US-09-996-634-136	Sequence 136, App

ALIGNMENTS

RESULT 1
US-10-491-733-22
; Sequence 22, Application US/10491733
; Publication No. US20040219675A1
; GENERAL INFORMATION:
; APPLICANT: Syngenta Participations AG
; APPLICANT: Sainz, Manuel
; APPLICANT: Salmeron, John
; APPLICANT: Weislo, Laura J.
; TITLE OF INVENTION: Nucleic Acid Molecules from Rice Encoding Proteins for Abiotic St
; TITLE OF INVENTION: Resistance, Yield, Disease Resistance and Nutritional Quality an
; FILE REFERENCE: 60127WOPCT
; CURRENT APPLICATION NUMBER: US/10/491,733
; CURRENT FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: 60/334,501
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 924
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-491-733-22

Query Match 9.2%; Score 87; DB 5; Length 924;
Best Local Similarity 23.0%; Pred. No. 8;
Matches 34; Conservative 16; Mismatches 44; Indels 54; Gaps 7;

```
Qy         55 DKLW----EAMPAEEFVGMVSSKQMLGDPTLRTQHFI------------GGTRWEKV--- 95
              ||||    ||:||:    :|       |||   :| :            |   |: :
Db        654 DKLWRFDTEALPAD----LVRRGMAEEDPT--AEHGLKLAIEDYPFANDGLLIWDAIKTW 707

Qy         96 ----------SEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDG----- 140
                       | | |  :|:           ||  |||     :  |: |:|
Db        708 VQAYVARFYPDADSVAGDEELQ--------AFWTEVRTKGHGDKKDAPWWPKLDSPESLA 759

Qy        141 ------VWKFAGLKPDIRWGEFDFDRIF 162
                   ||  |     : :|::||    |
Db        760 HTLTTIVWVAAAHHAAVNFGQYDFGGYF 787
```

RESULT 2
US-09-882-227-306
; Sequence 306, Application US/09882227
; Publication No. US20030158396A1
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean-Francois

; APPLICANT: Ooomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20030158396A1el Helicobacter Polypeptides in the
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 06132/047002
; CURRENT APPLICATION NUMBER: US/09/882,227
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 08/902,615
; PRIOR FILING DATE: 1997-07-29
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 306
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 118
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-882-227-306

Query Match 9.0%; Score 85; DB 3; Length 265;
Best Local Similarity 22.4%; Pred. No. 2.7;
Matches 39; Conservative 28; Mismatches 57; Indels 50; Gaps 7;

```
Qy          13 FSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKL--WEAMPAEEFVGMV 70
               |  :.|       ::|| ::   |:: |: |   :|  ||| :   |    | : :|:|
Db         102 FYQFVG-------FSDSCKNRRRXRVKCVLLPNESVDSLSFLYRSANWSEREAYDMLGIV 154

Qy          71 SSK----------QMLGDPTLRTQHFIGG--TRWEKVSE------DEVIGYHQ------ 105
                 |             :| | ||:    |    :| :| :       ||:|  |
Db         155 FDKHPYLKRLIMPHDWVGHPLLRSYPLKGDEFAQWYEVDKIFGKEYREVVGKEQRDSARV 214

Qy         106 --------LRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDGVWKFAGLKPDI 151
                     :: ::: |   :||| |         | :|||  |     : | |
Db         215 DEKDTFNFAKIGYEQGKGEELKEVEEK--------HAFKKIPFVKDLHKIAPTI 260
```

RESULT 3
US-10-847-972-60
; Sequence 60, Application US/10847972
; Publication No. US20050049195A1
; GENERAL INFORMATION:
; APPLICANT: ZOU, YIMIN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR NERVE REGENERATION
; FILE REFERENCE: ARCD:395US
; CURRENT APPLICATION NUMBER: US/10/847,972
; CURRENT FILING DATE: 2004-05-17
; PRIOR APPLICATION NUMBER: 60/470,913
; PRIOR FILING DATE: 2003-05-15
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-847-972-60

Query Match 8.9%; Score 84; DB 5; Length 349;
Best Local Similarity 31.1%; Pred. No. 4.8;
Matches 32; Conservative 11; Mismatches 36; Indels 24; Gaps 7;

```
Qy          84 QHFIGGTRW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-------ANLH- 133
               ||     ||    : |  | |  :|||  :     |    :|  | ||:         ||
Db          74 QHQFRFGRWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSN 130

Qy         134 ---------WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                      :| : :| ||: |   |:|:|  || | | | ||
Db         131 CGCDREKQGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171
```

RESULT 4
US-11-108-528-46

; Sequence 46, Application US/11108528
; Publication No. US20050261189A1
; GENERAL INFORMATION:
; APPLICANT: Larsen, Glenn
; APPLICANT: Marvin, Martha
; APPLICANT: Li, Dean Y.
; APPLICANT: Wang, Elizabeth
; APPLICANT: Chen, C. M. Amy
; APPLICANT: Shamah, Steven M.
; TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: HYDR-P01-041
; CURRENT APPLICATION NUMBER: US/11/108,528
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/563,137
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/598,368
; PRIOR FILING DATE: 2004-08-02
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Mouse
US-11-108-528-46

Query Match 8.9%; Score 84; DB 6; Length 349;
Best Local Similarity 31.1%; Pred. No. 4.8;
Matches 32; Conservative 11; Mismatches 36; Indels 24; Gaps 7;

```
Qy          84 QHFIGGTRW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-------ANLH- 133
               ||     ||    : |  | |  :|||  :     |    :|  | ||:         ||
Db          74 QHQFRFGRWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSN 130

Qy         134 ---------WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                      :| : :| ||: |   |:|:|  || | | | ||
Db         131 CGCDREKQGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171
```

RESULT 5
US-10-425-114-56305
; Sequence 56305, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 56305
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73131C10_FLI.pep
US-10-425-114-56305

Query Match 8.9%; Score 84; DB 4; Length 411;
Best Local Similarity 25.2%; Pred. No. 5.9;
Matches 35; Conservative 17; Mismatches 31; Indels 56; Gaps 10;

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Qy          26 WADSYDSKDW-DRLRKVIAPTLRIDYRSF--------LDK-----LW-EAMPAEEFVGMV 70
               | | :||  | | : : | | ||:  : |        ||:     ||  |:| :  | |
Db         171 WKDVFDSASWEDLIVRYIIPKLRLALQDFQINPANQKLDQFNWVMLWTSAIPVQLMVHM- 229

Qy          71 SSKQMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSA 130
```

```
                    |    |   ::|::|       || |  |:  : :
Db        230 ----------LEVDFF---SKWQQVL------YHWLCSPNPDFNEI-------------- 256

Qy        131 NLHWYKKIDGVWKFAGLKP 149
                ::|||     ||  || |
Db        257 -MNWYKG----WK--GLFP 268


RESULT 6
US-10-425-115-213325
; Sequence 213325, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 213325
;   LENGTH: 411
;   TYPE: PRT
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_126150C.1.pep
US-10-425-115-213325

  Query Match             8.9%;  Score 84;  DB 4;  Length 411;
  Best Local Similarity   25.2%;  Pred. No. 5.9;
  Matches   35;  Conservative   17;  Mismatches   31;  Indels   56;  Gaps   10;

Qy         26 WADSYDSKDW-DRLRKVIAPTLRIDYRSF--------LDK-----LW-EAMPAEEFVGMV 70
              | | :||  | | : : | | ||:  : |         ||:     ||  |:| :  | |
Db        171 WKDVPDSASWEDLIVRYIIPKLRLALQDFQINPANQKLDQFNWVMLWTSAIPVQLMVHM- 229

Qy         71 SSKQMLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSA 130
                        |    |   ::|::|       || |  |:  : :
Db        230 ----------LEVDFF---SKWQQVL------YHWLCSPNPDFNEI-------------- 256

Qy        131 NLHWYKKIDGVWKFAGLKP 149
                ::|||     ||  || |
Db        257 -MNWYKG----WK--GLFP 268


RESULT 7
US-10-285-976-21
; Sequence 21, Application US/10285976
; Publication No. US20030165500A1
; GENERAL INFORMATION:
;  APPLICANT: Rhee, Chae-Seo
;  APPLICANT:  Malini, Sen
;  APPLICANT:  Wu, Christina
;  APPLICANT:  Leoni, Lorenzo M.
;  APPLICANT:  Corr, Maripat
;  APPLICANT:  Carson, Dennis A.
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
;  TITLE OF INVENTION:  in Head and Neck Squamous Cell Carcinomas
;  FILE REFERENCE: 02307O-130320US
;  CURRENT APPLICATION NUMBER: US/10/285,976
;  CURRENT FILING DATE:  2002-11-01
;  PRIOR APPLICATION NUMBER: US 60/287,995
;  PRIOR FILING DATE: 2001-05-01
;  PRIOR APPLICATION NUMBER: WO PCT/US02/13802
;  PRIOR FILING DATE: 2002-05-01
;  NUMBER OF SEQ ID NOS: 232
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
;   LENGTH: 349
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: human Wnt-7b
US-10-285-976-21

  Query Match             8.6%;  Score 81;  DB 4;  Length 349;
  Best Local Similarity   31.2%;  Pred. No. 10;
  Matches   30;  Conservative   11;  Mismatches   31;  Indels   24;  Gaps    7;

Qy         91 RW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-------ANLH-------- 133
              ||    : |  | |  :|||  :    |    :|  | ||:        ||
Db         81 RWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSNCGCDREK 137

Qy        134 --WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                :| : :| ||: |    |:|:|  || | | | ||
Db        138 QGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171


RESULT 8
US-10-364-888-2
; Sequence 2, Application US/10364888
; Publication No. US20040023259A1
; GENERAL INFORMATION:
;  APPLICANT: Rastelli, Luca
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Gangolli, Esha
;  APPLICANT:  Guo, Xiaojia
;  APPLICANT:  Malyankar, Uriel
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Pena, Carol
;  APPLICANT:  Shimkets, Richard
;  APPLICANT:  Spytek, Kimberly
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Rieger, Daniel
;  APPLICANT:  Edinger, Shlomit
;  APPLICANT:  Burgess, Catherine
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 15966-744CIP
;  CURRENT APPLICATION NUMBER: US/10/364,888
;  CURRENT FILING DATE:  2003-02-12
;  PRIOR APPLICATION NUMBER: 60/356,375
;  PRIOR FILING DATE: 2002-02-12
;  PRIOR APPLICATION NUMBER: 60/387,082
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: 09/625,634
;  PRIOR FILING DATE: 2000-07-26
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 2
;   LENGTH: 349
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-364-888-2

  Query Match             8.6%;  Score 81;  DB 4;  Length 349;
  Best Local Similarity   31.2%;  Pred. No. 10;
  Matches   30;  Conservative   11;  Mismatches   31;  Indels   24;  Gaps    7;

Qy         91 RW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-------ANLH-------- 133
              ||    : |  | |  :|||  :    |    :|  | ||:        ||
Db         81 RWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSNCGCDREK 137

Qy        134 --WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                :| : :| ||: |    |:|:|  || | | | ||
Db        138 QGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171


RESULT 9
US-10-364-888-6
; Sequence 6, Application US/10364888
; Publication No. US20040023259A1
```

; GENERAL INFORMATION:
; APPLICANT: Rastelli, Luca
; APPLICANT: Zhong, Haihong
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gangolli, Esha
; APPLICANT: Guo, Xiaojia
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol
; APPLICANT: Shimkets, Richard
; APPLICANT: Spytek, Kimberly
; APPLICANT: Vernet, Corine
; APPLICANT: Rieger, Daniel
; APPLICANT: Edinger, Shlomit
; APPLICANT: Burgess, Catherine
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE:.15966-744CIP
; CURRENT APPLICATION NUMBER: US/10/364,888
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: 60/356,375
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/387,082
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 09/625,634
; PRIOR FILING DATE: 2000-07-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 6
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-364-888-6

Query Match 8.6%; Score 81; DB 4; Length 349;
Best Local Similarity 31.2%; Pred. No. 10;
Matches 30; Conservative 11; Mismatches 31; Indels 24; Gaps 7;

```
Qy          91 RW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-------ANLH-------- 133
               ||    : |  | |  :|||  :    |    :|  | ||:        ||
Db          81 RWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSNCGCDREK 137

Qy         134 --WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                 :| : :| ||: |   |:|:|  || | | | ||
Db         138 QGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171
```

RESULT 10
US-10-364-888-8
; Sequence 8, Application US/10364888
; Publication No. US20040023259A1
; GENERAL INFORMATION:
; APPLICANT: Rastelli, Luca
; APPLICANT: Zhong, Haihong
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gangolli, Esha
; APPLICANT: Guo, Xiaojia
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol
; APPLICANT: Shimkets, Richard
; APPLICANT: Spytek, Kimberly
; APPLICANT: Vernet, Corine
; APPLICANT: Rieger, Daniel
; APPLICANT: Edinger, Shlomit
; APPLICANT: Burgess, Catherine
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 15966-744CIP
; CURRENT APPLICATION NUMBER: US/10/364,888
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: 60/356,375
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/387,082
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 09/625,634
; PRIOR FILING DATE: 2000-07-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 8
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-364-888-8

Query Match 8.6%; Score 81; DB 4; Length 349;
Best Local Similarity 31.2%; Pred. No. 10;
Matches 30; Conservative 11; Mismatches 31; Indels 24; Gaps 7;

```
Qy          91 RW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-------ANLH-------- 133
               ||    : |  | |  :|||  :    |    :|  | ||:        ||
Db          81 RWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSNCGCDREK 137

Qy         134 --WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                 :| : :| ||: |   |:|:|  || | | | ||
Db         138 QGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171
```

RESULT 11
US-10-678-639-20
; Sequence 20, Application US/10678639
; Publication No. US20040247593A1
; GENERAL INFORMATION:
; APPLICANT: He, Biao
; APPLICANT: You, Liang
; APPLICANT: Xu, Zhidong
; APPLICANT: Jablons, David M.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Methods for Treating Cancer by Inhibiting Wnt Signaling
; FILE REFERENCE: 023070-125630US
; CURRENT APPLICATION NUMBER: US/10/678,639
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: US 10/264,825
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US 60/509,037
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US 60/491,350
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Wingless-type 7B (Wnt-7B) peptide sequence
US-10-678-639-20

Query Match 8.6%; Score 81; DB 5; Length 349;
Best Local Similarity 31.2%; Pred. No. 10;
Matches 30; Conservative 11; Mismatches 31; Indels 24; Gaps 7;

```
Qy          91 RW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-------ANLH-------- 133
               ||    : |  | |  :|||  :    |    :|  | ||:        ||
Db          81 RWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSNCGCDREK 137

Qy         134 --WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                 :| : :| ||: |   |:|:|  || | | | ||
Db         138 QGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171
```

RESULT 12
US-10-847-972-22
; Sequence 22, Application US/10847972
; Publication No. US20050049195A1
; GENERAL INFORMATION:
; APPLICANT: ZOU, YIMIN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR NERVE REGENERATION

```
;  FILE REFERENCE: ARCD:395US
;  CURRENT APPLICATION NUMBER: US/10/847,972
;  CURRENT FILING DATE:  2004-05-17
;  PRIOR APPLICATION NUMBER: 60/470,913
;  PRIOR FILING DATE: 2003-05-15
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 349
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-847-972-22

  Query Match             8.6%;  Score 81;  DB 5;  Length 349;
  Best Local Similarity   31.2%;  Pred. No. 10;
  Matches   30;  Conservative   11;  Mismatches   31;  Indels   24;  Gaps    7;

Qy          91 RW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-------ANLH-------- 133
               ||    : |  | |  :||| :    |    :|  | ||:        ||
Db          81 RWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSNCGCDREK 137

Qy         134 --WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                 :| : :| ||: |   |:|:|  || | | | ||
Db         138 QGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171


RESULT 13
US-11-108-528-44
; Sequence 44, Application US/11108528
; Publication No. US20050261189A1
; GENERAL INFORMATION:
;  APPLICANT: Larsen, Glenn
;  APPLICANT:  Marvin, Martha
;  APPLICANT:  Li, Dean Y.
;  APPLICANT:  Wang, Elizabeth
;  APPLICANT:  Chen, C. M. Amy
;  APPLICANT:  Shamah, Steven M.
;  TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
;  TITLE OF INVENTION:  PROLIFERATION
;  FILE REFERENCE: HYDR-P01-041
;  CURRENT APPLICATION NUMBER: US/11/108,528
;  CURRENT FILING DATE:  2005-04-18
;  PRIOR APPLICATION NUMBER: US 60/563,137
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: US 60/598,368
;  PRIOR FILING DATE: 2004-08-02
;  NUMBER OF SEQ ID NOS: 86
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
;   LENGTH: 349
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-108-528-44

  Query Match             8.6%;  Score 81;  DB 6;  Length 349;
  Best Local Similarity   31.2%;  Pred. No. 10;
  Matches   30;  Conservative   11;  Mismatches   31;  Indels   24;  Gaps    7;

Qy          91 RW--EKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHS-------ANLH-------- 133
               ||    : |  | |  :||| :    |    :|  | ||:        ||
Db          81 RWNCSALGEKTVFG-QELRVGSREAAFT--YAITAAGVAHAVTAACSQGNLSNCGCDREK 137

Qy         134 --WYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRE 167
                 :| : :| ||: |   |:|:|  || | | | ||
Db         138 QGYYNQAEG-WKWGGCSADVRYG-IDFSRRFVDARE 171


RESULT 14
US-11-096-568A-28399
; Sequence 28399, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28399
;   LENGTH: 614
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(614)
;   OTHER INFORMATION: Ceres Seq. ID no. 2717494
US-11-096-568A-28399

  Query Match             8.4%;  Score 79.5;  DB 6;  Length 614;
  Best Local Similarity   23.2%;  Pred. No. 29;
  Matches   57;  Conservative   29;  Mismatches   61;  Indels   99;  Gaps   15;

Qy           6 QKSDE----------ITFSDYLGLMTCVYEWADSYD-------------SKDWDRLRKVI 42
               | |||           :| | :|::   :    |  |              : : | |  :|
Db          29 QPSDEDLGTIIGPHQTSPDDEIGIVIGPHATVDDEDIDMDMGTTVGPQTNLNDDDLGTII 88

Qy          43 APTLRIDYRSFLDKLWEAMPAEEFVG-MVSSKQMLGDPTLRTQHFIGGTRW--------E 93
               |   |  : |         ||:   |  ||: |: |    :      | | |        |
Db          89 GPEFEIHKQDF--------PADFIFGTSVSAYQVEG---AKKGSGRGLTSWDEFTHMFPE 137

Qy          94 KVSE----DEVIGYHQLRVPHQRYKD--TTMKEVTMKGHAHSANLHWYKKI--------- 138
               || :    || : :      : ||||    |||:   |   |  : | : :
Db         138 KVQQNGDGDEGVDF------YTRYKDDIKLMKELNTNGFRFS--ISWTRILPYGTIKKGV 189

Qy         139 --DGVWKF----------AGLKP-------------DIRWGEFDFDRIFEDGRE------ 167
                 :|| ||           |::|             :: :| |  :|| || ||
Db         190 NEEGV-KFYNDLINELLANGIQPSVTLFHWESPLALEMEYGGFLNERIVEDFREFANFCF 248

Qy         168 -TFGDK 172
                |||:
Db         249 KEFGDR 254


RESULT 15
US-11-097-143-1701
; Sequence 1701, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
;  APPLICANT: Venter, J. Craig
;  APPLICANT:  et al.
;  TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
;  TITLE OF INVENTION:  ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
;  TITLE OF INVENTION:  DROSOPHILA GENES.
;  FILE REFERENCE: CL000728
;  CURRENT APPLICATION NUMBER: US/11/097,143
;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: 60/157,832
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: 60/160,191
;  PRIOR FILING DATE: 1999-10-19
;  PRIOR APPLICATION NUMBER: 60/161,932
;  PRIOR FILING DATE: 1999-10-28
;  PRIOR APPLICATION NUMBER: 60/164,769
;  PRIOR FILING DATE: 1999-11-12
;  PRIOR APPLICATION NUMBER: 60/173,383
;  PRIOR FILING DATE: 1999-12-28
;  PRIOR APPLICATION NUMBER: 60/175,693
;  PRIOR FILING DATE: 2000-01-12
;  PRIOR APPLICATION NUMBER: 60/184,831
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: 60/191,637
;  PRIOR FILING DATE: 2000-03-23
;  NUMBER OF SEQ ID NOS: 43008
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1701
```

; LENGTH: 1239
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-1701

Query Match 8.4%; Score 79.5; DB 6; Length 1239;
Best Local Similarity 27.6%; Pred. No. 71;
Matches 32; Conservative 20; Mismatches 51; Indels 13; Gaps 4;

```
Qy         34 DWDRLRKVIA--PTL---RIDYRSFLDKLWEAMPAEEFVGMVSSKQMLGDPTLRTQHFI- 87
              ||  :   |||  ||     |   :  |:    : ||| ||     : |  ||  |   |
Db        769 DWRQNNIVIADQPTFVKYLIKVVAINDRGESNVAAEEVVGYSGEDRPLDAPTNFTMRQIT 828

Qy         88 ----GGTRWEKVSEDEVIGY---HQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYK 136
                  |   |  |||: | |:   ::::   :   :  ::|: :||  |:| :  :|
Db        829 SSTSGYMAWTPVSEESVRGHFKGYKIQTWTENEGEEGLREIHVKGDTHNALVTQFK 884
```

Search completed: December 5, 2006, 01:44:31
Job time : 189 secs

GenCore version 5.1.9

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2006, 19:11:55 ; Search time 4365 Seconds
(without alignments)
3305.198 Million cell updates/sec

Title: US-10-507-132-2
Perfect score: 942
Sequence: 1 MGSQVQKSDEITFSDYLGLM.....WGEFDFDRIFEDGRETFGDK 172

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10507132/runat_04122006_143903_11302/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss07
-USER=US10507132_@CGN_1_1_6323_@runat_04122006_143903_11302 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	938	99.6	619	3	BM863356	BM863356 mgcm006xO
	2	933	99.0	657	3	BM864194	BM864194 mgcm008xJ
	3	932	98.9	664	3	BM863315	BM863315 mgcm006xE
	4	923	98.0	649	3	BM863340	BM863340 mgcm006xK
	5	861	91.4	593	3	BM863546	BM863546 mgcm006xF
	6	859	91.2	571	3	BM863710	BM863710 mgcm007xE
	7	853	90.6	599	3	BM864156	BM864156 mgcm008xD
	8	833	88.4	643	3	BM864467	BM864467 mgcm010xH
	9	785	83.3	523	3	BM863209	BM863209 mgcm005xD
	10	772	82.0	602	3	BM863558	BM863558 mgcm006xH
	11	748	79.4	486	3	BM863639	BM863639 mgcm007xG
c	12	715	75.9	781	3	BM864820	BM864820 mgap007xA
	13	703	74.6	510	3	BM863374	BM863374 mgcm006xC
	14	703	74.6	530	3	BM863357	BM863357 mgcm006xO
	15	694	73.7	600	3	BM864472	BM864472 mgcm010xJ
	16	685	72.7	552	5	CD275566	CD275566 T143B0121
	17	685	72.7	588	5	CD275905	CD275905 T143B0122
	18	675	71.7	515	3	BM861796	BM861796 mgcm001xI
	19	665	70.6	504	3	BM863499	BM863499 mgcm006xL
	20	649.5	68.9	473	3	BM864018	BM864018 mgcm008xG
	21	643	68.3	530	5	CD275940	CD275940 T143B0156
	22	629	66.8	499	5	CD273332	CD273332 T143B0196
	23	618	65.6	573	3	BQ109916	BQ109916 VD0100E09
	24	605	64.2	507	5	CD275678	CD275678 T143B0071
	25	596	63.3	430	4	CD028671	CD028671 mgcm007xH
	26	564	59.9	366	3	BM864053	BM864053 mgcm008xM
	27	560	59.4	429	5	CD274144	CD274144 T143B0403
c	28	548	58.2	541	4	CD036729	CD036729 mgsu011xC
c	29	530.5	56.3	570	4	CD034317	CD034317 mgmt015xP
	30	529	56.2	398	3	BM861952	BM861952 mgcm001xL
c	31	496	52.7	491	4	CD035038	CD035038 mgmt018xH
c	32	477	50.6	486	4	CD035120	CD035120 mgmt018xL
	33	463	49.2	377	5	CD276416	CD276416 T143B0271
c	34	452	48.0	489	3	BM863213	BM863213 mgcm005xD
	35	408	43.3	441	3	BM871833	BM871833 mgns015xB
	36	387.5	41.1	476	2	BG280255	BG280255 c2b06np.r
	37	355	37.7	563	5	CK906746	CK906746 rhzma0_00
c	38	269.5	28.6	670	7	BE188285	BE188285 PSI61F_In
	39	265	28.1	363	3	BP100008	BP100008 BP100008
c	40	253	26.9	881	9	DN476575	DN476575 altr207xo
	41	193.5	20.5	697	7	BE188286	BE188286 PSI61R3 I
	42	183	19.4	797	6	AB228194	AB228194 Aspergill
	43	142	15.1	495	8	CO151881	CO151881 EST826934
c	44	123	13.1	295	3	BM863872	BM863872 mgcm007xL
	45	110	11.7	146	5	CK434157	CK434157 rhzma0_00

ALIGNMENTS

RESULT 1
BM863356
LOCUS BM863356 619 bp mRNA linear EST 06-MAY-2003
DEFINITION mgcm006xO03f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm006xO03 5', mRNA sequence.
ACCESSION BM863356
VERSION BM863356.2 GI:30391591
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE 1 (bases 1 to 619)
AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.
TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe grisea
JOURNAL Unpublished (2002)
COMMENT On Mar 7, 2002 this sequence version replaced gi:19231038.
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone

dehydratase >gi|1127197|pdb|1STD|. . . 367 e-101
PCR PRimers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgcm006 row: O column: 03
Seq primer: T3.

FEATURES Location/Qualifiers
source 1. .619
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="Guy11"
/db_xref="taxon:148305"
/clone="mgcm006xO03"
/sex="Mat1-2 hermaphrodite"
/cell_type="mycelium"
/clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2: XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

ORIGIN

Alignment Scores:

Pred. No.:	5.51e-105	Length:	619
Score:	938.00	Matches:	171
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	99.4%	Mismatches:	0
Query Match:	99.6%	Indels:	0
DB:	3	Gaps:	0

US-10-507-132-2 (1-172) x BM863356 (1-619)

```
Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
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Db         53 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 112

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        113 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 172

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        173 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 232

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db        233 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 292

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 352

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 412

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
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Db        413 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 472

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
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Db        473 GTCTGGAAGTTCGCCGGCCTCAAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGG 532

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
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Db        533 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 568
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RESULT 2
BM864194
LOCUS BM864194 657 bp mRNA linear EST 06-MAY-2003
DEFINITION mgcm008xJ12f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm008xJ12 5', mRNA sequence.
ACCESSION BM864194
VERSION BM864194.2 GI:30390885
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE 1 (bases 1 to 657)
AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.
TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe grisea
JOURNAL Unpublished (2002)
COMMENT On Mar 7, 2002 this sequence version replaced gi:19231876.
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone dehydratase >gi|1127197|pdb|1STD|. . . 365 e-100
PCR PRimers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgcm008 row: J column: 12
Seq primer: T3.

FEATURES Location/Qualifiers
source 1. .657
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="Guy11"
/db_xref="taxon:148305"
/clone="mgcm008xJ12"
/sex="Mat1-2 hermaphrodite"
/cell_type="mycelium"
/clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2: XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

ORIGIN

Alignment Scores:

Pred. No.:	2.47e-104	Length:	657
Score:	933.00	Matches:	170
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	99.4%	Mismatches:	0
Query Match:	99.0%	Indels:	0
DB:	3	Gaps:	0

US-10-507-132-2 (1-172) x BM864194 (1-657)

```
Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db         91 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 150

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 210

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 270

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db        271 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 330

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 390

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 450

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
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Db        451 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 510

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
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Db        511 GTCTGGAAGTTCGCCGGCCTCAAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGG 570

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAsp 171
              |||||||||||||||||||||||||||||||||
Db        571 ATCTTTGAGGACGGACGGGAGACCTTTGGCGAC 603

RESULT 3
BM863315
LOCUS       BM863315                664 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm006xE21f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm006xE21 5', mRNA sequence.
ACCESSION   BM863315
VERSION     BM863315.2  GI:30391622
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 664)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19230997.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 364 e-100
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm006  row: E  column: 21
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .664
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm006xE21"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

Alignment Scores:
Pred. No.:              3.33e-104       Length:         664
Score:                  932.00          Matches:        170
Percent Similarity:     99.4%           Conservative:   1
Best Local Similarity:  98.8%           Mismatches:     1
Query Match:            98.9%           Indels:         0
DB:                     3               Gaps:           0

US-10-507-132-2 (1-172) x BM863315 (1-664)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 140

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 200

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 260

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db        261 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 320

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
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Db        321 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 380

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
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Db        381 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 440

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
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Db        441 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 500

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
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Db        501 GTCTGGAAGTTCGCCGGCCTCAAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGG 560

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
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Db        561 ATCTTTGAGGACGGACGGGAGACCTTGGGCGACAAA 596

RESULT 4
BM863340
LOCUS       BM863340                649 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm006xK09f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm006xK09 5', mRNA sequence.
ACCESSION   BM863340
VERSION     BM863340.2  GI:30391603
KEYWORDS    EST.
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SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 649)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19231022.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 361 5e-99
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm006  row: K  column: 09
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .649
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm006xK09"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

Alignment Scores:
Pred. No.:              4.18e-103       Length:         649
Score:                  923.00          Matches:        169
Percent Similarity:     99.4%           Conservative:   2
Best Local Similarity:  98.3%           Mismatches:     1
Query Match:            98.0%           Indels:         0
DB:                     3               Gaps:           0

US-10-507-132-2 (1-172) x BM863340 (1-649)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
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Db         84 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 143

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        144 ACTTGCGTCTATGAGTGGGCAGACAGCTACTACTCCAAGGACTGGGATAGGCTGCGAAAG 203

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 263

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||
Db        264 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 323

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 383

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 443

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db        444 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTTACTGGTACAAGAAGATCGACGGC 503

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 GTCTGGAAGTTCGCCGGCCTCAAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGG 563

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
              ||||||||||||||||||||||||||||||||||
Db        564 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 599

RESULT 5
BM863546
LOCUS       BM863546                593 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm006xF04f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm006xF04 5', mRNA sequence.
ACCESSION   BM863546
VERSION     BM863546.2  GI:30391437
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 593)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19231228.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 322 2e-87
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm006  row: F  column: 04
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .593
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm006xF04"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
```

150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

ORIGIN

Alignment Scores:

Pred. No.:	1.67e-95	Length:	593
Score:	861.00	Matches:	164
Percent Similarity:	95.9%	Conservative:	1
Best Local Similarity:	95.3%	Mismatches:	7
Query Match:	91.4%	Indels:	1
DB:	3	Gaps:	0

US-10-507-132-2 (1-172) x BM863546 (1-593)

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Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 138

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 198

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 258

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db        259 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 318

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        319 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGAGAGAAGGTGTCCGAGGACGAGGTC 378

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 ATCGGCTACCACCAGCTGCGCGTGCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 438

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 498

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
              |||||||||  |||||||||  |||||||||  ||||||||||||  |||  |||
Db        499 GTCTGGAAGTTNGCCGGCCTCAGCCCCGACATCCCGTGGGGCGAGTTCCACTTTAC-AGG 557

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
              |||||||||  ||||||||||||||||||||||||
Db        558 ATCTTTGAGGGCGGACGGGAGACCTTTGGCGACAAA 593
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RESULT 6
BM863710
LOCUS       BM863710                 571 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm007xE24f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm007xE24 5', mRNA sequence.
ACCESSION   BM863710
VERSION     BM863710.2  GI:30391295
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19231392.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 336 1e-91
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm007  row: E  column: 24
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .571
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm007xE24"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN
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Alignment Scores:

Pred. No.:	2.81e-95	Length:	571
Score:	859.00	Matches:	156
Percent Similarity:	98.8%	Conservative:	2
Best Local Similarity:	97.5%	Mismatches:	2
Query Match:	91.2%	Indels:	0
DB:	3	Gaps:	0

US-10-507-132-2 (1-172) x BM863710 (1-571)

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Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
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Db         92 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 151

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 211

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 271

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db        272 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 331

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 391

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 451
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Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
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Db        452 GTCACCATGAAGGGCCACGCCCACTCGGGAAACCTTCACTGGTACAAGAAGATCGACGGG 511

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
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Db        512 GTTTGGAAGTTTTCCGGTCTCAAGCCCGACATCCGGTGGGGCGAAGTCGATTTTGACAGG 571

RESULT 7
BM864156
LOCUS       BM864156                599 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm008xD02f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm008xD02 5', mRNA sequence.
ACCESSION   BM864156
VERSION     BM864156.2  GI:30390915
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 599)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19231838.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 302 3e-87
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm008  row: D  column: 02
            Seq primer: T3.
FEATURES             Location/Qualifiers
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                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm008xD02"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

Alignment Scores:
Pred. No.:              1.65e-94        Length:         599
Score:                  853.00          Matches:        160
Percent Similarity:     94.2%           Conservative:   3
Best Local Similarity:  92.5%           Mismatches:     9
Query Match:            90.6%           Indels:         1
DB:                     3               Gaps:           0
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US-10-507-132-2 (1-172) x BM864156 (1-599)

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Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
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Db         79 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 138

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 198

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 258

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db        259 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 318

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 378

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 ATCGGCTACCACCAGCTGCGCGTTCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 438

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 498

Qy        141 ValTrpLysPheAlaGlyLeu-LysProAspIleArgTrpGlyGluPheAspPheAspAr 160
              |||   ||||||      |||    ||||||   ||||||   ||||||:::||||||||
Db        499 GTTCTGAAGTTCATGAGCCTTTACGCCCGACAGTCGCTGGCGCGAGTTCGAGTTTGACCG 558

Qy        160 gIlePheGluAspGlyArgGluThrPheGlyAspLys 172
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Db        559 GAACTTTGACGACCGAACGGAGACCTTTGGGGACAAA 595
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RESULT 8
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LOCUS       BM864467                643 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm010xH12f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm010xH12 5', mRNA sequence.
ACCESSION   BM864467
VERSION     BM864467.2  GI:30390655
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 643)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19232149.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 320 8e-87
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm010  row: H  column: 12
            Seq primer: T3.
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FEATURES             Location/Qualifiers
     source          1. .643
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                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm010xH12"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

Alignment Scores:
Pred. No.:                5.33e-92        Length:         643
Score:                    833.00          Matches:        160
Percent Similarity:       96.4%           Conservative:   2
Best Local Similarity:    95.2%           Mismatches:     3
Query Match:              88.4%           Indels:         3
DB:                       3               Gaps:           0

US-10-507-132-2 (1-172) x BM864467 (1-643)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 204

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 264

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 324

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db        325 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 384

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 444

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 504

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db        505 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTTACTGGTACAAGAAGATCGACGGC 564

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArg-TrpGlyGluPheAsp-PheAspA 160
              ||||||||||||||||||      |||||||||||| |||||||||||||| |||   |
Db        565 GTTTGGAAGTTCGCCGGCCCCANGCCCGACATCCGCTTGGGGCGAGTTCGACTTTTTACA 624

Qy        160 rgIle-PheGluAspGly 165
              ||||| ||||||||||||
Db        625 GGATTCTTTGAGGACGGA 642

RESULT 9
BM863209
LOCUS       BM863209                523 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm005xD02f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm005xD02 5', mRNA sequence.
ACCESSION   BM863209
VERSION     BM863209.2  GI:30391705
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 523)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19230891.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 308 3e-83
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm005  row: D  column: 02
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .523
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm005xD02"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

Alignment Scores:
Pred. No.:                3.42e-86        Length:         523
Score:                    785.00          Matches:        144
Percent Similarity:       99.3%           Conservative:   1
Best Local Similarity:    98.6%           Mismatches:     1
Query Match:              83.3%           Indels:         0
DB:                       3               Gaps:           0

US-10-507-132-2 (1-172) x BM863209 (1-523)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 145

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 205
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Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 265

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db        266 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 325

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Db        326 CTCCGCACGCAGCACTTGATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 385

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        386 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 445

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        446 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 505

Qy        141 ValTrpLysPheAlaGly 146
              |||||||||||||||||
Db        506 GTCTGGAAGTTCGCCGGC 523

RESULT 10
BM863558
LOCUS       BM863558                602 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm006xH04f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm006xH04 5', mRNA sequence.
ACCESSION   BM863558
VERSION     BM863558.2  GI:30391426
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 602)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19231240.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 272 3e-72
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm006  row: H  column: 04
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .602
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm006xH04"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

Alignment Scores:
Pred. No.:                1.66e-84        Length:          602
Score:                    772.00          Matches:         154
Percent Similarity:       93.5%           Conservative:    4
Best Local Similarity:    91.1%           Mismatches:      10
Query Match:              82.0%           Indels:          3
DB:                       3               Gaps:            0

US-10-507-132-2 (1-172) x BM863558 (1-602)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 154

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        155 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 214

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 274

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db        275 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 334

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        335 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGNGAGAAGGTGTCCGAGGACGAGGTC 394

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAA 454

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              |||||||||   ||||||||||||||||||||||||:::   ||||||||||||||||||
Db        455 GTCACCATGAA-GGGCACGCCCACTCGGCAAACCTTTACTTGTACAAGAAGATCGACGGC 513

Qy        141 -ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspAr 160
               |||:::||||||||||||   ||||||   ||||||||||||||   |||   ||
Db        514 GGCTTGGAGGTTCGCGGGCCTAAACCCCGACTT-CGGTGGGGCGAGTTCCAATTTTACAG 572

Qy        160 gIlePheGluAspGlyArgGluThr 168
              |:::      |||||||||||||||
Db        573 GGTTCTTTAGGACGGACGGGAAACC 597

RESULT 11
BM863639
LOCUS       BM863639                486 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm007xG13f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm007xG13 5', mRNA sequence.
ACCESSION   BM863639
VERSION     BM863639.2  GI:30391353
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 486)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
```

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COMMENT     On Mar 7, 2002 this sequence version replaced gi:19231321.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 293 5e-79
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm007  row: G  column: 13
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .486
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm007xG13"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

Alignment Scores:
Pred. No.:                1.15e-81      Length:          486
Score:                    748.00        Matches:         140
Percent Similarity:       97.9%         Conservative:    1
Best Local Similarity:    97.2%         Mismatches:      3
Query Match:              79.4%         Indels:          0
DB:                       3             Gaps:            0

US-10-507-132-2 (1-172) x BM863639 (1-486)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         55 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 114

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 174

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 234

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db        235 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 294

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 354

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 ATCGGCTACCACCAGCTGCGCGTTCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 414

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              ||||||||||||||   ||||||||||||||||||||     ||||||||||||||
Db        415 GTCACCATGAAGGGCCCCGCCCACTCGGCAAACCTTCACTGTGACAAGAAGATCGACGGG 474

Qy        141 ValTrpLysPhe 144
              |||||||||||
Db        475 GTCTGGAAGTTC 486

RESULT 12
BM864820/c
LOCUS       BM864820                781 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgap007xA05f.b Magnaporthe grisea Ap Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgap007xA05 5', mRNA sequence.
ACCESSION   BM864820
VERSION     BM864820.2  GI:30390364
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 781)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19232502.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 271 1e-71
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgap007  row: A  column: 05
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .781
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="70-15"
                     /db_xref="taxon:148305"
                     /clone="mgap007xA05"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="Appressorium"
                     /clone_lib="Magnaporthe grisea Ap Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK+; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Appressorium library. Conidia were germ inated on an
                     inductive surface for 5-8 h. Sequences were processed by
                     one of two methods. Where a full-length alignment to the
                     M. grisea genome sequence was available, the EST sequence
                     was trimed according to the alignment, otherwise sequence
                     quality was assessed using phredPhrap version 991019 and
                     trimmed according to phd files (0.05) and for vector
                     seqs."
ORIGIN

Alignment Scores:
Pred. No.:                2.56e-77      Length:          781
Score:                    715.00        Matches:         143
Percent Similarity:       88.4%         Conservative:    9
Best Local Similarity:    83.1%         Mismatches:      19
Query Match:              75.9%         Indels:          4
DB:                       3             Gaps:            0
```

```
US-10-507-132-2 (1-172) x BM864820 (1-781)

Qy          2 GlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMetThr 21
              |||       :::   |||:::|||   |||          ||||||||||||   |||
Db        723 GGGTTGTCAATTCCAAAAAACGATTAAATACCTTGTCCTGACTACCTGGGCTCAATGCT- 665

Qy         22 CysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArg-LysVa 41
              ||||||||||||||   |||||||||   |||||||||||||||||||||||| |||||
Db        664 TGCGTGTATGAGTGGCA-GACAGTTACGCCTCCAAGGACTGGGATAGGCTGAGGAAAGGT 606

Qy         41 lIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMe 61
              |:::|||   ::::::   |||:::   ||||||   |||||||||   ||||||   ||
Db        605 CATGGCGCTATCTGTGGGCATTGAATC-CGCTCCCTCCTCGACAAGTTTTGGGAGCCAAT 547

Qy         61 tProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThrLe 81
              ||||   :::|||||||||||||||   ||||||||||||::::::|||||||||||||
Db        546 GCCGACGAAGGAGTTCGTCGGCATGTTCTCGAGCAAGCAGGTGGTGGGCGACCCCACCCT 487

Qy         81 uArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluValIl 101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CCGCACGCAGCATTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCAT 427

Qy        101 eGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluVa 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 CGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGT 367

Qy        121 lThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGlyVa 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 CACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGT 307

Qy        141 lTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArgIl 161
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 CTGGAAGTTCGCCGGCCTCAAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGGAT 247

Qy        161 ePheGluAspGlyArgGluThrPheGlyAspLys 172
              |||||||||||||||||||||||||||||||||
Db        246 CTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 213

RESULT 13
BM863374
LOCUS       BM863374                 510 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm006xC10f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm006xC10 5', mRNA sequence.
ACCESSION   BM863374
VERSION     BM863374.2  GI:30391576
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 510)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19231056.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 276 1e-73
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm006  row: C  column: 10
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .510
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm006xC10"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

Alignment Scores:
Pred. No.:                4.39e-76       Length:          510
Score:                    703.00         Matches:         131
Percent Similarity:       100.0%         Conservative:    1
Best Local Similarity:    99.2%          Mismatches:      0
Query Match:              74.6%          Indels:          0
DB:                       3              Gaps:            0

US-10-507-132-2 (1-172) x BM863374 (1-510)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 142

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 202

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 262

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db        263 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 322

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 382

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 442

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeu 132
              |||||||||||||||||||||||||||||||||||
Db        443 GTCACCATGAAGGGCCACGCTCACTCGGCAAACCTT 478

RESULT 14
BM863357
LOCUS       BM863357                 530 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm006xO05f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm006xO05 5', mRNA sequence.
ACCESSION   BM863357
VERSION     BM863357.1  GI:19231039
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 530)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 276 1e-73
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm006  row: O  column: 05
            Seq primer: T3.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm006xO05"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

Alignment Scores:
Pred. No.:                4.62e-76      Length:          530
Score:                    703.00        Matches:         131
Percent Similarity:       100.0%        Conservative:    1
Best Local Similarity:    99.2%         Mismatches:      0
Query Match:              74.6%         Indels:          0
DB:                       3             Gaps:            0

US-10-507-132-2 (1-172) x BM863357 (1-530)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
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Db         83 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 142

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
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Db        143 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 202

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 262

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db        263 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 322

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 382

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 442

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeu 132
              |||||||||||||||||||||||||||||||||||
Db        443 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTT 478

RESULT 15
BM864472
LOCUS       BM864472                 600 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm010xJ04f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm010xJ04 5', mRNA sequence.
ACCESSION   BM864472
VERSION     BM864472.2  GI:30390651
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 600)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19232154.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 268 5e-71
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm010  row: J  column: 04
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .600
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm010xJ04"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

Alignment Scores:
Pred. No.:                7.04e-75      Length:          600
Score:                    694.00        Matches:         144
Percent Similarity:       94.8%         Conservative:    1
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Best Local Similarity:  94.1%          Mismatches:    8
Query Match:            73.7%          Indels:        4
DB:                     3              Gaps:          0

US-10-507-132-2 (1-172) x BM864472 (1-600)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 204

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 264

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 324

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db        325 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 384

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 444

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||   ||||||||||||||   ||||||||||||||||||||
Db        445 ATCGGCTACCACCAGCTGGGCGTCCCGCACCAGAGGGACAAGGACACCACCATGAAGGAG 504

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              ||||||||||||||||||||||||||   |||   ||||||   ||||||||||||||||
Db        505 GTCACCATGAAGGGCCACGCCCACTCGCAAAACCT-CATTGGAC-AAGAAGATCGACGGC 562

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrp 153
              |||   |||||||||   |||||||||   |||||||||
Db        563 GTCTGAAAGTTCGCCGC-CTCAAGCCGAC-ATCCGTTGG 599


Search completed: December  4, 2006, 21:49:49
Job time : 4367 secs
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GenCore version 5.1.9

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2006, 20:22:27 ; Search time 628 Seconds
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Title: US-10-507-132-2
Perfect score: 942
Sequence: 1 MGSQVQKSDEITFSDYLGLM.....WGEFDFDRIFEDGRETFGDK 172

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2931743 seqs, 1025338116 residues

Total number of hits satisfying chosen parameters: 5863486

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
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-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss04
-USER=US10507132_@CGN_1_1_271_@runat_04122006_143935_12137 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	942	100.0	516	6	US-10-507-132-1	Sequence 1, Appli
2	938	99.6	516	6	US-10-507-132-3	Sequence 3, Appli
3	938	99.6	600	6	US-10-507-132-13	Sequence 13, Appl
4	938	99.6	610	6	US-10-507-132-16	Sequence 16, Appl
5	921	97.8	538	6	US-10-507-132-15	Sequence 15, Appl
6	921	97.8	545	6	US-10-507-132-14	Sequence 14, Appl
7	872.5	92.6	729	6	US-10-507-132-18	Sequence 18, Appl
8	870	92.4	732	6	US-10-507-132-17	Sequence 17, Appl
9	87	9.2	3196	6	US-10-449-902-16327	Sequence 16327, A
10	80.5	8.5	1611	9	US-11-174-307B-3703	Sequence 3703, Ap
11	79.5	8.4	1845	9	US-11-056-355B-70677	Sequence 70677, A
12	79.5	8.4	1848	9	US-11-056-355B-78749	Sequence 78749, A
13	77.5	8.2	2451	8	US-11-217-529-78037	Sequence 78037, A
14	77	8.2	1116	8	US-11-266-748A-85042	Sequence 85042, A
c 15	77	8.2	1116	8	US-11-266-748A-137853	Sequence 137853,
16	77	8.2	1517	9	US-11-056-355B-65438	Sequence 65438, A
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20	76.5	8.1	2101	6	US-10-449-902-18695	Sequence 18695, A
21	76.5	8.1	2973	6	US-10-449-902-13104	Sequence 13104, A
22	76.5	8.1	40070	6	US-10-540-898-747	Sequence 747, App
23	76.5	8.1	200033	8	US-11-266-748A-23936	Sequence 23936, A
24	76	8.1	1510	8	US-11-266-748A-260498	Sequence 260498,
25	76	8.1	1510	8	US-11-266-748A-279244	Sequence 279244,
c 26	76	8.1	1510	8	US-11-266-748A-321015	Sequence 321015,
27	76	8.1	2104	6	US-10-953-349-24959	Sequence 24959, A
28	76	8.1	3330	8	US-11-217-529-3074	Sequence 3074, Ap
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c 30	76	8.1	1971884	10	US-11-184-236-70	Sequence 70, Appl
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33	75.5	8.0	2065	8	US-11-293-697-1789	Sequence 1789, Ap
c 34	75.5	8.0	1317241	10	US-11-184-236-73	Sequence 73, Appl
35	75	8.0	1600	8	US-11-216-545-4433	Sequence 4433, Ap
36	74.5	7.9	1391	6	US-10-953-349-22946	Sequence 22946, A
37	74.5	7.9	1578	9	US-11-348-413-18390	Sequence 18390, A
38	74	7.9	1908	8	US-11-216-545-1060	Sequence 1060, Ap
c 39	74	7.9	4894	8	US-11-266-748A-32577	Sequence 32577, A
40	74	7.9	82027	8	US-11-266-748A-29375	Sequence 29375, A
41	74	7.9	294540	8	US-11-266-748A-23953	Sequence 23953, A
42	73.5	7.8	1698	8	US-11-266-748A-188286	Sequence 188286,
43	73.5	7.8	1698	8	US-11-266-748A-194649	Sequence 194649,
c 44	73.5	7.8	1698	8	US-11-266-748A-242302	Sequence 242302,
45	73.5	7.8	2668	9	US-11-056-355B-76446	Sequence 76446, A

ALIGNMENTS

RESULT 1
US-10-507-132-1
; Sequence 1, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
; APPLICANT: Koichiro KAKU et al.
; TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
; TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
; FILE REFERENCE: 1254-0258PUS1
; CURRENT APPLICATION NUMBER: US/10/507,132
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: JP 2002-66955
; PRIOR FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Pyricularia oryzae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(516)
US-10-507-132-1

Alignment Scores:

Pred. No.:	7.47e-118	Length:	516
Score:	942.00	Matches:	172
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0

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DB:                    6              Gaps:          0

US-10-507-132-2 (1-172) x US-10-507-132-1 (1-516)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
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Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
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Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
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Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
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Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
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Db        481 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516

RESULT 2
US-10-507-132-3
; Sequence 3, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU et al.
;  TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
;  TITLE OF INVENTION:  AGRICULTURAL FUNGICIDAL AGENT
;  FILE REFERENCE: 1254-0258PUS1
;  CURRENT APPLICATION NUMBER: US/10/507,132
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: JP 2002-66955
;  PRIOR FILING DATE: 2002-03-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 516
;   TYPE: DNA
;   ORGANISM: Pyricularia oryzae
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(516)
US-10-507-132-3

Alignment Scores:
Pred. No.:              2.6e-117      Length:         516
Score:                  938.00        Matches:        171
Percent Similarity:     100.0%        Conservative:   1
Best Local Similarity:  99.4%         Mismatches:     0
Query Match:            99.6%         Indels:         0
DB:                     6             Gaps:           0

US-10-507-132-2 (1-172) x US-10-507-132-3 (1-516)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
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Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||
Db        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 240

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
              ||||||||||||||||||||||||||||||||||
Db        481 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516

RESULT 3
US-10-507-132-13
; Sequence 13, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU et al.
;  TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
;  TITLE OF INVENTION:  AGRICULTURAL FUNGICIDAL AGENT
;  FILE REFERENCE: 1254-0258PUS1
;  CURRENT APPLICATION NUMBER: US/10/507,132
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: JP 2002-66955
;  PRIOR FILING DATE: 2002-03-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 600
;   TYPE: DNA
;   ORGANISM: Pyricularia oryzae
US-10-507-132-13

Alignment Scores:
Pred. No.:              3.24e-117     Length:         600
Score:                  938.00        Matches:        171
Percent Similarity:     100.0%        Conservative:   1
Best Local Similarity:  99.4%         Mismatches:     0
Query Match:            99.6%         Indels:         0
DB:                     6             Gaps:           0

US-10-507-132-2 (1-172) x US-10-507-132-13 (1-600)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 140

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
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Db        141 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 200

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60

Db        201 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 260

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80

Db        261 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 320

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100

Db        321 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 380

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120

Db        381 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 440

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140

Db        441 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 500

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160

Db        501 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 560

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172

Db        561 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 596

RESULT 4
US-10-507-132-16
; Sequence 16, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU et al.
;  TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
;  TITLE OF INVENTION:  AGRICULTURAL FUNGICIDAL AGENT
;  FILE REFERENCE: 1254-0258PUS1
;  CURRENT APPLICATION NUMBER: US/10/507,132
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: JP 2002-66955
;  PRIOR FILING DATE: 2002-03-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 610
;   TYPE: DNA
;   ORGANISM: Pyricularia oryzae
US-10-507-132-16

Alignment Scores:
Pred. No.:              3.32e-117      Length:         610
Score:                  938.00         Matches:        171
Percent Similarity:     100.0%         Conservative:   1
Best Local Similarity:  99.4%          Mismatches:     0
Query Match:            99.6%          Indels:         0
DB:                     6              Gaps:           0

US-10-507-132-2 (1-172) x US-10-507-132-16 (1-610)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20

Db         81 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 140

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40

Db        141 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 200

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60

Db        201 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 260

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80

Db        261 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 320

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100

Db        321 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 380

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120

Db        381 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 440

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140

Db        441 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 500

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160

Db        501 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 560

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172

Db        561 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 596

RESULT 5
US-10-507-132-15
; Sequence 15, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU et al.
;  TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
;  TITLE OF INVENTION:  AGRICULTURAL FUNGICIDAL AGENT
;  FILE REFERENCE: 1254-0258PUS1
;  CURRENT APPLICATION NUMBER: US/10/507,132
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: JP 2002-66955
;  PRIOR FILING DATE: 2002-03-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 538
;   TYPE: DNA
;   ORGANISM: Pyricularia oryzae
US-10-507-132-15

Alignment Scores:
Pred. No.:              5.58e-115      Length:         538
Score:                  921.00         Matches:        168
Percent Similarity:     100.0%         Conservative:   1
Best Local Similarity:  99.4%          Mismatches:     0
Query Match:            97.8%          Indels:         0
DB:                     6              Gaps:           0

US-10-507-132-2 (1-172) x US-10-507-132-15 (1-538)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20

Db         31 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 90

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40

Db         91 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 150

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60

Db        151 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 210

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80

Db        211 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 270

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
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Db        271 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 330

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120

Db        331 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 390

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140

Db        391 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 450

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160

Db        451 GTCTGGAAGTTCGCCGGCCTCAAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGG 510

Qy        161 IlePheGluAspGlyArgGluThrPhe 169

Db        511 ATCTTTGAGGACGGACGGGAGACCTTT 537

RESULT 6
US-10-507-132-14
; Sequence 14, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU et al.
;  TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
;  TITLE OF INVENTION:  AGRICULTURAL FUNGICIDAL AGENT
;  FILE REFERENCE: 1254-0258PUS1
;  CURRENT APPLICATION NUMBER: US/10/507,132
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: JP 2002-66955
;  PRIOR FILING DATE: 2002-03-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 545
;   TYPE: DNA
;   ORGANISM: Pyricularia oryzae
US-10-507-132-14

Alignment Scores:
Pred. No.:              5.69e-115      Length:         545
Score:                  921.00         Matches:        168
Percent Similarity:     100.0%         Conservative:   1
Best Local Similarity:  99.4%          Mismatches:     0
Query Match:            97.8%          Indels:         0
DB:                     6              Gaps:           0

US-10-507-132-2 (1-172) x US-10-507-132-14 (1-545)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20

Db         38 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 97

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40

Db         98 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 157

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60

Db        158 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 217

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80

Db        218 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 277

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100

Db        278 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 337

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120

Db        338 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 397

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140

Db        398 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 457

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160

Db        458 GTCTGGAAGTTCGCCGGCCTCAAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGG 517

Qy        161 IlePheGluAspGlyArgGluThrPhe 169

Db        518 ATCTTTGAGGACGGACGGGAGACCTTT 544

RESULT 7
US-10-507-132-18
; Sequence 18, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU et al.
;  TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
;  TITLE OF INVENTION:  AGRICULTURAL FUNGICIDAL AGENT
;  FILE REFERENCE: 1254-0258PUS1
;  CURRENT APPLICATION NUMBER: US/10/507,132
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: JP 2002-66955
;  PRIOR FILING DATE: 2002-03-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 729
;   TYPE: DNA
;   ORGANISM: Pyricularia oryzae
US-10-507-132-18

Alignment Scores:
Pred. No.:              3.26e-108      Length:         729
Score:                  872.50         Matches:        171
Percent Similarity:     75.4%          Conservative:   1
Best Local Similarity:  75.0%          Mismatches:     0
Query Match:            92.6%          Indels:         56
DB:                     6              Gaps:           2

US-10-507-132-2 (1-172) x US-10-507-132-18 (1-729)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSer---------- 14

Db         48 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGGTGAGCATAATATCCCC 107

Qy         14 ---------- 14

Db        108 CTCCAAAAAGAAAATAGCGGTGAAGCCACCAACGACAGTACCGCTGACCCTAATTCCCCT 167

Qy         15 ---AspTyrLeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerLys 33

Db        168 CCAGACTACCTGGGCCTCATGACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAG 227

Qy         34 AspTrpAspArgLeuArgLysValIleAlaProThrLeuArg---------- 47

Db        228 GACTGGGATAGGCTGCGAAAGGTCATTGCGCCTACTCTGCGCGTATGTTCCGCCCTGCCA 287

Qy         47 ---------- 47

Db        288 TGTTTATTTTTACTTTCCCACACCAAATCCAGACTTTAACAGCGACGACCAAAAAAAAAA 347

Qy         48 -------IleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetProAlaGluGl 65

Db        348 AAAACAGATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGA 407

Qy         65 uPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThrLeuArgThrGlnHi 85

Db        408 GTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACCCTCCGCACGCAGCA 467

Qy         85 sPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluValIleGlyTyrHisGl 105
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Db        468 CTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCA 527

Qy        105 nLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGl 125

Db        528 GCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGG 587

Qy        125 yHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGlyValTrpLysPheAl 145

Db        588 CCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGC 647

Qy        145 aGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArgIlePheGluAspGl 165

Db        648 CGGCCTCAAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGGATCTTTGAGGACGG 707

Qy        165 yArgGluThrPheGlyAspLys 172

Db        708 ACGGGAGACCTTTGGCGACAAA 729

RESULT 8
US-10-507-132-17
; Sequence 17, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU et al.
;  TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
;  TITLE OF INVENTION:  AGRICULTURAL FUNGICIDAL AGENT
;  FILE REFERENCE: 1254-0258PUS1
;  CURRENT APPLICATION NUMBER: US/10/507,132
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: JP 2002-66955
;  PRIOR FILING DATE: 2002-03-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
;   LENGTH: 732
;   TYPE: DNA
;   ORGANISM: Pyricularia oryzae
US-10-507-132-17

Alignment Scores:
Pred. No.:              7.15e-108      Length:         732
Score:                  870.00         Matches:        170
Percent Similarity:     74.7%          Conservative:   1
Best Local Similarity:  74.2%          Mismatches:     1
Query Match:            92.4%          Indels:         58
DB:                     6              Gaps:           2

US-10-507-132-2 (1-172) x US-10-507-132-17 (1-732)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSer---------- 14

Db         47 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGGTGAGCATAATATCCCC 106

Qy         14 ----------------------------------------------------- 14

Db        107 CTCCAAAAAGAAAATAGCGGTGAAGCCACCAACGACAGTACCGCTGACCCTAATTCCCCT 166

Qy         15 ---AspTyrLeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerLys 33

Db        167 CCAGACTACCTGGGCCTCATGACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAG 226

Qy         34 AspTrpAspArgLeuArgLysValIleAlaProThrLeu---------- 46

Db        227 GACTGGGATAGGCTGCGAAAGGTCATTGCGCCTACTCTGCGCGTATGTTCCGCCCTGCCA 286

Qy         46 ----------------------------------------------------- 46

Db        287 TGTTTATTTTTACTTTCCCACACCAAATCCAGACTTTAACAGCGACGACCAAAAAAAAAA 346

Qy         47 ---------ArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetProAla 63

Db        347 AAAAAAAACAGATT-GACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCC 405

Qy         64 GluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThrLeuArgThr 83

Db        406 GAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACCCTCCGCACG 465

Qy         84 GlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluValIleGlyTyr 103

Db        466 CAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTAC 525

Qy        104 HisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMet 123

Db        526 CACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATG 585

Qy        124 LysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGlyValTrpLys 143

Db        586 AAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAG 645

Qy        144 PheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArgIlePheGlu 163

Db        646 TTCGCCGGCCTCAAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGGATCTTTGAG 705

Qy        164 AspGlyArgGluThrPheGlyAspLys 172

Db        706 GACGGACGGGAGACCTTTGGCGACAAA 732

RESULT 9
US-10-449-902-16327
; Sequence 16327, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
;  APPLICANT: National Institute of Agrobiological Sciences.
;  APPLICANT:  Bio-oriented Technology Research Advancement Institution.
;  APPLICANT:  The Institute of Physical and Chemical Research.
;  APPLICANT:  Foundation for Advancement of International Science.
;  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
;  FILE REFERENCE: MOA-A0205Y1-US
;  CURRENT APPLICATION NUMBER: US/10/449,902
;  CURRENT FILING DATE:  2003-05-29
;  PRIOR APPLICATION NUMBER: JP 2002-203269
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: JP 2002-383870
;  PRIOR FILING DATE: 2002-12-11
;  NUMBER OF SEQ ID NOS: 56791
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16327
;   LENGTH: 3196
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: AK066825
;   DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-16327

Alignment Scores:
Pred. No.:              0.85           Length:         3196
Score:                  87.00          Matches:        34
Percent Similarity:     33.8%          Conservative:   16
Best Local Similarity:  23.0%          Mismatches:     44
Query Match:            9.2%           Indels:         54
DB:                     6              Gaps:           7

US-10-507-132-2 (1-172) x US-10-449-902-16327 (1-3196)

Qy         55 AspLysLeuTrp----------GluAlaMetProAlaGluGluPheValGlyMetVal 70

Db       2160 GACAAGCTCTGGCGCTTCGACATGGAGGCGCTCCCCGCCGAC----------CTCGTC 2207

Qy         71 SerSerLysGlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIle--------- 87

Db       2208 CGCCGCGGCATGGCCGAGGAGGACCCCACG------GCGGAGCACGGCCTCAGGCTCGCC 2261

Qy         88 -------------------------GlyGlyThrArgTrpGluLysVal--------- 95
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Db       2262 ATCGAGGACTACCCGTTCGCCAACGACGGCCTCCTCATCTGGGACGCCATCAAGACCTGG 2321

Qy         96 ----------------------------SerGluAspGluValIleGlyTyrHisGln 105

Db       2322 GTCCAGGCGTACGTCGCGCGGTTCTACCCCGACGCCGACAGCGTCGCCGGCGACGAGGAG 2381

Qy        106 LeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGly 125

Db       2382 CTCCAG----------------------GCGTTCTGGACCGAGGTGCGCACCAAGGGG 2417

Qy        126 HisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly-------------- 140

Db       2418 CACGGCGACAAGAAGGACGCCCCGTGGTGGCCGAAGTTGGACTCGCCGGAGAGCCTCGCC 2477

Qy        141 ------------------ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGly 154

Db       2478 CACACGCTGACCACCATCGTCTGGGTCGCGGCGGCGCACCACGCCGCCGTCAACTTCGGG 2537

Qy        155 GluPheAspPheAspArgIlePhe 162

Db       2538 CAGTACGACTTCGGCGGCTACTTC 2561

RESULT 10
US-11-174-307B-3703
; Sequence 3703, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai
;  APPLICANT:  BROVER, Vyacheslav
;  TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
;  TITLE OF INVENTION:  USEFUL FOR MODIFYING PLANT CHARACTERISTICS
;  FILE REFERENCE: 2750-1601PUS2
;  CURRENT APPLICATION NUMBER: US/11/174,307B
;  CURRENT FILING DATE:  2005-06-30
;  PRIOR APPLICATION NUMBER: 60/583,671
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,781
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,651
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 3703
;   LENGTH: 1611
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1611)
;   OTHER INFORMATION: Ceres cDNA ID no. 21665863
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1611)
;   OTHER INFORMATION: Ceres CLONE  ID no. 779290
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1611)
;   OTHER INFORMATION: Also known as  Ceres CDNA ID no. 25088318
US-11-174-307B-3703

Alignment Scores:
Pred. No.:              2.39          Length:        1611
Score:                  80.50         Matches:       35
Percent Similarity:     40.5%         Conservative:  25
Best Local Similarity:  23.6%         Mismatches:    45
Query Match:            8.5%          Indels:        43
DB:                     9             Gaps:          7

US-10-507-132-2 (1-172) x US-11-174-307B-3703 (1-1611)

Qy         54 LeuAspLysLeuTrpGluAlaMetProAlaGluGluPheValGly-------------- 68

Db        568 TTGGCCAAGCTCAGGGAGTCG------GCCGAGGCGTACCTCGGCCGTGCAATCCAGGAG 621

Qy         69 ---MetValSerSerLysGlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIle 87

Db        622 GCCATCGTCACCGTCCCGCAGCAGTACAACGATCCG----------------------- 657

Qy         88 GlyGlyThrArgTrpGluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArg 107

Db        658 ------TCAAGGTATTCGATGTTGAGGGCCGCGGAGCTCGCCGGCCTGCGCGTCACGAGG 711

Qy        108 Val----------------------------------ProHisGlnArgTyrLysAsp 115

Db        712 ATGATCGACGAGCCGACCGCGGCTGCCGTCGCTCACGGCCTCCACAGGAAGCTGCGCGAC 771

Qy        116 Thr---ThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrp 134

Db        772 GAGGGCAACGTCCTCGTCCTCCACGTCGGCGGCGGGACGTCAGACGCGAGCGTCATGTGG 831

Qy        135 TyrLysLysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGly 154

Db        832 TAT------GTGGACGGCGTCTTCGAGTTCATGGGAGCAGACGAGGACCCTTTCTTTGGA 885

Qy        155 GluPheAspPheAspArgIlePheGluAsp---------------------------- 164

Db        886 GGACAGGACTTCGACCAGAGGATCGTCGACCACTTCGTGGAGCTGATCAGGAAGAAGCAC 945

Qy        165 GlyArgGluThrPheGlyAspLys 172

Db        946 GGCAAGGACCTGAGCAACGACAAG 969

RESULT 11
US-11-056-355B-70677
; Sequence 70677, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 70677
;   LENGTH: 1845
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1845)
;   OTHER INFORMATION: Ceres Seq. ID no. 2717493
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1845)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13600220
;   OTHER INFORMATION: as cited in SEQ ID NO 0
US-11-056-355B-70677

Alignment Scores:
Pred. No.:              3.98          Length:        1845
Score:                  79.50         Matches:       57
Percent Similarity:     35.0%         Conservative:  29
Best Local Similarity:  23.2%         Mismatches:    61
Query Match:            8.4%          Indels:        99
DB:                     9             Gaps:          15

US-10-507-132-2 (1-172) x US-11-056-355B-70677 (1-1845)

Qy          6 GlnLysSerAspGlu----------------------------IleThrPheSerAsp 15

Db         85 CAACCAAGTGATGAGGATCTTGGTACCATCATTGGACCTCATCAAACTAGCTTCGATGAC 144

Qy         16 TyrLeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAsp------------ 31
```

```
                 :::|||::::::         :::        |||      |||
Db        145 GAGATAGGCATCGTGATTGGACCACATGCGACCGTAGATGACGAAGACATTGACATGGAC 204

Qy         32 -------------------------SerLysAspTrpAspArgLeuArgLysValIle 42
                                       :::   :::   |||   |||      :::|||
Db        205 ATGGGCACCACCGTTGGACCGCAGACCAACCTAAATGATGATGATTTGGGCACCATCATT 264

Qy         43 AlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetPro 62
              |||         |||     :::   |||                          |||
Db        265 GGACCCGAGTTTGAGATCCACAAGCAAGATTTC----------------------CCC 300

Qy         63 AlaGluGluPheValGly---MetValSerSerLysGlnMetLeuGlyAspProThrLeu 81
              |||:::       |||     ||||||:::   |||:::   |||
Db        301 GCAGATTTCATATTTGGAACATCTGTTTCCGCATATCAGGTTGAAGGT---------GCT 351

Qy         82 ArgThrGlnHisPheIleGlyGlyThrArgTrp----------------------Glu 93
              :::                 |||   |||   |||                      |||
Db        352 AAAAAGGGTTCTGGGAGAGGCTTGACCTCATGGGACGAATTTACACACATGTTTCCTGAG 411

Qy         94 LysValSerGlu------------AspGluValIleGlyTyrHisGlnLeuArgValPro 109
              ||||||   :::             ||||||   :::   :::
Db        412 AAGGTTCAACAAAATGGCGATGGAGATGAGGGAGTCGACTTC----------------- 453

Qy        110 HisGlnArgTyrLysAsp------ThrThrMetLysGluValThrMetLysGlyHisAla 127
              :::   ||||||||||||       |||||||||:::       |||
Db        454 TATACCCGTTACAAGGATGATATAAAATTAATGAAGGAGTTGAACACGAATGGCTTCAGA 513

Qy        128 HisSerAlaAsnLeuHisTrpTyrLysLysIle-------------------------- 138
              |||      :::   |||   :::   :::
Db        514 TTTTCA------ATCTCATGGACCAGGATCTTGCCTTATGGAACTATTAAAAAAGGTGTA 567

Qy        139 ------AspGlyValTrpLysPhe-----------------------------AlaGly 146
                    :::||||||   ||||||                             |||
Db        568 AACGAGGAGGGGGTG---AAGTTCTACAACGATCTTATAAATGAACTTTTAGCTAATGGA 624

Qy        147 LeuLysPro-------------------------------------AspIleArgTrp 153
              ::::::|||                                     ::::::   :::
Db        625 ATTCAGCCTTCGGTTACTCTCTTTCACTGGGAATCTCCACTTGCTCTAGAAATGGAGTAC 684

Qy        154 GlyGluPheAspPheAspArgIlePheGluAspGlyArgGlu------------------ 167
              |||   |||      :::||||||   ||||||   ||||||
Db        685 GGAGGTTTCCTAAACGAAAGGATAGTAGAGGATTTCCGTGAGTTTGCAAACTTTTGCTTC 744

Qy        168 ---ThrPheGlyAspLys 172
                 |||||||||:::
Db        745 AAGGAATTTGGAGATAGG 762

RESULT 12
US-11-056-355B-78749
; Sequence 78749, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 78749
;   LENGTH: 1848
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1848)
;   OTHER INFORMATION: Ceres Seq. ID no. 12644995
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1848)
;   OTHER INFORMATION: Ortholog of  Ceres SEQ ID NO 13600220
;   OTHER INFORMATION: as cited in SEQ ID NO 0
US-11-056-355B-78749

Alignment Scores:
Pred. No.:              3.99          Length:          1848
Score:                  79.50         Matches:         57
Percent Similarity:     35.0%         Conservative:    29
Best Local Similarity:  23.2%         Mismatches:      61
Query Match:            8.4%          Indels:          99
DB:                     9             Gaps:            15

US-10-507-132-2 (1-172) x US-11-056-355B-78749 (1-1848)

Qy          6 GlnLysSerAspGlu----------------------------IleThrPheSerAsp 15
              |||   |||||||||                            :::|||   |||
Db         85 CAACCAAGTGATGAGGATCTTGGTACCATCATTGGACCTCATCAAACTAGCTTCGATGAC 144

Qy         16 TyrLeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAsp------------ 31
                 :::|||::::::         :::         |||      |||
Db        145 GAGATAGGCATCGTGATTGGACCACATGCGACCGTAGATGACGAAGACATTGACATGGAC 204

Qy         32 -------------------------SerLysAspTrpAspArgLeuArgLysValIle 42
                                       :::   :::   |||   |||      :::|||
Db        205 ATGGGCACCACCGTTGGACCGCAGACCAACCTAAATGATGATGATTTGGGCACCATCATT 264

Qy         43 AlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetPro 62
              |||         |||     :::   |||                          |||
Db        265 GGACCCGAGTTTGAGATCCACAAGCAAGATTTC----------------------CCC 300

Qy         63 AlaGluGluPheValGly---MetValSerSerLysGlnMetLeuGlyAspProThrLeu 81
              |||:::       |||     ||||||:::   |||:::   |||
Db        301 GCAGATTTCATATTTGGAACATCTGTTTCCGCATATCAGGTTGAAGGT---------GCT 351

Qy         82 ArgThrGlnHisPheIleGlyGlyThrArgTrp----------------------Glu 93
              :::                 |||   |||   |||                      |||
Db        352 AAAAAGGGTTCTGGGAGAGGCTTGACCTCATGGGACGAATTTACACACATGTTTCCTGAG 411

Qy         94 LysValSerGlu------------AspGluValIleGlyTyrHisGlnLeuArgValPro 109
              ||||||   :::             ||||||   :::   :::
Db        412 AAGGTTCAACAAAATGGCGATGGAGATGAGGGAGTCGACTTC----------------- 453

Qy        110 HisGlnArgTyrLysAsp------ThrThrMetLysGluValThrMetLysGlyHisAla 127
              :::   ||||||||||||       |||||||||:::       |||
Db        454 TATACCCGTTACAAGGATGATATAAAATTAATGAAGGAGTTGAACACGAATGGCTTCAGA 513

Qy        128 HisSerAlaAsnLeuHisTrpTyrLysLysIle-------------------------- 138
              |||      :::   |||   :::   :::
Db        514 TTTTCA------ATCTCATGGACCAGGATCTTGCCTTATGGAACTATTAAAAAAGGTGTA 567

Qy        139 ------AspGlyValTrpLysPhe-----------------------------AlaGly 146
                    :::||||||   ||||||                             |||
Db        568 AACGAGGAGGGGGTG---AAGTTCTACAACGATCTTATAAATGAACTTTTAGCTAATGGA 624

Qy        147 LeuLysPro-------------------------------------AspIleArgTrp 153
              ::::::|||                                     ::::::   :::
Db        625 ATTCAGCCTTCGGTTACTCTCTTTCACTGGGAATCTCCACTTGCTCTAGAAATGGAGTAC 684

Qy        154 GlyGluPheAspPheAspArgIlePheGluAspGlyArgGlu------------------ 167
              |||   |||      :::||||||   ||||||   ||||||
Db        685 GGAGGTTTCCTAAACGAAAGGATAGTAGAGGATTTCCGTGAGTTTGCAAACTTTTGCTTC 744

Qy        168 ---ThrPheGlyAspLys 172
                 |||||||||:::
Db        745 AAGGAATTTGGAGATAGG 762

RESULT 13
US-11-217-529-78037
; Sequence 78037, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
;  APPLICANT: SUNTORY LIMITED
;  APPLICANT:  NAKAO, YOSHIHIRO
```

```
;  APPLICANT:  NAKAMURA, NORIHISA
;  APPLICANT:  KODAMA, YUKIKO
;  APPLICANT:  FUJIMURA, TOMOKO
;  APPLICANT:  ASHIKARI, TOSHIHIKO
;  TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
;  FILE REFERENCE: S-38-285
;  CURRENT APPLICATION NUMBER: US/11/217,529
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 10/932,182
;  PRIOR FILING DATE: 2004-09-02
;  NUMBER OF SEQ ID NOS: 197023
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78037
;   LENGTH: 2451
;   TYPE: DNA
;   ORGANISM: Saccharomyces pastorianus
US-11-217-529-78037

Alignment Scores:
Pred. No.:              11.2          Length:         2451
Score:                  77.50         Matches:        44
Percent Similarity:     31.5%         Conservative:   19
Best Local Similarity:  22.0%         Mismatches:     56
Query Match:            8.2%          Indels:         81
DB:                     8             Gaps:           10

US-10-507-132-2 (1-172) x US-11-217-529-78037 (1-2451)

Qy         24 TyrGluTrpAlaAspSerTyrAspSerLys---------------------------- 33
              |||         ||||||   :::||||||
Db       1321 TATAGGCGGATAGATTCTAGTGAATCTAAACTAGTTCAGGATGCATTGGATTGGCTCTTG 1380

Qy         34 ---AspTrpAspArgLeuArg--------------------------------LysVal 41
                 :::||||||      |||
Db       1381 TTCAATTGGGATACGTTTCGACTGACATTTTTTGGTAAGCTTTATGATAATTTTATGACA 1440

Qy         42 IleAlaProThrLeuArgIleAspTyrArg------SerPheLeuAspLysLeuTrpGlu 59
              |||:::      |||   |||||||||          |||      ||||||
Db       1441 ATTTCAGAAAAACTTGCTATAGATTATAATCACCCTAAAATCTTGAGAAATTTATGG--- 1497

Qy         60 AlaMetProAlaGluGluPheValGlyMetValSerSerLysGlnMet------------ 75
                                          :::   |||   |||
Db       1498 ----------------------------TGCAATGGGAAGTACATGGGCATTGATTTA 1527

Qy         76 ----------------------------------------------------LeuGlyAsp 78
                                                              :::   |||
Db       1528 AAGAATGCTAATAATTTAAACCTTGATACCGATGATGAAGCAACTAGTAACATTAATGAC 1587

Qy         79 ProThrLeuArgThrGlnHisPheIleGlyGly--------------------------- 89
                 :::||||||   :::|||
Db       1588 GTCCATGTAAGGACCCCTAATTTTGAATCGAGATTGAAGATTCCCACCAACAGACTTTTC 1647

Qy         90 ------ThrArgTrpGluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArg 107
                  |||   |||:::   :::         |||   :::||||||   |||
Db       1648 GAAATAACCTTATGGGATATTTTGATGATAACGGAGAATTTAGGATATAAACAATTT--- 1704

Qy        108 ValPro-----------------------------HisGlnArgTyrLysAspThrThr 117
              :::|||                          :::   :::   |||   |||
Db       1705 ATTCCCATAATTAATTTACTAAGTCCTTTTTTTATTTCAAGGTCATTTAATGATTACACA 1764

Qy        118 MetLysGluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLys 137
              :::          |||   :::   :::|||   |||      |||   ::::::
Db       1765 TTGCCTCCAAATATTAGGAAACAGTACCAGAACAGC---AACAAAATCTGGCTTCAAGAA 1821

Qy        138 IleAspGlyValTrpLysPheAlaGly------LeuLysProAspIleArgTrpGlyGlu 155
              :::|||      ||||||      |||      |||      |||   |||  ||||||
Db       1822 ATGGACAGTAAGTGGAAAATGAATGGTCATCAACTCAATTACGACCAAAGGGAGGGTGAA 1881

RESULT 14
US-11-266-748A-85042
; Sequence 85042, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 85042
;   LENGTH: 1116
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (119)..(119)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-85042

Alignment Scores:
Pred. No.:              4.18          Length:         1116
Score:                  77.00         Matches:        31
Percent Similarity:     35.8%         Conservative:   22
Best Local Similarity:  20.9%         Mismatches:     37
Query Match:            8.2%          Indels:         58
DB:                     8             Gaps:           6

US-10-507-132-2 (1-172) x US-11-266-748A-85042 (1-1116)

Qy         57 LeuTrpGluAlaMetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeu 76
              ||||||   ::::::                  |||:::   |||   |||      |||
Db       512 CTGTGGAATTCAATCCAT--------------GGACTCCAGAGCCCCAAGTCTCCTTTA 556

Qy         77 GlyAspProThrLeuArgThrGln---------------------------------- 84
              |||  |||           |||
Db       557 GGCCGACCTGAGAGCTTGCTCCAGTCTAATACCCTGATGCTCCCTTTGCAGCCCTGTACC 616

Qy         85 ------------------------------------------------------His 85
                                                                    |||
Db       617 TCCGTTATGCCAATGCTCAGGGCAGCATTTGTGGATGAGAATTTGCCTGATGGGACTCAC 676

Qy         86 PheIleGlyGlyThrArgTrpGluLysValSerGluAspGluValIleGlyTyrHisGln 105
                    ||||||::::::   |||      |||||||||
Db       677 CTTCAGCCAGGAACCAAGTTTATCAAACCACTGGAGGATGAA------------------ 718

Qy        106 LeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGly 125
                          :::|||:::      |||:::  |||          |||
Db       719 -----------------AAATACAGGAAATGTACAGTG---GAGTGCAGACACAAAGCT 757

Qy        126 HisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGlyValTrpLysPheAla 145
                    |||         |||  |||:::::::::   :::|||:::
Db       758 CAAGTTCATGTGGGGAAACTGATTTGGTTCCAAAGAAAAGAAGGATTGTTGGGTTGCCCT 817

Qy        146 GlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArgIlePheGlu------ 163
              ||||||:::|||            |||   ::::::::::::|||      :::
Db       818 GGCCTAAGGCCG------------GGCAGCTGGGAGTGGAATCGCGCGAGTAAGTGCACC 865
```

```
Qy        164 ---------AspGlyArgGluThr 168
                      :::|||::::::|||
Db        866 AAGCCTAGGGAGGGGAAGGATACA 889

RESULT 15
US-11-266-748A-137853/c
; Sequence 137853, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 137853
;   LENGTH: 1116
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (998)..(998)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-137853

Alignment Scores:
Pred. No.:              4.18          Length:         1116
Score:                  77.00         Matches:        31
Percent Similarity:     35.8%         Conservative:   22
Best Local Similarity:  20.9%         Mismatches:     37
Query Match:            8.2%          Indels:         58
DB:                     8             Gaps:           6

US-10-507-132-2 (1-172) x US-11-266-748A-137853 (1-1116)

Qy         57 LeuTrpGluAlaMetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeu 76
              ||||||   ::::::                  |||:::   |||   |||      |||
Db        605 CTGTGGAATTCAATCCAT--------------GGACTCCAGAGCCCCAAGTCTCCTTTA 561

Qy         77 GlyAspProThrLeuArgThrGln---------------------------------- 84
              |||   |||             |||
Db        560 GGCCGACCTGAGAGCTTGCTCCAGTCTAATACCCTGATGCTCCCTTTGCAGCCCTGTACC 501

Qy         85 ------------------------------------------------------------His 85
                                                                          |||
Db        500 TCCGTTATGCCAATGCTCAGGGCAGCATTTGTGGATGAGAATTTGCCTGATGGGACTCAC 441

Qy         86 PheIleGlyGlyThrArgTrpGluLysValSerGluAspGluValIleGlyTyrHisGln 105
                  ||||||::::::   |||      |||||||||
Db        440 CTTCAGCCAGGAACCAAGTTTATCAAACCACTGGAGGATGAA----------------- 399

Qy        106 LeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGly 125
                                  :::|||:::      |||:::   |||      |||
Db        398 -----------------AAATACAGGAAATGTACAGTG---GAGTGCAGACACAAAGCT 360

Qy        126 HisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGlyValTrpLysPheAla 145
                  |||         |||   |||:::::::::   :::|||:::
Db        359 CAAGTTCATGTGGGGAAACTGATTTGGTTCCAAAGAAAAGAAGGATTGTTGGGTTGCCCT 300

Qy        146 GlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArgIlePheGlu------ 163
              ||||||:::|||            |||   ::::::::::::|||      :::
Db        299 GGCCTAAGGCCG-----------GGCAGCTGGGAGTGGAATCGCGCGAGTAAGTGCACC 252

Qy        164 ---------AspGlyArgGluThr 168
                      :::|||::::::|||
Db        251 AAGCCTAGGGAGGGGAAGGATACA 228


Search completed: December  4, 2006, 22:06:05
Job time : 632 secs
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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2006, 20:11:49 ; Search time 893 Seconds
(without alignments)
3550.067 Million cell updates/sec

Title: US-10-507-132-2
Perfect score: 942
Sequence: 1 MGSQVQKSDEITFSDYLGLM.....WGEFDFDRIFEDGRETFGDK 172

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abss/ABSSWEB_spool/US10507132/runat_04122006_143928_11899/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06h
-USER=US10507132_@CGN_1_1_1334_@runat_04122006_143928_11899 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	87	9.2	2775	9	US-10-491-733-21	Sequence 21, Appl
	2	85	9.0	864	3	US-09-882-227-305	Sequence 305, App
	3	84	8.9	850	3	US-09-964-238-8	Sequence 8, Appli
	4	84	8.9	1454	8	US-10-425-114-31125	Sequence 31125, A
	5	84	8.9	1454	9	US-10-425-115-28662	Sequence 28662, A
	6	84	8.9	3154	10	US-10-847-972-59	Sequence 59, Appl
	7	84	8.9	3154	15	US-11-108-528-45	Sequence 45, Appl
	8	82.5	8.8	88232	6	US-10-087-192-1699	Sequence 1699, Ap
	9	81.5	8.7	1473	8	US-10-335-977-2219	Sequence 2219, Ap
	10	81	8.6	1047	8	US-10-364-888-1	Sequence 1, Appli
	11	81	8.6	1070	7	US-10-305-810-1	Sequence 1, Appli
	12	81	8.6	1070	8	US-10-364-888-5	Sequence 5, Appli
	13	81	8.6	2160	8	US-10-364-888-7	Sequence 7, Appli
	14	81	8.6	2250	7	US-10-285-976-22	Sequence 22, Appl
	15	81	8.6	2250	10	US-10-847-972-21	Sequence 21, Appl
	16	81	8.6	2250	15	US-11-108-528-43	Sequence 43, Appl
	17	80.5	8.5	2280	10	US-10-469-204-36	Sequence 36, Appl
	18	80.5	8.5	2503	10	US-10-481-032A-69	Sequence 69, Appl
	19	79.5	8.4	1845	16	US-11-096-568A-28398	Sequence 28398, A
c	20	79.5	8.4	2623	8	US-10-437-963-61451	Sequence 61451, A
	21	79.5	8.4	4041	13	US-11-097-143-1700	Sequence 1700, Ap
	22	79.5	8.4	20510	13	US-11-097-143-1699	Sequence 1699, Ap
	23	79	8.4	801	8	US-10-335-977-1665	Sequence 1665, Ap
	24	79	8.4	2109	7	US-10-369-493-47161	Sequence 47161, A
c	25	79	8.4	6588	8	US-10-437-963-79084	Sequence 79084, A
	26	79	8.4	11096	7	US-10-149-736-4	Sequence 4, Appli
	27	79	8.4	11096	10	US-10-964-536-4	Sequence 4, Appli
c	28	79	8.4	2256646	8	US-10-470-565-1	Sequence 1, Appli
	29	78.5	8.3	1122	7	US-10-156-761-124	Sequence 124, App
c	30	78.5	8.3	13734	8	US-10-287-226-303	Sequence 303, App
	31	78.5	8.3	9025608	7	US-10-156-761-1	Sequence 1, Appli
	32	78	8.3	1400	16	US-11-136-527-4457	Sequence 4457, Ap
c	33	78	8.3	1462	8	US-10-424-599-139221	Sequence 139221,
	34	78	8.3	1947	8	US-10-152-319A-2121	Sequence 2121, Ap
	35	78	8.3	1947	10	US-10-486-706-279	Sequence 279, App
	36	78	8.3	1947	16	US-11-136-527-361	Sequence 361, App
	37	78	8.3	1947	16	US-11-036-196-2121	Sequence 2121, Ap
	38	78	8.3	2163	8	US-10-335-977-2753	Sequence 2753, Ap
	39	78	8.3	2355	8	US-10-335-977-2754	Sequence 2754, Ap
	40	78	8.3	2694	3	US-09-815-242-7512	Sequence 7512, Ap
	41	78	8.3	2694	8	US-10-335-977-2755	Sequence 2755, Ap
	42	78	8.3	4647	13	US-11-097-143-34924	Sequence 34924, A
	43	77.5	8.2	719	6	US-10-027-632-18936	Sequence 18936, A
	44	77.5	8.2	719	7	US-10-027-632-18936	Sequence 18936, A
	45	77.5	8.2	1116	10	US-10-469-204-93	Sequence 93, Appl

ALIGNMENTS

RESULT 1
US-10-491-733-21
; Sequence 21, Application US/10491733
; Publication No. US20040219675A1
; GENERAL INFORMATION:
; APPLICANT: Syngenta Participations AG
; APPLICANT: Sainz, Manuel
; APPLICANT: Salmeron, John
; APPLICANT: Weislo, Laura J.
; TITLE OF INVENTION: Nucleic Acid Molecules from Rice Encoding Proteins for Abiotic St
; TITLE OF INVENTION: Resistance, Yield, Disease Resistance and Nutritional Quality an
; FILE REFERENCE: 60127WOPCT
; CURRENT APPLICATION NUMBER: US/10/491,733
; CURRENT FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: 60/334,501
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 2775
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-491-733-21

Alignment Scores:

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Pred. No.:              2.63          Length:        2775
Score:                  87.00         Matches:       34
Percent Similarity:     33.8%         Conservative:  16
Best Local Similarity:  23.0%         Mismatches:    44
Query Match:            9.2%          Indels:        54
DB:                     9             Gaps:          7

US-10-507-132-2 (1-172) x US-10-491-733-21 (1-2775)

Qy         55 AspLysLeuTrp----------GluAlaMetProAlaGluGluPheValGlyMetVal 70
              ||||||||||||          ||||||:::||||||:::            :::|||
Db       1960 GACAAGCTCTGGCGCTTCGACACGGAGGCGCTCCCCGCCGAC----------CTCGTC 2007

Qy         71 SerSerLysGlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIle--------- 87
                                 |||||||||         :::|||   :::
Db       2008 CGCCGCGGCATGGCCGAGGAGGACCCCACG------GCGGAGCACGGCCTCAAGCTCGCC 2061

Qy         88 --------------------------GlyGlyThrArgTrpGluLysVal--------- 95
                                        |||         |||:::   :::
Db       2062 ATCGAGGACTACCCGTTCGCCAACGACGGCCTCCTCATCTGGGACGCCATCAAGACCTGG 2121

Qy         96 ----------------------------SerGluAspGluValIleGlyTyrHisGln 105
                                           |||   |||   |||       :::
Db       2122 GTCCAGGCGTACGTCGCGCGGTTCTACCCCGACGCCGACAGCGTCGCCGGCGACGAGGAG 2181

Qy        106 LeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGly 125
              |||:::                                    ||||||      ||||||
Db       2182 CTCCAG----------------------GCGTTCTGGACCGAGGTGCGCACCAAGGGG 2217

Qy        126 HisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly-------------- 140
              |||         :::      |||:::   |||:::|||
Db       2218 CACGGCGACAAGAAGGACGCCCCGTGGTGGCCGAAGTTGGACTCGCCGGAGAGCCTCGCC 2277

Qy        141 ------------------ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGly 154
                               ||||||      |||             :::   ::::||
Db       2278 CACACGCTGACCACCATCGTCTGGGTGGCGGCGGCGCACCACGCCGCCGTCAACTTCGGG 2337

Qy        155 GluPheAspPheAspArgIlePhe 162
              ::::::||||||         |||
Db       2338 CAGTACGACTTCGGCGGCTACTTC 2361

RESULT 2
US-09-882-227-305
; Sequence 305, Application US/09882227
; Publication No. US20030158396A1
; GENERAL INFORMATION:
;  APPLICANT: Kleanthous, Harold
;  APPLICANT:  Al-Garawi, Amal
;  APPLICANT:  Miller, Charles
;  APPLICANT:  Tomb, Jean-Francois
;  APPLICANT:  Ooomen, Raymond P.
;  TITLE OF INVENTION: Identification of Polynucleotides
;  TITLE OF INVENTION:  Encoding No. US20030158396A1el Helicobacter Polypeptides in the
;  TITLE OF INVENTION:  Genome
;  FILE REFERENCE: 06132/047002
;  CURRENT APPLICATION NUMBER: US/09/882,227
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: US 08/902,615
;  PRIOR FILING DATE: 1997-07-29
;  NUMBER OF SEQ ID NOS: 638
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 305
;   LENGTH: 864
;   TYPE: DNA
;   ORGANISM: Helicobacter pylori
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (37)...(831)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 388
;   OTHER INFORMATION: n = A,T,C or G
US-09-882-227-305

Alignment Scores:
Pred. No.:              0.964         Length:        864
Score:                  85.00         Matches:       43
Percent Similarity:     41.1%         Conservative:  31
Best Local Similarity:  23.9%         Mismatches:    54
Query Match:            9.0%          Indels:        54
DB:                     3             Gaps:          8

US-10-507-132-2 (1-172) x US-09-882-227-305 (1-864)

Qy         18 GlyLeuMetThrCysValTyrGlu---------TrpAlaAspSerTyrAspSerLysAsp 34
              |||::::::   |||   |||:::         ::::::||||||      ::::::
Db        326 GGCATTTTGAATTGTTT-TATCAGTTCGTGGGCTTTAGCGATAGCTGCAAGAACCGCCGT 384

Qy         35 TrpAspArgLeuArgLysValIleAlaProThrLeuArgIleAspTyrArgSerPheLeu 54
                    |||::::::   |||:::   |||          :::|||      |||||||||
Db        385 AGGNTGCGCGTGAAGTGCGTTTTGTTGCCTAATGAGAGCGTGGATTCTTTGAGTTTTTTA 444

Qy         55 AspLysLeu------TrpGluAlaMetProAlaGluGluPheValGlyMetValSerSer 72
                 :::         |||             |||   :::   :::|||:::|||
Db        445 TACCGATCGGCTAATTGGAGCGAAAGGGAAGCGTATGACATGCTTGGTATTGTGTTTGAC 504

Qy         73 Lys--------------------------------GlnMetLeuGlyAspProThrLeu 81
              |||                                        :::|||   |||   |||
Db        505 AAACACCCCTATTTGAAACGCCTTATTATGCCGCATGATTGGGTAGGCCACCCATTATTG 564

Qy         82 ArgThrGlnHisPheIleGlyGly------ThrArgTrpGluLysValSerGlu------ 97
              |||:::             |||             :::|||   :::|||   :::
Db        565 CGCTCTTACCCGCTCAAAGGCGATGAATTCGCCCAATGGTATGAAGTGGATAAAATTTTT 624

Qy         98 -----------AspGluValIleGlyTyrHisGln----------------------- 105
                         ||||||::|||       |||
Db        625 GGTAAAGAATACCGAGAAGTGGTGGGTAAAGAGCAGAGAGACAGCGCAAGAGTGGATGAA 684

Qy        106 -----------------LeuArgValProHisGlnArgTyrLysAspThrThrMetLys 119
                              ::::::   :::::::::   |||         :::|||
Db        685 AAAGACACTTTCAATTTTGCAAAAATTGGCTATGAACAGGGCAAGGGCGAAGAATTAAAA 744

Qy        120 GluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAsp 139
              ||||||      |||                  |||   :::|||||||||
Db        745 GAAGTAGAAGAAAAG----------------------CATGCGTTTAAGAAAATCCCT 780

Qy        140 GlyValTrpLysPheAlaGlyLeuLysProAsp-----------------IleArgTrp 153
                 |||   :::||||||      :::|||                        |||:::|||
Db        781 TTTGTCAA-AGATTTGCACAAAATCGCCCCCACTATCTTAAAAAAGAGGCTATAAAATGG 839

RESULT 3
US-09-964-238-8
; Sequence 8, Application US/09964238
; Patent No. US20020035246A1
; GENERAL INFORMATION:
;  APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnology
;  TITLE OF INVENTION: SMAD-INTERACTING POLYPEPTIDES AND THEIR USE
;  FILE REFERENCE: 2676-4232US
;  CURRENT APPLICATION NUMBER: US/09/964,238
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 09/449,285
;  PRIOR FILING DATE: 1999-11-24
;  PRIOR APPLICATION NUMBER: PCT/EP98/03193
;  PRIOR FILING DATE: 1998-05-28
;  PRIOR APPLICATION NUMBER: 97201645.5
;  PRIOR FILING DATE: 1997-06-02
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
;   LENGTH: 850
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-964-238-8

Alignment Scores:
Pred. No.:              1.29          Length:        850
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Score:                  84.00          Matches:       32
Percent Similarity:     41.7%          Conservative:  11
Best Local Similarity:  31.1%          Mismatches:    36
Query Match:            8.9%           Indels:        24
DB:                     3              Gaps:          7

US-10-507-132-2 (1-172) x US-09-964-238-8 (1-850)

Qy         84 GlnHisPheIleGlyGlyThrArgTrp------GluLysValSerGluAspGluValIle 101
              ||||||                ||||||          :::   |||     |||
Db        536 CAGCACCAGTTCCGATTCGGCCGCTGGAACTGCTCCGCCCTGGGCGAGAAGACCGTCTTC 595

Qy        102 GlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluVal 121
              |||      :::|||||||||      :::           |||           :::
Db        596 GGG---CAAGAACTCCGAGTAGGGAGTCGAGAGGCTGCCTTCACC------TATGCCATC 646

Qy        122 ThrMetLysGlyHisAlaHisSer--------------------AlaAsnLeuHis--- 133
              |||      |||   ||||||:::                          ||||||
Db        647 ACGGCGGCGGGCGTGGCGCATGCTGTCACCGCTGCCTGCAGCCAGGGCAATCTGAGCAAT 706

Qy        134 --------------------------TrpTyrLysLysIleAspGlyValTrpLysPhe 144
                                       :::|||   :::   :::|||   ||||||:::
Db        707 TGTGGCTGTGACCGGGAGAAGCAAGGCTACTACAACCAGGCGGAAGGC---TGGAAGTGG 763

Qy        145 AlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArgIlePheGluAsp 164
              |||         |||:::|||:::|||      ||||||  |||   |||  |||
Db        764 GGGGGCTGCTCAGCGGACGTCCGCTACGGC---ATCGACTTTTCTCGTCGCTTTGTGGAT 820

Qy        165 GlyArgGlu 167
              ||||||
Db        821 GCCCGTGAG 829

RESULT 4
US-10-425-114-31125
; Sequence 31125, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 31125
;   LENGTH: 1454
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: UC-ZMFLB73131C10_FLI
US-10-425-114-31125

Alignment Scores:
Pred. No.:              2.74           Length:        1454
Score:                  84.00          Matches:       35
Percent Similarity:     37.4%          Conservative:  17
Best Local Similarity:  25.2%          Mismatches:    31
Query Match:            8.9%           Indels:        56
DB:                     8              Gaps:          10

US-10-507-132-2 (1-172) x US-10-425-114-31125 (1-1454)

Qy         26 TrpAlaAspSerTyrAspSerLysAspTrp---AspArgLeuArgLysValIleAlaPro 44
              |||   |||   :::||||||      |||   |||  :::   :::   |||   |||
Db        512 TGGAAAGACGTGTTTGATTCGGCAAGCTGGGAAGACCTGATTGTGCGGTATATCATTCCT 571

Qy         45 ThrLeuArgIleAspTyrArgSerPhe----------------------LeuAspLys 56
                 ||||||:::      :::   |||                     ||||||:::
Db        572 AAACTGAGATTGGCGTTGCAAGACTTTCAGATCAACCCAGCAAACCAGAAGCTCGATCAG 631

Qy         57 --------------LeuTrp---GluAlaMetProAlaGluGluPheValGlyMetVal 70
                           ||||||     |||:::|||   :::      |||   |||
Db        632 TTCAACTGGGTGATGTTGTGGACATCTGCAATCCCAGTACAGCTCATGGTCCATATG--- 688

Qy         71 SerSerLysGlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThr 90
                                          |||           |||         :::
Db        689 ----------------------------TTGGAAGTCGATTTCTTC---------AGC 709

Qy         91 ArgTrpGluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgValProHis 110
              :::|||::::::|||                        ||||||   |||      |||:::
Db        710 AAGTGGCAGCAGGTTCTT-----------------TACCACTGGTTGTGCTCACCAAAT 751

Qy        111 GlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlyHisAlaHisSerAla 130
                    :::   :::
Db        752 CCTGATTTCAATGAGATA---------------------------------------- 769

Qy        131 AsnLeuHisTrpTyrLysLysIleAspGlyValTrpLysPheAlaGlyLeuLysPro 149
                  ::::::|||||||||              ||||||      ||||||   |||
Db        770 ---ATGAACTGGTATAAGGGA-----------TGGAAG------GGCCTTTTCCCA 805

RESULT 5
US-10-425-115-28662
; Sequence 28662, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 28662
;   LENGTH: 1454
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_126150C.1
US-10-425-115-28662

Alignment Scores:
Pred. No.:              2.74           Length:        1454
Score:                  84.00          Matches:       35
Percent Similarity:     37.4%          Conservative:  17
Best Local Similarity:  25.2%          Mismatches:    31
Query Match:            8.9%           Indels:        56
DB:                     9              Gaps:          10

US-10-507-132-2 (1-172) x US-10-425-115-28662 (1-1454)

Qy         26 TrpAlaAspSerTyrAspSerLysAspTrp---AspArgLeuArgLysValIleAlaPro 44
              |||   |||   :::||||||      |||   |||  :::   :::   |||   |||
Db        512 TGGAAAGACGTGTTTGATTCGGCAAGCTGGGAAGACCTGATTGTGCGGTATATCATTCCT 571

Qy         45 ThrLeuArgIleAspTyrArgSerPhe----------------------LeuAspLys 56
                 ||||||:::      :::   |||                     ||||||:::
Db        572 AAACTGAGATTGGCGTTGCAAGACTTTCAGATCAACCCAGCAAACCAGAAGCTCGATCAG 631

Qy         57 --------------LeuTrp---GluAlaMetProAlaGluGluPheValGlyMetVal 70
                           ||||||     |||:::|||   :::      |||   |||
Db        632 TTCAACTGGGTGATGTTGTGGACATCTGCAATCCCAGTACAGCTCATGGTCCATATG--- 688

Qy         71 SerSerLysGlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThr 90
                                          |||           |||         :::
Db        689 ----------------------------TTGGAAGTCGATTTCTTC---------AGC 709

Qy         91 ArgTrpGluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgValProHis 110
              :::|||::::::|||                        ||||||   |||      |||:::
```

```
Db        710 AAGTGGCAGCAGGTTCTT-----------------TACCACTGGTTGTGCTCACCAAAT 751

Qy        111 GlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlyHisAlaHisSerAla 130
                  :::   :::
Db        752 CCTGATTTCAATGAGATA---------------------------------------- 769

Qy        131 AsnLeuHisTrpTyrLysLysIleAspGlyValTrpLysPheAlaGlyLeuLysPro 149
              ::::::|||||||||              ||||||      ||||||   |||
Db        770 ---ATGAACTGGTATAAGGGA-----------TGGAAG------GGCCTTTTCCCA 805

RESULT 6
US-10-847-972-59
; Sequence 59, Application US/10847972
; Publication No. US20050049195A1
; GENERAL INFORMATION:
;  APPLICANT: ZOU, YIMIN
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR NERVE REGENERATION
;  FILE REFERENCE: ARCD:395US
;  CURRENT APPLICATION NUMBER: US/10/847,972
;  CURRENT FILING DATE:  2004-05-17
;  PRIOR APPLICATION NUMBER: 60/470,913
;  PRIOR FILING DATE: 2003-05-15
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
;   LENGTH: 3154
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (133)..(1182)
US-10-847-972-59

Alignment Scores:
Pred. No.:              8.12          Length:        3154
Score:                  84.00         Matches:       32
Percent Similarity:     41.7%         Conservative:  11
Best Local Similarity:  31.1%         Mismatches:    36
Query Match:            8.9%          Indels:        24
DB:                     10            Gaps:          7

US-10-507-132-2 (1-172) x US-10-847-972-59 (1-3154)

Qy         84 GlnHisPheIleGlyGlyThrArgTrp------GluLysValSerGluAspGluValIle 101
              ||||||                ||||||           :::   |||      |||
Db        352 CAGCACCAGTTCCGATTCGGCCGCTGGAACTGCTCCGCCCTGGGCGAGAAGACCGTCTTC 411

Qy        102 GlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluVal 121
              |||      :::||||||||      :::             |||           :::
Db        412 GGG---CAAGAACTCCGAGTAGGGAGTCGAGAGGCTGCCTTCACC------TATGCCATC 462

Qy        122 ThrMetLysGlyHisAlaHisSer--------------------AlaAsnLeuHis--- 133
              |||      |||   ||||||:::                          ||||||
Db        463 ACGGCGGCGGGCGTGGCGCATGCTGTCACCGCTGCCTGCAGCCAGGGCAATCTGAGCAAT 522

Qy        134 -------------------------TrpTyrLysLysIleAspGlyValTrpLysPhe 144
                                      :::|||   :::   :::|||   ||||||:::
Db        523 TGTGGCTGTGACCGGGAGAAGCAAGGCTACTACAACCAGGCGGAAGGC---TGGAAGTGG 579

Qy        145 AlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArgIlePheGluAsp 164
              |||         |||:::|||:::|||      ||||||   |||   |||   |||
Db        580 GGGGGCTGCTCAGCGGACGTCCGCTACGGC---ATCGACTTTTCTCGTCGTCTTTGTGGAT 636

Qy        165 GlyArgGlu 167
              ||||||
Db        637 GCCCGTGAG 645

RESULT 7
US-11-108-528-45
; Sequence 45, Application US/11108528
; Publication No. US20050261189A1
; GENERAL INFORMATION:
;  APPLICANT: Larsen, Glenn
;  APPLICANT: Marvin, Martha
;  APPLICANT: Li, Dean Y.
;  APPLICANT: Wang, Elizabeth
;  APPLICANT: Chen, C. M. Amy
;  APPLICANT: Shamah, Steven M.
;  TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
;  TITLE OF INVENTION:  PROLIFERATION
;  FILE REFERENCE: HYDR-P01-041
;  CURRENT APPLICATION NUMBER: US/11/108,528
;  CURRENT FILING DATE:  2005-04-18
;  PRIOR APPLICATION NUMBER: US 60/563,137
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: US 60/598,368
;  PRIOR FILING DATE: 2004-08-02
;  NUMBER OF SEQ ID NOS: 86
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
;   LENGTH: 3154
;   TYPE: DNA
;   ORGANISM: Mouse
US-11-108-528-45

Alignment Scores:
Pred. No.:              8.12          Length:        3154
Score:                  84.00         Matches:       32
Percent Similarity:     41.7%         Conservative:  11
Best Local Similarity:  31.1%         Mismatches:    36
Query Match:            8.9%          Indels:        24
DB:                     15            Gaps:          7

US-10-507-132-2 (1-172) x US-11-108-528-45 (1-3154)

Qy         84 GlnHisPheIleGlyGlyThrArgTrp------GluLysValSerGluAspGluValIle 101
              ||||||                ||||||           :::   |||      |||
Db        352 CAGCACCAGTTCCGATTCGGCCGCTGGAACTGCTCCGCCCTGGGCGAGAAGACCGTCTTC 411

Qy        102 GlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluVal 121
              |||      :::||||||||      :::             |||           :::
Db        412 GGG---CAAGAACTCCGAGTAGGGAGTCGAGAGGCTGCCTTCACC------TATGCCATC 462

Qy        122 ThrMetLysGlyHisAlaHisSer--------------------AlaAsnLeuHis--- 133
              |||      |||   ||||||:::                          ||||||
Db        463 ACGGCGGCGGGCGTGGCGCATGCTGTCACCGCTGCCTGCAGCCAGGGCAATCTGAGCAAT 522

Qy        134 -------------------------TrpTyrLysLysIleAspGlyValTrpLysPhe 144
                                      :::|||   :::   :::|||   ||||||:::
Db        523 TGTGGCTGTGACCGGGAGAAGCAAGGCTACTACAACCAGGCGGAAGGC---TGGAAGTGG 579

Qy        145 AlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArgIlePheGluAsp 164
              |||         |||:::|||:::|||      ||||||   |||   |||   |||
Db        580 GGGGGCTGCTCAGCGGACGTCCGCTACGGC---ATCGACTTTTCTCGTCGTCTTTGTGGAT 636

Qy        165 GlyArgGlu 167
              ||||||
Db        637 GCCCGTGAG 645

RESULT 8
US-10-087-192-1699
; Sequence 1699, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Engelhard, Eric K.
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
;  TITLE OF INVENTION:  CANCER
;  FILE REFERENCE: 529452000122
;  CURRENT APPLICATION NUMBER: US/10/087,192
;  CURRENT FILING DATE:  2002-03-01
;  PRIOR APPLICATION NUMBER: US 09/747,377
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 2059
```

```
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1699
;   LENGTH: 88232
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(88232)
;   OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1699

Alignment Scores:
Pred. No.:              1.39e+03        Length:         88232
Score:                  82.50           Matches:        28
Percent Similarity:     37.7%           Conservative:   12
Best Local Similarity:  26.4%           Mismatches:     45
Query Match:            8.8%            Indels:         21
DB:                     6               Gaps:           4

US-10-507-132-2 (1-172) x US-10-087-192-1699 (1-88232)

Qy         22 CysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArg------ 39
              |||||||||:::|||         :::           |||      |||
Db      26290 TGTGTATATGATTGGATTCTTTATTTCCCCCTAAGTACATGGCAGACGTTGAATTTCTGG 26349

Qy         40 ---------------LysValIleAlaProThrLeuArgIleAspTyrArgSerPheLeu 54
                            :::::|||   |||     ::::::          |||
Db      26350 CCACCTTCAGGACCTTCCTCTATGTCTCCACTATTGAACTGTGAGCACTGGCCTGTGCTC 26409

Qy         55 AspLysLeuTrpGluAlaMetProAlaGluGluPheValGly----------MetVal 70
                 |||||::::::   |||         :::|||          :::|||
Db      26410 TCCACACTTTGGGACTCCTCCCCTCCCCACATGCTCTTAGGACTTAGATTTTTTTTGGTA 26469

Qy         71 SerSerLysGlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThr 90
                 ||||||         |||                     |||   |||
Db      26470 GGTATAAAACAAAACAACAACGACAAAAAACCTGCTGACCTTGAAATGATT---GGATAT 26526

Qy         91 ArgTrpGluLysVal--------------------------SerGluAspGluValIle 101
              :::   |||   |||                         ||||||      :::
Db      26527 CAACTGGAGGTGGTTTGAAATCTGGCACTCATTTTCTAGGACTCAGAGCAGGGACTGTGG 26586

Qy        102 GlyTyrHisGlnLeuArg 107
              ||||||||||||   |||
Db      26587 GGATACCACCAGGCCAGA 26604

RESULT 9
US-10-335-977-2219
; Sequence 2219, Application US/10335977
; Publication No. US20040052799A1
;   GENERAL INFORMATION:
;        APPLICANT: DOUGLAS SMITH et al
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
;                            RELATING TO HELICOBACTER PYLORI FOR
;                            DIAGNOSTICS AND THERAPEUTICS
;        NUMBER OF SEQUENCES: 10031
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: LAHIVE & COCKFIELD
;             STREET: 28 State Street
;             CITY: Boston
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02109-1875
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD/ROM ISO9660
;             COMPUTER: IBM PC Compatible
;             OPERATING SYSTEM: Windows NT 4.0
;             SOFTWARE: UNIX
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/335,977
;             FILING DATE: 30-Dec-2002
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/993,002
;             FILING DATE: 17-DEC-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Mandragouras, Amy E.
;             REGISTRATION NUMBER: 36,207
;             REFERENCE/DOCKET NUMBER: GTN-018
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617)227-7400
;             TELEFAX: (617)742-4214
;   INFORMATION FOR SEQ ID NO: 2219:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1473 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: circular
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        ORIGINAL SOURCE:
;             ORGANISM: Helicobacter pylori
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION: (B) LOCATION 1...1473
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2219:
US-10-335-977-2219

Alignment Scores:
Pred. No.:              6.15            Length:         1473
Score:                  81.50           Matches:        35
Percent Similarity:     44.1%           Conservative:   25
Best Local Similarity:  25.7%           Mismatches:     68
Query Match:            8.7%            Indels:         8
DB:                     8               Gaps:           4

US-10-507-132-2 (1-172) x US-10-335-977-2219 (1-1473)

Qy         23 ValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLysValIle 42
              |||||||||:::|||         :::           |||   ::::::   :::
Db        106 GTCTATGAATTCGCGCAAAAAGCGAATTTGAATTTAGCCGATGTGATTAAAACCCTCTTC 165

Qy         43 AlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetPro 62
                    |||   :::           ||||||||||||                :::
Db        166 AATTTAGGGCTTATGGTAACTAAAAACGACTTTTTGGATAAGGATAGCATAGAGATTTTA 225

Qy         63 AlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThrLeuArg 82
              ||||||||||||         :::|||   :::      |||   :::
Db        226 GCCGAAGAGTTTCATTTAGAAATTTCTGTTCAAAACACCTTAGAAGAA------TTTGAA 279

Qy         83 ThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluValIleGly 102
                 :::      :::   |||   :::   |||:::                 ::::::|||
Db        280 GTAGAAGAGGTGCTAGAGGGGGTGAAAAAAGAGCGCCCGCCTGTGGTTACTATCATGGGG 339

Qy        103 TyrHisGln-LeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluValTh 122
              :::      :::   :::||||||        |||              :::      ||
Db        340 CATGTTGATCATGGTAATACCTCACTACTGGATAAAATCCGTGATAAGAGAGTCGCCCAC 399

Qy        122 rMetLys------GlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIle---As 139
              |:::|||      |||         :::      |||   |||:::||||||||   ::
Db        400 ACTGAAGCCGGGGGGATCACTCAGCACATTGGTGCTTACATGGTGGAAAAAAATAACAAA 459

Qy        139 pGlyValTrpLysPheAla------GlyLeuLysProAspIleArg 152
              :|||                    |||:::||||||      |||
Db        460 TGGGTGTCTTTCATTGACACCCCAGGGCATGAAGCCTTCAGCCAGA 505

RESULT 10
US-10-364-888-1
; Sequence 1, Application US/10364888
; Publication No. US20040023259A1
; GENERAL INFORMATION:
;  APPLICANT: Rastelli, Luca
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Gangolli, Esha
;  APPLICANT:  Guo, Xiaojia
;  APPLICANT:  Malyankar, Uriel
```

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;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Pena, Carol
;  APPLICANT:  Shimkets, Richard
;  APPLICANT:  Spytek, Kimberly
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Rieger, Daniel
;  APPLICANT:  Edinger, Shlomit
;  APPLICANT:  Burgess, Catherine
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 15966-744CIP
;  CURRENT APPLICATION NUMBER: US/10/364,888
;  CURRENT FILING DATE:  2003-02-12
;  PRIOR APPLICATION NUMBER: 60/356,375
;  PRIOR FILING DATE: 2002-02-12
;  PRIOR APPLICATION NUMBER: 60/387,082
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: 09/625,634
;  PRIOR FILING DATE: 2000-07-26
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 1
;   LENGTH: 1047
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1047)
US-10-364-888-1

Alignment Scores:
Pred. No.:              4.47          Length:        1047
Score:                  81.00         Matches:       30
Percent Similarity:     42.7%         Conservative:  11
Best Local Similarity:  31.2%         Mismatches:    31
Query Match:            8.6%          Indels:        24
DB:                     8             Gaps:          7

US-10-507-132-2 (1-172) x US-10-364-888-1 (1-1047)

Qy          91 ArgTrp------GluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgVal 108
               ||||||      :::   |||     |||   |||     :::||||||||||
Db         241 CGCTGGAACTGCTCTGCCCTCGGCGAGAAGACCGTCTTCGGG---CAAGAGCTCCGAGTA 297

Qy         109 ProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlyHisAlaHis 128
                  :::           |||           :::|||     |||   ||||||
Db         298 GGGAGCCGTGAGGCTGCCTTCACG------TACGCCATCACCGCGGCTGGCGTGGCGCAC 351

Qy         129 Ser--------------------AlaAsnLeuHis---------------------- 133
                  :::                 ||||||
Db         352 GCCGTCACCGCTGCCTGCAGCCAAGGGAACCTGAGCAACTGCGGCTGCGACCGCGAGAAG 411

Qy         134 ------TrpTyrLysLysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIle 151
                  :::|||   :::   :::|||   ||||||:::   |||         |||:::
Db         412 CAGGGCTACTACAACCAAGCCGAGGGC---TGGAAGTGGGGCGGCTGCTCGGCCGACGTG 468

Qy         152 ArgTrpGlyGluPheAspPheAspArgIlePheGluAspGlyArgGlu 167
               |||:::|||     ||||||  |||   |||   |||   ||||||
Db         469 CGTTACGGC---ATCGACTTCTCCCGGCGCTTCGTGGACGCTCGGGAG 513

RESULT 11
US-10-305-810-1
; Sequence 1, Application US/10305810
; Publication No. US20030176385A1
; GENERAL INFORMATION:
;  APPLICANT: Ju, Jingfang
;  APPLICANT:  Huang, Chunli
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Simons, Jan Fredrik
;  APPLICANT:  Tailon, Bruce E.
;  APPLICANT:  Chant, John S.
;  APPLICANT:  Peyman, John A.
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Millet, Isabelle
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN EXPRESSION
;  FILE REFERENCE: 21402-501
;  CURRENT APPLICATION NUMBER: US/10/305,810
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: 60/334,148
;  PRIOR FILING DATE: 2001-11-29
;  PRIOR APPLICATION NUMBER: 60/336,572
;  PRIOR FILING DATE: 2001-12-04
;  PRIOR APPLICATION NUMBER: 09/625,634
;  PRIOR FILING DATE: 2000-07-26
;  PRIOR APPLICATION NUMBER: 60/192,838
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: 60/194,256
;  PRIOR FILING DATE: 2000-04-03
;  PRIOR APPLICATION NUMBER: 09/957,187
;  PRIOR FILING DATE: 2001-09-19
;  PRIOR APPLICATION NUMBER: 60/233,798
;  PRIOR FILING DATE: 2000-09-19
;  PRIOR APPLICATION NUMBER: 09/970,813
;  PRIOR FILING DATE: 2001-10-04
;  PRIOR APPLICATION NUMBER: 60/182,637
;  PRIOR FILING DATE: 2000-02-15
;  PRIOR APPLICATION NUMBER: 60/240,316
;  PRIOR FILING DATE: 2000-10-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 1
;   LENGTH: 1070
;   TYPE: DNA
;   ORGANISM: WNT-7B
US-10-305-810-1

Alignment Scores:
Pred. No.:              4.61          Length:        1070
Score:                  81.00         Matches:       30
Percent Similarity:     42.7%         Conservative:  11
Best Local Similarity:  31.2%         Mismatches:    31
Query Match:            8.6%          Indels:        24
DB:                     7             Gaps:          7

US-10-507-132-2 (1-172) x US-10-305-810-1 (1-1070)

Qy          91 ArgTrp------GluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgVal 108
               ||||||            :::   |||     |||   |||     :::||||||||||
Db         241 CGCTGGAACTGCTCTGCCCTCGGCGAGAAGACCGTCTTCGGG---CAAGAGCTCCGAGTA 297

Qy         109 ProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlyHisAlaHis 128
                  :::           |||           :::|||     |||   ||||||
Db         298 GGGAGCCGTGAGGCTGCCTTCACG------TACGCCATCACCGCGGCTGGCGTGGCGCAC 351

Qy         129 Ser--------------------AlaAsnLeuHis---------------------- 133
                  :::                 ||||||
Db         352 GCCGTCACCGCTGCCTGCAGCCAAGGGAACCTGAGCAACTGCGGCTGCGACCGCGAGAAG 411

Qy         134 ------TrpTyrLysLysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIle 151
                  :::|||   :::   :::|||   ||||||:::   |||         |||:::
Db         412 CAGGGCTACTACAACCAAGCCGAGGGC---TGGAAGTGGGGCGGCTGCTCGGCCGACGTG 468

Qy         152 ArgTrpGlyGluPheAspPheAspArgIlePheGluAspGlyArgGlu 167
               |||:::|||     ||||||  |||   |||   |||   ||||||
Db         469 CGTTACGGC---ATCGACTTCTCCCGGCGCTTCGTGGACGCTCGGGAG 513

RESULT 12
US-10-364-888-5
; Sequence 5, Application US/10364888
; Publication No. US20040023259A1
; GENERAL INFORMATION:
;  APPLICANT: Rastelli, Luca
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Gangolli, Esha
;  APPLICANT:  Guo, Xiaojia
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;  APPLICANT:  Malyankar, Uriel
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Pena, Carol
;  APPLICANT:  Shimkets, Richard
;  APPLICANT:  Spytek, Kimberly
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Rieger, Daniel
;  APPLICANT:  Edinger, Shlomit
;  APPLICANT:  Burgess, Catherine
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 15966-744CIP
;  CURRENT APPLICATION NUMBER: US/10/364,888
;  CURRENT FILING DATE:  2003-02-12
;  PRIOR APPLICATION NUMBER: 60/356,375
;  PRIOR FILING DATE: 2002-02-12
;  PRIOR APPLICATION NUMBER: 60/387,082
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: 09/625,634
;  PRIOR FILING DATE: 2000-07-26
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 5
;   LENGTH: 1070
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1047)
US-10-364-888-5

Alignment Scores:
Pred. No.:              4.61          Length:        1070
Score:                  81.00         Matches:       30
Percent Similarity:     42.7%         Conservative:  11
Best Local Similarity:  31.2%         Mismatches:    31
Query Match:            8.6%          Indels:        24
DB:                     8             Gaps:          7

US-10-507-132-2 (1-172) x US-10-364-888-5 (1-1070)

Qy          91 ArgTrp------GluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgVal 108
               ||||||            :::   |||      |||   |||      :::||||||||||
Db         241 CGCTGGAACTGCTCTGCCCTCGGCGAGAAGACCGTCTTCGGG---CAAGAGCTCCGAGTA 297

Qy         109 ProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlyHisAlaHis 128
               :::          |||          :::|||      |||   ||||||
Db         298 GGGAGCCGTGAGGCTGCCTTCACG------TACGCCATCACCGCGGCTGGCGTGGCGCAC 351

Qy         129 Ser--------------------AlaAsnLeuHis----------------------- 133
               :::                    ||||||
Db         352 GCCGTCACCGCTGCCTGCAGCCAAGGGAACCTGAGCAACTGCGGCTGCGACCGCGAGAAG 411

Qy         134 ------TrpTyrLysLysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIle 151
                   ::|||   :::   :::|||   ||||||:::   |||         ||:::
Db         412 CAGGGCTACTACAACCAAGCCGAGGGC---TGGAAGTGGGGCGGCTGCTCGGCCGACGTG 468

Qy         152 ArgTrpGlyGluPheAspPheAspArgIlePheGluAspGlyArgGlu 167
               |||:::|||      ||||||   |||   |||   |||   ||||||
Db         469 CGTTACGGC---ATCGACTTCTCCCGGCGCTTCGTGGACGCTCGGGAG 513

RESULT 13
US-10-364-888-7
; Sequence 7, Application US/10364888
; Publication No. US20040023259A1
; GENERAL INFORMATION:
;  APPLICANT: Rastelli, Luca
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Gangolli, Esha
;  APPLICANT:  Guo, Xiaojia
;  APPLICANT:  Malyankar, Uriel
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Pena, Carol
;  APPLICANT:  Shimkets, Richard
;  APPLICANT:  Spytek, Kimberly
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Rieger, Daniel
;  APPLICANT:  Edinger, Shlomit
;  APPLICANT:  Burgess, Catherine
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
;  FILE REFERENCE: 15966-744CIP
;  CURRENT APPLICATION NUMBER: US/10/364,888
;  CURRENT FILING DATE:  2003-02-12
;  PRIOR APPLICATION NUMBER: 60/356,375
;  PRIOR FILING DATE: 2002-02-12
;  PRIOR APPLICATION NUMBER: 60/387,082
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: 09/625,634
;  PRIOR FILING DATE: 2000-07-26
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 7
;   LENGTH: 2160
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (6)..(1052)
US-10-364-888-7

Alignment Scores:
Pred. No.:              12.3          Length:        2160
Score:                  81.00         Matches:       30
Percent Similarity:     42.7%         Conservative:  11
Best Local Similarity:  31.2%         Mismatches:    31
Query Match:            8.6%          Indels:        24
DB:                     8             Gaps:          7

US-10-507-132-2 (1-172) x US-10-364-888-7 (1-2160)

Qy          91 ArgTrp------GluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgVal 108
               ||||||            :::   |||      |||   |||      :::||||||||||
Db         246 CGCTGGAACTGCTCTGCCCTCGGCGAGAAGACCGTCTTCGGG---CAAGAGCTCCGAGTA 302

Qy         109 ProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlyHisAlaHis 128
               :::          |||          :::|||      |||   ||||||
Db         303 GGGAGCCGTGAGGCTGCCTTCACG------TACGCCATCACCGCGGCTGGCGTGGCGCAC 356

Qy         129 Ser--------------------AlaAsnLeuHis----------------------- 133
               :::                    ||||||
Db         357 GCCGTCACCGCTGCCTGCAGCCAAGGGAACCTGAGCAACTGCGGCTGCGACCGCGAGAAG 416

Qy         134 ------TrpTyrLysLysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIle 151
                   ::|||   :::   :::|||   ||||||:::   |||         ||:::
Db         417 CAGGGCTACTACAACCAAGCCGAGGGC---TGGAAGTGGGGCGGCTGCTCGGCCGACGTG 473

Qy         152 ArgTrpGlyGluPheAspPheAspArgIlePheGluAspGlyArgGlu 167
               |||:::|||      ||||||   |||   |||   |||   ||||||
Db         474 CGTTACGGC---ATCGACTTCTCCCGGCGCTTCGTGGACGCTCGGGAG 518

RESULT 14
US-10-285-976-22
; Sequence 22, Application US/10285976
; Publication No. US20030165500A1
; GENERAL INFORMATION:
;  APPLICANT: Rhee, Chae-Seo
;  APPLICANT:  Malini, Sen
;  APPLICANT:  Wu, Christina
;  APPLICANT:  Leoni, Lorenzo M.
;  APPLICANT:  Corr, Maripat
;  APPLICANT:  Carson, Dennis A.
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
;  TITLE OF INVENTION:  in Head and Neck Squamous Cell Carcinomas
;  FILE REFERENCE: 023070-130320US
;  CURRENT APPLICATION NUMBER: US/10/285,976
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;  CURRENT FILING DATE:  2002-11-01
;  PRIOR APPLICATION NUMBER: US 60/287,995
;  PRIOR FILING DATE: 2001-05-01
;  PRIOR APPLICATION NUMBER: WO PCT/US02/13802
;  PRIOR FILING DATE: 2002-05-01
;  NUMBER OF SEQ ID NOS: 232
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 2250
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: human Wnt-7b
US-10-285-976-22

Alignment Scores:
Pred. No.:              13              Length:         2250
Score:                  81.00           Matches:        30
Percent Similarity:     42.7%           Conservative:   11
Best Local Similarity:  31.2%           Mismatches:     31
Query Match:            8.6%            Indels:         24
DB:                     7               Gaps:           7

US-10-507-132-2 (1-172) x US-10-285-976-22 (1-2250)

Qy         91 ArgTrp------GluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgVal 108
              ||||||             :::   |||       |||   |||       :::|||||||||
Db        336 CGCTGGAACTGCTCTGCCCTCGGCGAGAAGACCGTCTTCGGG---CAAGAGCTCCGAGTA 392

Qy        109 ProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlyHisAlaHis 128
              :::           |||           :::|||      |||   ||||||
Db        393 GGGAGCCGTGAGGCTGCCTTCACG------TACGCCATCACCGCGGCTGGCGTGGCGCAC 446

Qy        129 Ser--------------------AlaAsnLeuHis---------------------- 133
              :::                   ||||||
Db        447 GCCGTCACCGCTGCCTGCAGCCAAGGGAACCTGAGCAACTGCGGCTGCGACCGCGAGAAG 506

Qy        134 ------TrpTyrLysLysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIle 151
                   :::|||   :::   :::|||   ||||||:::   |||          ||:::
Db        507 CAGGGCTACTACAACCAAGCCGAGGGC---TGGAAGTGGGGCGGCTGCTCGGCCGACGTG 563

Qy        152 ArgTrpGlyGluPheAspPheAspArgIlePheGluAspGlyArgGlu 167
              |||:::|||      ||||||   |||   |||   |||   ||||||
Db        564 CGTTACGGC---ATCGACTTCTCCCGGCGCTTCGTGGACGCTCGGGAG 608

RESULT 15
US-10-847-972-21
; Sequence 21, Application US/10847972
; Publication No. US20050049195A1
; GENERAL INFORMATION:
;  APPLICANT: ZOU, YIMIN
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR NERVE REGENERATION
;  FILE REFERENCE: ARCD:395US
;  CURRENT APPLICATION NUMBER: US/10/847,972
;  CURRENT FILING DATE:  2004-05-17
;  PRIOR APPLICATION NUMBER: 60/470,913
;  PRIOR FILING DATE: 2003-05-15
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
;   LENGTH: 2250
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (96)..(1145)
US-10-847-972-21

Alignment Scores:
Pred. No.:              13              Length:         2250
Score:                  81.00           Matches:        30
Percent Similarity:     42.7%           Conservative:   11
Best Local Similarity:  31.2%           Mismatches:     31
Query Match:            8.6%            Indels:         24
DB:                     10              Gaps:           7

US-10-507-132-2 (1-172) x US-10-847-972-21 (1-2250)

Qy         91 ArgTrp------GluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgVal 108
              ||||||             :::   |||       |||   |||       :::|||||||||
Db        336 CGCTGGAACTGCTCTGCCCTCGGCGAGAAGACCGTCTTCGGG---CAAGAGCTCCGAGTA 392

Qy        109 ProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlyHisAlaHis 128
              :::           |||           :::|||      |||   ||||||
Db        393 GGGAGCCGTGAGGCTGCCTTCACG------TACGCCATCACCGCGGCTGGCGTGGCGCAC 446

Qy        129 Ser--------------------AlaAsnLeuHis---------------------- 133
              :::                   ||||||
Db        447 GCCGTCACCGCTGCCTGCAGCCAAGGGAACCTGAGCAACTGCGGCTGCGACCGCGAGAAG 506

Qy        134 ------TrpTyrLysLysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIle 151
                   :::|||   :::   :::|||   ||||||:::   |||          ||:::
Db        507 CAGGGCTACTACAACCAAGCCGAGGGC---TGGAAGTGGGGCGGCTGCTCGGCCGACGTG 563

Qy        152 ArgTrpGlyGluPheAspPheAspArgIlePheGluAspGlyArgGlu 167
              |||:::|||      ||||||   |||   |||   |||   ||||||
Db        564 CGTTACGGC---ATCGACTTCTCCCGGCGCTTCGTGGACGCTCGGGAG 608


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GenCore version 5.1.9

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Run on: December 4, 2006, 19:19:24 ; Search time 143 Seconds
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Title: US-10-507-132-2
Perfect score: 942
Sequence: 1 MGSQVQKSDEITFSDYLGLM.....WGEFDFDRIFEDGRETFGDK 172

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
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7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	94.5	10.0	462	3	US-09-328-352-44	Sequence 44, Appl
	2	84	8.9	850	3	US-09-449-285A-8	Sequence 8, Appli
	3	84	8.9	850	3	US-09-964-238-8	Sequence 8, Appli
	4	84	8.9	1017	3	US-09-543-681A-477	Sequence 477, App
	5	81	8.6	1070	3	US-09-625-634A-1	Sequence 1, Appli
	6	79	8.4	11096	3	US-10-149-736-4	Sequence 4, Appli
c	7	77	8.2	687	3	US-09-252-991A-12976	Sequence 12976, A
	8	77	8.2	2103	3	US-09-252-991A-12501	Sequence 12501, A
c	9	77	8.2	3045	3	US-09-252-991A-13297	Sequence 13297, A
	10	76.5	8.1	24070	3	US-09-949-016-16153	Sequence 16153, A
	11	76	8.1	1806	3	US-09-248-796A-1708	Sequence 1708, Ap
	12	75.5	8.0	1776	3	US-09-614-221A-97	Sequence 97, Appl
c	13	75	8.0	1830121	3	US-09-557-884-1	Sequence 1, Appli
c	14	75	8.0	1830121	3	US-09-643-990A-1	Sequence 1, Appli
c	15	75	8.0	1830121	3	US-10-158-865-1	Sequence 1, Appli
	16	74.5	7.9	1382	3	US-09-477-135A-122	Sequence 122, App
	17	74.5	7.9	48318	3	US-09-949-016-15717	Sequence 15717, A
c	18	74.5	7.9	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	19	74.5	7.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	20	74	7.9	882	5	US-09-974-300-2748	Sequence 2748, Ap
	21	74	7.9	2307	3	US-09-489-039A-3960	Sequence 3960, Ap
	22	73.5	7.8	1839	3	US-09-540-236-1428	Sequence 1428, Ap
	23	73.5	7.8	66986	3	US-09-596-002-29	Sequence 29, Appl
c	24	73.5	7.8	325791	3	US-09-768-185A-1	Sequence 1, Appli
c	25	73	7.7	8961	3	US-09-949-016-15910	Sequence 15910, A
	26	72.5	7.7	1249	5	US-09-984-429-401	Sequence 401, App
	27	72.5	7.7	1557	3	US-09-489-039A-1236	Sequence 1236, Ap
	28	72.5	7.7	2498	2	US-07-943-843-3	Sequence 3, Appli
	29	72.5	7.7	2498	2	US-08-347-003-3	Sequence 3, Appli
	30	72.5	7.7	49931	3	US-09-949-016-13727	Sequence 13727, A
	31	72.5	7.7	49931	3	US-09-949-016-13728	Sequence 13728, A
	32	72.5	7.7	49931	3	US-09-949-016-13729	Sequence 13729, A
	33	72.5	7.7	92344	3	US-09-949-016-16802	Sequence 16802, A
	34	72	7.6	781	5	US-09-974-300-90	Sequence 90, Appl
	35	72	7.6	1191	3	US-09-328-352-3721	Sequence 3721, Ap
	36	72	7.6	1209	5	US-09-974-300-4488	Sequence 4488, Ap
	37	72	7.6	4282	3	US-09-976-594-799	Sequence 799, App
	38	72	7.6	6474	3	US-09-949-016-1717	Sequence 1717, Ap
	39	71.5	7.6	1503	3	US-09-949-016-5826	Sequence 5826, Ap
	40	71.5	7.6	1956	3	US-09-715-858-1	Sequence 1, Appli
	41	71.5	7.6	2191	3	US-09-039-555B-12	Sequence 12, Appl
	42	71.5	7.6	2312	5	US-09-984-429-371	Sequence 371, App
	43	71.5	7.6	3816	3	US-09-540-236-1820	Sequence 1820, Ap
	44	71.5	7.6	5140	3	US-10-098-600B-14	Sequence 14, Appl
	45	71.5	7.6	5140	3	US-10-098-600B-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-328-352-44
; Sequence 44, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 44
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-44

Alignment Scores:
Pred. No.: 0.00957 Length: 462
Score: 94.50 Matches: 31
Percent Similarity: 43.7% Conservative: 28
Best Local Similarity: 23.0% Mismatches: 59
Query Match: 10.0% Indels: 17
DB: 3 Gaps: 6

US-10-507-132-2 (1-172) x US-09-328-352-44 (1-462)

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Qy         15 AspTyrLeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAsp 34
              ||||||      ::::::      :::      :::          :::|||   |||:::
Db         37 GACTACCATCGTATTTTAGAGGTCATTACGCGTTTTCAATTGGTTTTTGACCAGAAAAAT 96
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Qy         35 TrpAspArgLeuArgLysValIleAlaProThrLeuArgIleAspTyrArgSerPheLeu 54
              ||||||          :::::::::|||      |||   :::||||||      |||
Db         97 TGGGATGCGTTTGATGAGTTGTTAGCCGATCAACTTGAGGTGGACTATTTGCAGTTTAGA 156

Qy         55 AspLysLeuTrpGluAlaMetProAlaGluGluPheValGlyMetValSerSerLysGln 74
                 :::             :::         |||:::   |||       |||   ::|||
Db        157 GGGGAGCCTTTATGTGTGGTGTCTTGTCATGAATATAAAGGT------TCACGGCAACAA 210

Qy         75 MetLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLys 94
               |||           ||||||   ||||||   :::                   :::
Db        211 GCTTTGTCACAT------TTGCGGCTACAGCACAATTTAAGCAATCCT---CTTATTCGG 261

Qy         95 ValSerGluAspGluValIleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLys 114
              :::   :::|||:::                  |||         :::|||   |||:::
Db        262 ATTGAACAAGATCAAGCA------------TGGTTAGAATGTAATTATCAAATTTATCGT 309

Qy        115 AspThrThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrp 134
                                  :::         :::   ||||||         ::::::
Db        310 -----------------TTTTCGGAAAATGATTATTTTCATTCTTTTGGTCGCTATTAT 351

Qy        135 Tyr------LysLysIleAspGlyValTrpLysPheAlaGlyLeu 147
              :::      |||     |||:::||||||      |||:::
Db        352 TTTACTTTGGCAAAACAACAGGGCATATGGAAAATTACCGGAATT 396

RESULT 2
US-09-449-285A-8
; Sequence 8, Application US/09449285A
; Patent No. 6313280
; GENERAL INFORMATION:
;  APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnology
;  TITLE OF INVENTION: SMAD-INTERACTING POLYPEPTIDES AND THEIR USE
;  FILE REFERENCE: 2676-4232US
;  CURRENT APPLICATION NUMBER: US/09/449,285A
;  CURRENT FILING DATE:  1999-11-24
;  PRIOR APPLICATION NUMBER: PCT/EP98/03193
;  PRIOR FILING DATE: 1998-05-28
;  PRIOR APPLICATION NUMBER: 97201645.5
;  PRIOR FILING DATE: 1997-06-02
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
;   LENGTH: 850
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-449-285A-8

Alignment Scores:
Pred. No.:              0.479          Length:         850
Score:                  84.00          Matches:        32
Percent Similarity:     41.7%          Conservative:   11
Best Local Similarity:  31.1%          Mismatches:     36
Query Match:            8.9%           Indels:         24
DB:                     3              Gaps:           7

US-10-507-132-2 (1-172) x US-09-449-285A-8 (1-850)

Qy         84 GlnHisPheIleGlyGlyThrArgTrp------GluLysValSerGluAspGluValIle 101
              ||||||                ||||||          :::   |||       |||
Db        536 CAGCACCAGTTCCGATTCGGCCGCTGGAACTGCTCCGCCCTGGGCGAGAAGACCGTCTTC 595

Qy        102 GlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluVal 121
              |||      :::||||||||||      :::             |||           :::
Db        596 GGG---CAAGAACTCCGAGTAGGGAGTCGAGAGGCTGCCTTCACC------TATGCCATC 646

Qy        122 ThrMetLysGlyHisAlaHisSer--------------------AlaAsnLeuHis--- 133
              |||      |||   ||||||:::                          ||||||
Db        647 ACGGCGGCGGGCGTGGCGCATGCTGTCACCGCTGCCTGCAGCCAGGGCAATCTGAGCAAT 706

Qy        134 -------------------------TrpTyrLysLysIleAspGlyValTrpLysPhe 144
                                        :::|||   :::   :::|||   ||||||:::
Db        707 TGTGGCTGTGACCGGGAGAAGCAAGGCTACTACAACCAGGCGGAAGGC---TGGAAGTGG 763

Qy        145 AlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArgIlePheGluAsp 164
              \
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                 |||         |||:::|||:::|||      ||||||   |||   |||   |||
Db        764 GGGGGCTGCTCAGCGGACGTCCGCTACGGC---ATCGACTTTTCTCGTCGCTTTGTGGAT 820

Qy        165 GlyArgGlu 167
                 ||||||
Db        821 GCCCGTGAG 829

RESULT 3
US-09-964-238-8
; Sequence 8, Application US/09964238
; Patent No. 6884779
; GENERAL INFORMATION:
;  APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnology
;  TITLE OF INVENTION: SMAD-INTERACTING POLYPEPTIDES AND THEIR USE
;  FILE REFERENCE: 2676-4232US
;  CURRENT APPLICATION NUMBER: US/09/964,238
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 09/449,285
;  PRIOR FILING DATE: 1999-11-24
;  PRIOR APPLICATION NUMBER: PCT/EP98/03193
;  PRIOR FILING DATE: 1998-05-28
;  PRIOR APPLICATION NUMBER: 97201645.5
;  PRIOR FILING DATE: 1997-06-02
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
;   LENGTH: 850
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-964-238-8

Alignment Scores:
Pred. No.:              0.479          Length:         850
Score:                  84.00          Matches:        32
Percent Similarity:     41.7%          Conservative:   11
Best Local Similarity:  31.1%          Mismatches:     36
Query Match:            8.9%           Indels:         24
DB:                     3              Gaps:           7

US-10-507-132-2 (1-172) x US-09-964-238-8 (1-850)

Qy         84 GlnHisPheIleGlyGlyThrArgTrp------GluLysValSerGluAspGluValIle 101
              ||||||                ||||||          :::   |||       |||
Db        536 CAGCACCAGTTCCGATTCGGCCGCTGGAACTGCTCCGCCCTGGGCGAGAAGACCGTCTTC 595

Qy        102 GlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluVal 121
              |||      :::||||||||||      :::             |||           :::
Db        596 GGG---CAAGAACTCCGAGTAGGGAGTCGAGAGGCTGCCTTCACC------TATGCCATC 646

Qy        122 ThrMetLysGlyHisAlaHisSer--------------------AlaAsnLeuHis--- 133
              |||      |||   ||||||:::                          ||||||
Db        647 ACGGCGGCGGGCGTGGCGCATGCTGTCACCGCTGCCTGCAGCCAGGGCAATCTGAGCAAT 706

Qy        134 -------------------------TrpTyrLysLysIleAspGlyValTrpLysPhe 144
                                        :::|||   :::   :::|||   ||||||:::
Db        707 TGTGGCTGTGACCGGGAGAAGCAAGGCTACTACAACCAGGCGGAAGGC---TGGAAGTGG 763

Qy        145 AlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArgIlePheGluAsp 164
                 |||         |||:::|||:::|||      ||||||   |||   |||   |||
Db        764 GGGGGCTGCTCAGCGGACGTCCGCTACGGC---ATCGACTTTTCTCGTCGCTTTGTGGAT 820

Qy        165 GlyArgGlu 167
                 ||||||
Db        821 GCCCGTGAG 829

RESULT 4
US-09-543-681A-477
; Sequence 477, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
;  APPLICANT: GARY BRETON
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
;  TITLE OF INVENTION:  DIAGNOSTICS AND THERAPEUTICS
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;  FILE REFERENCE: 2709.1002-001
;  CURRENT APPLICATION NUMBER: US/09/543,681A
;  CURRENT FILING DATE:  2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/128,706
;  PRIOR FILING DATE: 1999-04-09
;  NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 477
;   LENGTH: 1017
;   TYPE: DNA
;   ORGANISM: Proteus mirabilis
US-09-543-681A-477

Alignment Scores:
Pred. No.:              0.615          Length:        1017
Score:                  84.00          Matches:       39
Percent Similarity:     37.3%          Conservative:  18
Best Local Similarity:  25.5%          Mismatches:    42
Query Match:            8.9%           Indels:        54
DB:                     3              Gaps:          10

US-10-507-132-2 (1-172) x US-09-543-681A-477 (1-1017)

Qy          35 TrpAspArgLeuArgLysValIleAlaProThrLeuArgIleAspTyrArgSerPheLeu 54
               ||||||:::   ::::::                                        |||
Db         280 TGGGATAAAGCACAACGA----------------------------GAAGATGTGCTT 309

Qy          55 AspLysLeuTrpGluAlaMetProAlaGluGluPheValGlyMetValSerSerLysGln 74
               ||||||::::::|||      |||   :::   ||||||
Db         310 GATAAAATGTTTGAAACAGCGCCA---CAGTCTTTCGTG-------------------- 345

Qy          75 MetLeuGlyAspProThrLeuArg---ThrGlnHisPheIleGlyGlyThrArgTrpGlu 93
               ||||||   |||      ||||||      :::|||   :::      |||   ||||||
Db         346 ATGCTTGCAGATCTTTGTTTAAGAGGGGCTAAACACACATTACAGCGTACCTCTTGGGAA 405

Qy          94 LysValSerGluAspGluValIleGlyTyrHisGlnLeuArg----------------- 107
                  :::         |||:::|||         :::|||:::
Db         406 GGGATA---------GAGATTATA------GAGCGCTTAAAAGCACAAGGGCGTAATGTT 450

Qy         108 ---------ValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLys 124
                      |||||||||          |||                 :::      |||
Db         451 ATTTTTATGGTACCGCATGGATGGGCTGTTGATGTACCTGCCATGTTATTGGCTGCTAAA 510

Qy         125 GlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLys------IleAspGlyValTrp 142
               |||         :::|||      |||      |||            |||   :::|||
Db         511 GGGCAAAAAATGGCAGCAATGTTTCACCACCAAAAAGATCCGGTGACTGATTATTTATGG 570

Qy         143 ------------------------------------LysPheAlaGlyLeuLysPro 149
                                                  :::   ||||||:::||||||
Db         571 AATAAAGCACGTTACCATTTCGGCGGACGTTTACACTCGCGCGAAGCGGGGATAAAACCT 630

Qy         150 AspIleArg-----------------TrpGlyGluPhe 156
               |||                     ||||||   :::
Db         631 TTTATTTCAACGGTGCGCCAAGGGTTTTGGGGGTATTAT 669

RESULT 5
US-09-625-634A-1
; Sequence 1, Application US/09625634A
; Patent No. 6653448
; GENERAL INFORMATION:
;  APPLICANT: Vernet, Corine
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Herrmann, John
;  TITLE OF INVENTION: WNT-7B-LIKE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
;  TITLE OF INVENTION:  SAME
;  FILE REFERENCE: Cura-244 (15966-744) US
;  CURRENT APPLICATION NUMBER: US/09/625,634A
;  CURRENT FILING DATE:  2000-07-26
;  PRIOR APPLICATION NUMBER: USSN 60/194,256
;  PRIOR FILING DATE: 2000-04-03
;  PRIOR APPLICATION NUMBER: USSN 60/192,838
;  PRIOR FILING DATE: 2000-03-29
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1070
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1047)
US-09-625-634A-1

Alignment Scores:
Pred. No.:              1.58           Length:        1070
Score:                  81.00          Matches:       30
Percent Similarity:     42.7%          Conservative:  11
Best Local Similarity:  31.2%          Mismatches:    31
Query Match:            8.6%           Indels:        24
DB:                     3              Gaps:          7

US-10-507-132-2 (1-172) x US-09-625-634A-1 (1-1070)

Qy          91 ArgTrp------GluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgVal 108
               ||||||            :::   |||      |||   |||       :::||||||||||
Db         241 CGCTGGAACTGCTCTGCCCTCGGCGAGAAGACCGTCTTCGGG---CAAGAGCTCCGAGTA 297

Qy         109 ProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlyHisAlaHis 128
                  :::             |||            :::|||      |||   ||||||
Db         298 GGGAGCCGTGAGGCTGCCTTCACG------TACGCCATCACCGCGGCTGGCGTGGCGCAC 351

Qy         129 Ser---------------------AlaAsnLeuHis----------------------- 133
               :::                          ||||||
Db         352 GCCGTCACCGCTGCCTGCAGCCAAGGGAACCTGAGCAACTGCGGCTGCGACCGCGAGAAG 411

Qy         134 ------TrpTyrLysLysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIle 151
                    :::|||   :::   :::|||   ||||||:::   |||       |||:::
Db         412 CAGGGCTACTACAACCAAGCCGAGGGC---TGGAAGTGGGGCGGCTGCTCGGCCGACGTG 468

Qy         152 ArgTrpGlyGluPheAspPheAspArgIlePheGluAspGlyArgGlu 167
               |||:::|||      ||||||  |||   |||   |||   ||||||
Db         469 CGTTACGGC---ATCGACTTCTCCCGGCGCTTCGTGGACGCTCGGGAG 513

RESULT 6
US-10-149-736-4
; Sequence 4, Application US/10149736
; Patent No. 6869777
; GENERAL INFORMATION:
;  APPLICANT: Chamberlain, Jeffrey S.
;  APPLICANT:  Harper, Scott Q.
;  TITLE OF INVENTION: Mini-Dystrophin Nucleic Acids and Peptide Sequences
;  FILE REFERENCE: UM-06968
;  CURRENT APPLICATION NUMBER: US/10/149,736
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: PCT/US01/31126
;  PRIOR FILING DATE: 2001-10-04
;  PRIOR APPLICATION NUMBER: 60/238,848
;  PRIOR FILING DATE: 2000-10-06
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 11096
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-149-736-4

Alignment Scores:
Pred. No.:              74.9           Length:        11096
Score:                  79.00          Matches:       39
Percent Similarity:     35.0%          Conservative:  23
Best Local Similarity:  22.0%          Mismatches:    71
Query Match:            8.4%           Indels:        44
DB:                     3              Gaps:          5

US-10-507-132-2 (1-172) x US-10-149-736-4 (1-11096)

Qy          15 AspTyrLeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAsp 34
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           :::|||   |||      |||         |||            |||
Db       7201 GAATACAGTGGCGATGACACAAGGAATGTGGAAGAAACCACGGAGTACTTGAAAACATCA 7260

Qy         35 TrpAspArgLeuArgLysValIleAla---------------------------------- 43
           |||      |||::::::   ||||||
Db       7261 TGGGTCAATCTCAAACAAAGCATCGCTGATAGACAGAGTGCCTTGGAGGCTGAGCTACAG 7320

Qy         44 ------ProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMet 61
                  |||   |||   |||      :::|||:::      |||   ||||||
Db       7321 ACAGTGCAGACTTCTCGTAGAGACCTGGAGAACTTTGTCAAGTGGCTTCAGGAAGCAGAA 7380

Qy         62 ProAlaGluGluPheValGlyMetValSerSerLysGln---MetLeuGlyAspProThr 80
                        :::          |||   ::::::      |||   |||
Db       7381 ACCACAGCAAATGTGCTGGCCGATGCCTCTCAGCGGGAGAATGCTCTTCAGGACAGTGTC 7440

Qy         81 LeuArgThrGln------------------------------------------------ 84
           |||      |||
Db       7441 CTGGCCCGGCAGCTCCGACAGCAGATGCTGGACATCCAGGCAGAAATTGATGCCCACAAT 7500

Qy         85 ---------HisPheIleGlyGlyThrArgTrpGluLysVal---------------Ser 96
                      |||   |||   |||   :::   |||                 |||
Db       7501 GACATATTTAAAAGCATCGATGGAAACCGGCAGAAGATGGTGAAAGCTCTGGGGAATTCT 7560

Qy         97 GluAspGluValIleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThr 116
              |||:::      :::    |||:::|||         :::|||||:::   |||
Db       7561 GAGGAAGCAACAATGCTTCAACATCGACTGGATGACATGAACCAAAGATGGAATGATTTG 7620

Qy        117 ThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLys 136
                 |||      :::::::::   |||      ::::::         |||   :::
Db       7621 AAGGCAAAATCTGCTAGCATCAGGGCCCATTTGGAGGCCAGTGCTGAGAAATGGAACCGG 7680

Qy        137 LysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIleArgTrp 153
               :::                  |||   |||:::      |||:::|||
Db       7681 TTGCTG----------------GCATCGCTGGAAGAGCTGATCAAATGG 7713

RESULT 7
US-09-252-991A-12976/c
; Sequence 12976, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 12976
;   LENGTH: 687
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12976

Alignment Scores:
Pred. No.:              2.73          Length:         687
Score:                  77.00         Matches:        25
Percent Similarity:     44.9%         Conservative:   15
Best Local Similarity:  28.1%         Mismatches:     35
Query Match:            8.2%          Indels:         14
DB:                     3             Gaps:           4

US-10-507-132-2 (1-172) x US-09-252-991A-12976 (1-687)

Qy         59 GluAlaMetProAlaGluGluPheValGlyMet---ValSerSerLysGlnMetLeuGly 77
              |||      |||||||||:::   :::|||      |||:::         :::||||||
Db        300 GAAGATCAGCCAGCCGAACAGCGCCTTGGTCAGCGCGTTGCTCCAGGACATATCCTGGGC 241

Qy         78 AspProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrp--------------- 92
                 |||      |||      |||   :::      :::
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Db       240 TACCCCGAGGATCGCGTCGCCCATCGAGTACAGCGGAGCCCGCAGTGTCGGCAGGCGGTC 181

Qy         93 ---GluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgValProHisGln 111
                 |||   |||   :::   |||   :::|||:::|||   :::         ||||||
Db       180 GCCGAGGTCGTAGAACAGGGTGAAGACGTTGGTCATCACCACATAGAGGAAGGTCACCAG 121

Qy        112 ArgTyrLys--------------AspThrThrMetLysGluValThrMetLysGlyHis 126
              |||::::::              |||:::   :::   |||               |||
Db       120 CGTCATCGCCGCCAGCAGGAAGGCGATAGCGCCCTCCTCGAAGCGGTTCCAGACGCGCAC 61

Qy        127 ------AlaHisSerAlaAsnLeuHis 133
                    |||   :::   ||||||
Db        60 GAGTCGATTCATCGCAGCGTTCTCCAC 34

RESULT 8
US-09-252-991A-12501
; Sequence 12501, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 12501
;   LENGTH: 2103
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12501

Alignment Scores:
Pred. No.:              13.1          Length:         2103
Score:                  77.00         Matches:        25
Percent Similarity:     44.9%         Conservative:   15
Best Local Similarity:  28.1%         Mismatches:     35
Query Match:            8.2%          Indels:         14
DB:                     3             Gaps:           4

US-10-507-132-2 (1-172) x US-09-252-991A-12501 (1-2103)

Qy         59 GluAlaMetProAlaGluGluPheValGlyMet---ValSerSerLysGlnMetLeuGly 77
              |||      |||||||||:::   :::|||      |||:::         :::||||||
Db       421 GAAGATCAGCCAGCCGAACAGCGCCTTGGTCAGCGCGTTGCTCCAGGACATATCCTGGGC 480

Qy         78 AspProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrp--------------- 92
                 |||      |||      |||   :::      :::
Db       481 TACCCCGAGGATCGCGTCGCCCATCGAGTACAGCGGAGCCCGCAGTGTCGGCAGGCGGTC 540

Qy         93 ---GluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgValProHisGln 111
                 |||   |||   :::   |||   :::|||:::|||   :::         ||||||
Db       541 GCCGAGGTCGTAGAACAGGGTGAAGACGTTGGTCATCACCACATAGAGGAAGGTCACCAG 600

Qy        112 ArgTyrLys--------------AspThrThrMetLysGluValThrMetLysGlyHis 126
              |||::::::              |||:::   :::   |||               |||
Db       601 CGTCATCGCCGCCAGCAGGAAGGCGATAGCGCCCTCCTCGAAGCGGTTCCAGACGCGCAC 660

Qy        127 ------AlaHisSerAlaAsnLeuHis 133
                    |||   :::   ||||||
Db       661 GAGTCGATTCATCGCAGCGTTCTCCAC 687

RESULT 9
US-09-252-991A-13297/c
; Sequence 13297, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 13297
;   LENGTH: 3045
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13297

Alignment Scores:
Pred. No.:                21.9          Length:        3045
Score:                    77.00         Matches:       25
Percent Similarity:       44.9%         Conservative:  15
Best Local Similarity:    28.1%         Mismatches:    35
Query Match:              8.2%          Indels:        14
DB:                       3             Gaps:          4

US-10-507-132-2 (1-172) x US-09-252-991A-13297 (1-3045)

Qy         59 GluAlaMetProAlaGluGluPheValGlyMet---ValSerSerLysGlnMetLeuGly 77
              |||      |||||||||:::   :::|||      |||:::         :::||||||
Db       1378 GAAGATCAGCCAGCCGAACAGCGCCTTGGTCAGCGCGTTGCTCCAGGACATATCCTGGGC 1319

Qy         78 AspProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrp-------------- 92
              |||       |||      |||   :::      :::
Db       1318 TACCCCGAGGATCGCGTCGCCCATCGAGTACAGCGGAGCCCGCAGTGTCGGCAGGCGGTC 1259

Qy         93 ---GluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgValProHisGln 111
                 |||   |||   :::   |||   :::|||:::|||   :::         ||||||
Db       1258 GCCGAGGTCGTAGAACAGGGTGAAGACGTTGGTCATCACCACATAGAGGAAGGTCACCAG 1199

Qy        112 ArgTyrLys--------------AspThrThrMetLysGluValThrMetLysGlyHis 126
              |||::::::               |||:::   :::   |||               |||
Db       1198 CGTCATCGCCGCCAGCAGGAAGGCGATAGCGCCCTCCTCGAAGCGGTTCCAGACGCGCAC 1139

Qy        127 ------AlaHisSerAlaAsnLeuHis 133
                    |||   :::   ||||||
Db       1138 GAGTCGATTCATCGCAGCGTTCTCCAC 1112

RESULT 10
US-09-949-016-16153
; Sequence 16153, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16153
;   LENGTH: 24070
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-16153

Alignment Scores:
Pred. No.:                459           Length:        24070
Score:                    76.50         Matches:       56
Percent Similarity:       30.3%         Conservative:  18
Best Local Similarity:    23.0%         Mismatches:    79
Query Match:              8.1%          Indels:        91
DB:                       3             Gaps:          11

US-10-507-132-2 (1-172) x US-09-949-016-16153 (1-24070)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAsp---------TyrLeu 17
              |||||||||:::         |||                 |||
Db      12678 ATGGGAAGCAGAGCATCCATGTCGAGCCGTGCATTTACGAGCAGTCGTGCAGCCATGTGC 12737

Qy         18 GlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArg 37
              |||        |||||||||   ||||||                  |||:::
Db      12738 GGGTGTGCATGCTGTGTGTACATCTGGGCGTGTGTGTGTGTGCATGTGGGGTGGAATTGT 12797

Qy         38 LeuArgLysValIle---------------------------------------------- 42
              |||         :::
Db      12798 CTGTGTGTTGCTGTGTGGGAATGGACTGCTGTGGTTTGTCTGGTGCCTGAGGGCCTAGGG 12857

Qy         42 ---------------------------------------------------------- 42

Db      12858 AGCGTGTACTTGTGTGAGCGTGTGGCTACTGGGCATGGGCATGCCTGTGCGTGTATGGAC 12917

Qy         43 ----------------------------------------------AlaProThrLeuArg 47
                                                            ||||||:::
Db      12918 ATGTGGCTGGGGTTGGCTTCAGCCTCAGGCCTGTGGCTTCCACATGCACCCTCCCGGGCC 12977

Qy         48 IleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetProAlaGluGluPheVal 67
              |||       :::|||:::|||   |||                 |||          |||
Db      12978 ATCAGTAGAAAATCATGGTTGCCTAAGGCAGGCTTTGAGTCCCCGGAT---------GTG 13028

Qy         68 GlyMetValSerSer------LysGlnMetLeuGlyAspProThrLeuArgThr------ 83
              |||:::      |||            :::||||||||||||   |||   |||
Db      13029 GGTTTGAGCCCCAGCCCTGTCTCTGGTTTGCTGGGTGACCCCAGGCTGGCCACTTCCCTC 13088

Qy         84 Gln-HisPheIleGlyGlyThrArgTrpGlu-----------LysValSerGluAspGl 99
                 |||       ||||||:::              |||:::::|||   ||
Db      13089 TCTGGACCTCATTTCTTCTGTACGCTGGGATTGTAATCTCCTGAAGATCGCAGAGGGGGA 13148

Qy         99 uValIleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLy 119
              ||||  |||         |||      ||||||
Db      13149 GGTCTGTGGGCTAGGATGGCTGGGCTTCCCCCAT------------------------- 13182

Qy        119 sGluValThrMetLysGlyHisAlaHisSer-AlaAsnLeuHisTrpTyrLysLysIleA 139
                             ||||||       |||   |||         :::   :::
Db      13183 ---------------GCCCATGCACTGCCTGGCCAGGCTC---CTGAGAAGGCCTGTCC 13223

Qy        139 spGlyValTrpLysPhe-----------------AlaGlyLeuLysProAspIleArgT 153
              |||   |||                      :::   |||   ||||||      |
Db      13224 CTGGCTGCTGGAGCCTCTGCCCCTGCCTCCGGGGCTCAGCCTTGTTCCCTGATGCCATTT 13283

Qy        153 rp---------GlyGluPheAspPheAspArgIlePheGluAspGlyArgGluThrPheG 170
              ||         |||   :::   :::      :::      |||||||||:::   |||
Db      13284 GGGCGTCTCTTGGCCTCTGGTCCTACCCAGGCCTGCTG---GATGGGAGGAAACTTTTCC 13340

Qy        170 lyAspLys 172
                 |||
Db      13341 GGCCAAAA 13348

RESULT 11
US-09-248-796A-1708
; Sequence 1708, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
;  APPLICANT: Keith Weinstock et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
;  TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 107196.132
;  CURRENT APPLICATION NUMBER: US/09/248,796A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER: US 60/074,725
;  PRIOR FILING DATE: 1998-02-13
;  PRIOR APPLICATION NUMBER: US 60/096,409
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;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 1708
;    LENGTH: 1806
;    TYPE: DNA
;    ORGANISM: Candida albicans
US-09-248-796A-1708

Alignment Scores:
Pred. No.:              14.1          Length:         1806
Score:                  76.00         Matches:        39
Percent Similarity:     36.5%         Conservative:   23
Best Local Similarity:  22.9%         Mismatches:     57
Query Match:            8.1%          Indels:         51
DB:                     3             Gaps:           6

US-10-507-132-2 (1-172) x US-09-248-796A-1708 (1-1806)

Qy          4 GlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMetThrCysVal 23
              |||   :::   |||   |||||||||      :::|||   |||             |||
Db        307 CAAGAGAAATCGTCTGTGGAAATTACCATTGAAAATTATGAAGGTCACTCACCTATAGTA 366

Qy         24 TyrGluTrpAlaAspSerTyrAspSerLysAspTrp-----------AspArgLeuArg 39
                 :::         :::          :::|||               |||
Db        367 ATTAAAAGAGAGTTTACTGCCAAAGAATCAAATTGGACAGTTAACAACAAGCGGGCCACT 426

Qy         40 LysValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGlu 59
              :::               :::|||      :::         ||||||   |||
Db        427 GAATCAAAAATCAAAGATATAAGAACCAAATTCAATATCCAACTAGACAACCTTTGTCAT 486

Qy         60 AlaMetProAlaGlu---------GluPheValGly-----------------MetVal 70
                :::|||   |||       ||||||   |||                  ::::::
Db        487 TTTTTGCCGCAAGAAAGAGTAGCAGAATTTGCAGGACTTTCCCCAGAGAAATTGTTGATG 546

Qy         71 SerSerLysGlnMetLeuGlyAspProThrLeuArgThrGlnHis--------------- 85
              :::::::::   |||||||||      |||         |||
Db        547 GAGACAGAACGTACTCTTGGTGATGGCCATTTGTTGATCATGCACGAAGATTTGATTGCC 606

Qy         86 ---------------------------------------PheIleGlyGlyThrArgTrp 92
                                                     |||   |||   |||
Db        607 AAAGATAACGAAAGTCAGCAATTGGGCAACAAGATTAAAGACATTGAAGGG---AGATTA 663

Qy         93 GluLysValSerGluAsp------------------------------------------ 98
              |||:::   ||||||
Db        664 GCCAAATTACACGAGGATAGATCAAAATTGGAAGAAGAAGCACGAAAATTAGAGGAGTAC 723

Qy         99 -----------GluValIleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLys 114
                      |||   :::      |||:::|||   :::|||:::   :::|||:::
Db        724 GATAGAAAGTCTGAAGAAGTTGATAATCACCGTCTTTTGATCCCGTATGCAAAATACCAA 783

Qy        115 AspThr-ThrMetLysGluValThrMet 123
              |||          ||||||:::|||:::
Db        784 GACTTGAAAAACCAAAGAACTCACCTTA 811

RESULT 12
US-09-614-221A-97
; Sequence 97, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
;  APPLICANT: Karunanandaa, Balasulojini
;  APPLICANT:  Yu, Jaehyuk
;  APPLICANT:  Kishore, Ganesh M.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
;  TITLE OF INVENTION:  WITH STEROL SYNTHESIS AND METABOLISM
;  FILE REFERENCE: 16516.075
;  CURRENT APPLICATION NUMBER: US/09/614,221A
;  CURRENT FILING DATE:  2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/142,981
;  PRIOR FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 626
; SEQ ID NO 97
;    LENGTH: 1776
;    TYPE: DNA
;   ORGANISM: Saccharomyces cerevisiae
US-09-614-221A-97

Alignment Scores:
Pred. No.:              16            Length:         1776
Score:                  75.50         Matches:        42
Percent Similarity:     32.5%         Conservative:   25
Best Local Similarity:  20.4%         Mismatches:     68
Query Match:            8.0%          Indels:         71
DB:                     3             Gaps:           8

US-10-507-132-2 (1-172) x US-09-614-221A-97 (1-1776)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              |||   :::               |||   :::   :::   ||||||
Db        964 ATGAACGCTTCAAAAGCTGGTGGCGATATCCTTAAGTATTTCGATTAT---------CCT 1014

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSer---LysAspTrpAspArgLeuArg 39
              |||          |||       |||   |||   |||||||||:::   |||
Db       1015 ACCACAGCGAGTGGATGGAATCAAATGTACCATTCTGCCAAAGATTGGGAGGTACTTGCC 1074

Qy         40 LysValIleAlaProThr---------------------------------------- 45
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Db       1075 AAAGGGCAGGTTCCCACCGCCCCCTCTTTAAAGACATTGAGGAATGAAAAAGGTTCGGGT 1134

Qy         46 LeuArgIleAspTyrArgSerPhe--------------------LeuAspLysLeuTrp 58
              ::::::   ||||||   :::|||                 :::   |||:::
Db       1135 GTGAAAGCTGATTATGACACTTTTGCTAAAATTTTGCTTGCTGGGATTGCAAAAATTAAC 1194

Qy         59 GluAlaMetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAsp 78
              |||     |||       :::       ::::::              ||||||
Db       1195 GAGGTTGAACCAAAGGTTACTTGGTACGATACCATTGCA--------------GGAGAT 1239

Qy         79 ProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAsp 98
                           |||                |||||   |||
Db       1240 GGTGATTGCGGAACTACTCTTGTGTCCGGTGGTGAAGCATTGGAA--------------- 1284

Qy         99 GluValIleGlyTyrHisGlnLeuArgValProHis----------------------- 110
              |||   |||      |||   ||||||:::
Db       1285 GAAGCTATTAAAAACCATACGTTGCGCCTCGAGGATGCTGCTCTTGGTATCGAAGATATT 1344

Qy        110 ------------------------------------------------------------ 110

Db       1345 GCGTATATGGTTGAGGATTCTATGGGTGGTACGTCCGGTGGTCTGTACTCTATCTATCTT 1404

Qy        111 -----------GlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlyHis 126
                        |||      :::|||:::      ||||||:::|||   :::
Db       1405 TCTGCTCTCGCACAAGGAGTTAGGGATTCTGGGGACAAGGAACTTACTGCGGAAACTTTC 1464

Qy        127 AlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGlyValTrpLysPheAlaGly 146
                    ::::::|||:::               :::|||   ::::::|||:::
Db       1465 AAAAAGGCATCAAACGTT-----------GCACTAGATGCTTTGTATAAGTATACGAGA 1512

Qy        147 LeuLysProAspIleArg 152
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Db       1513 GCCCGTCCTGGTTACAGG 1530

RESULT 13
US-09-557-884-1/c
; Sequence 1, Application US/09557884
; Patent No. 6506581
;   GENERAL INFORMATION:
;        APPLICANT: Fleischmann et al.
;        TITLE OF INVENTION: The Nucleotide sequence of
;                            the Haemophilus influenzae Rd Genome, Fragments
;                            Thereof, and Uses Thereof
;        NUMBER OF SEQUENCES: 1
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: MD
;             COUNTRY: USA
```

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;           ZIP: 20850
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: 3 1/2 inch diskette
;           COMPUTER: Dell Pentium
;           OPERATING SYSTEM: MS DOS v6.22
;           SOFTWARE: ASCII Text
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/557,884
;           FILING DATE: 25-Apr-2000
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: 08/476,102
;           FILING DATE: JUN-5-1995
;       ATTORNEY/AGENT INFORMATION:
;           NAME: Michelle S. Marks
;           REGISTRATION NUMBER: 41,971
;           REFERENCE/DOCKET NUMBER: PB186P3
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: 301-309-8504
;           TELEFAX: 301-309-8439
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 1830121 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: double
;           TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

Alignment Scores:
Pred. No.:              2.89e+05      Length:         1830121
Score:                  75.00         Matches:        44
Percent Similarity:     35.9%         Conservative:   25
Best Local Similarity:  22.9%         Mismatches:     81
Query Match:            8.0%          Indels:         42
DB:                     3             Gaps:           8

US-10-507-132-2 (1-172) x US-09-557-884-1 (1-1830121)

Qy         15 AspTyrLeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAsp 34
              ||||||      |||   |||      ||||||:::      |||
Db     227712 GATTATCCGCAACTTTGTACTTACTTCTATGAGTTTAATCTTTCCGATCCTGTGTTACAA 227653

Qy         35 TrpAspArgLeuArgLysValIleAlaProThrLeuArgIleAsp---------------- 49
                  :::||||||   |||         :::      :::
Db     227652 AAAAGTGCGGTAAGAAAAGCGATTGTTTCGATGATTTCTACCAATAATTTGGTTGCAGAT 227593

Qy         50 ------------------TyrArgSerPheLeuAspLys---------------------- 56
                                 :::||||||   |||
Db     227592 ATTGCTCATCTTTATCCTAACAATACTTTTTTGCCAAAATCTATGCTAGGTGAGCAAGAA 227533

Qy         57 ---LeuTrpGluAlaMetProAlaGluGluPheValGlyMetValSerSerLysGlnMet 75
                 :::||||||   :::   ||||||:::         :::   |||      |||:::
Db     227532 TCTGTTTGGGAGCCAGTTGTTGCAGAACAG---------CTCTTTTCCCAAAATCAAATT 227482

Qy         76 LeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysVal 95
                      |||:::   :::                  |||::::::   :::
Db     227481 AGTGAAACTCGTCCATTGAAATTACGT--------------ATTCGTTATGATGATTTA 227437

Qy         96 SerGluAspGluValIleGlyTyr---------HisGln-----------------Leu 106
              |||   ::::::   |||              ||||||                  |||
Db     227436 TCTCTGAATCAAACCATTGCAATGCGATTAAATCATCAATTATCACAATCTGATTTATTA 227377

Qy        107 ArgValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlyHis 126
              ||||||   :::|||                :::::            ||||||
Db     227376 CGAGTTGAAAATCAAGGGATGAGCTGGCAAGAATTGCAAACCGCCCGCACAAAAGGCGAT 227317

Qy        127 AlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGlyValTrpLysPheAlaGly 146
                              |||           :::          |||
Db     227316 TTTCAATTAATTCGTTCTGGCTGGTGTGCTGATTTTAATGATCCTGCAGCATTTCTAAAT 227257

Qy        147 Leu------------LysProAspIleArgTrpGly------GluPheAspPheAspArg 160
              |||           ||||||   :::   |||           :::||||||||||
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Db     227256 TTATTCTATTCAAAAAGCCCAGATAACAAAAATGGCTATAAAAATGCGGAATTTGATCGT 227197

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
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Db     227196 TTATTTGAAAGTGCAATGACGACGATATCCGAAAAA 227161

RESULT 14
US-09-643-990A-1/c
; Sequence 1, Application US/09643990A
; Patent No. 6528289
;   GENERAL INFORMATION:
;       APPLICANT: Robert D. Fleischmann
;                  Mark D. Adams
;                  Owen White
;                  Hamilton O. Smith
;                  J. Craig Venter
;       TITLE OF INVENTION: The Nucleotide sequence of
;                           the Haemophilus influenzae Rd Genome, Fragments
;                           Thereof, and Uses Thereof
;       NUMBER OF SEQUENCES: 1
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Human Genome Sciences, Inc.
;           STREET: 9410 Key West Avenue
;           CITY: Rockville,
;           STATE: MD
;           COUNTRY: USA
;           ZIP: 20850
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: 3 1/2 inch diskette
;           COMPUTER: Dell Pentium
;           OPERATING SYSTEM: MS DOS v6.22
;           SOFTWARE: ASCII Text
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/643,990A
;           FILING DATE: 23-Aug-2000
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: 08/487,429
;           FILING DATE: 1995-06-07
;           APPLICATION NUMBER: 08/426,787
;           FILING DATE: 1995-04-21
;       ATTORNEY/AGENT INFORMATION:
;           NAME: Kenley K. Hoover
;           REGISTRATION NUMBER: 40,302
;           REFERENCE/DOCKET NUMBER: PB186P1C1
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: 301-610-5790
;           TELEFAX: 310-309-8439
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 1830121 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: double
;           TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1

Alignment Scores:
Pred. No.:              2.89e+05      Length:         1830121
Score:                  75.00         Matches:        44
Percent Similarity:     35.9%         Conservative:   25
Best Local Similarity:  22.9%         Mismatches:     81
Query Match:            8.0%          Indels:         42
DB:                     3             Gaps:           8

US-10-507-132-2 (1-172) x US-09-643-990A-1 (1-1830121)

Qy         15 AspTyrLeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAsp 34
              ||||||      |||   |||      ||||||:::      |||
Db     227712 GATTATCCGCAACTTTGTACTTACTTCTATGAGTTTAATCTTTCCGATCCTGTGTTACAA 227653

Qy         35 TrpAspArgLeuArgLysValIleAlaProThrLeuArgIleAsp---------------- 49
                  :::||||||   |||         :::      :::
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Db     227652 AAAAGTGCGGTAAGAAAAGCGATTGTTTCGATGATTTCTACCAATAATTTGGTTGCAGAT 227593

Qy         50 ------------------TyrArgSerPheLeuAspLys---------------------- 56
                                 :::||||||   |||
Db     227592 ATTGCTCATCTTTATCCTAACAATACTTTTTTGCCAAAATCTATGCTAGGTGAGCAAGAA 227533

Qy         57 ---LeuTrpGluAlaMetProAlaGluGluPheValGlyMetValSerSerLysGlnMet 75
                 :::|||||||   :::   ||||||:::         :::   |||      |||:::
Db     227532 TCTGTTTGGGAGCCAGTTGTTGCAGAACAG---------CTCTTTTCCCAAAATCAAATT 227482

Qy         76 LeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysVal 95
                        |||:::   :::                  |||::::::   :::
Db     227481 AGTGAAACTCGTCCATTGAAATTACGT---------------ATTCGTTATGATGATTTA 227437

Qy         96 SerGluAspGluValIleGlyTyr---------HisGln------------------Leu 106
              |||   ::::::   |||              ||||||                  |||
Db     227436 TCTCTGAATCAAACCATTGCAATGCGATTAAATCATCAATTATCACAATCTGATTTATTA 227377

Qy        107 ArgValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlyHis 126
              ||||||   :::|||                  ::::::              ||||||
Db     227376 CGAGTTGAAAATCAAGGGATGAGCTGGCAAGAATTGCAAACCGCCCGCACAAAAGGCGAT 227317

Qy        127 AlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGlyValTrpLysPheAlaGly 146
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Db     227316 TTTCAATTAATTCGTTCTGGCTGGTGTGCTGATTTTAATGATCCTGCAGCATTTCTAAAT 227257

Qy        147 Leu------------LysProAspIleArgTrpGly------GluPheAspPheAspArg 160
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Db     227256 TTATTCTATTCAAAAAGCCCAGATAACAAAAATGGCTATAAAAATGCGGAATTTGATCGT 227197

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
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Db     227196 TTATTTGAAAGTGCAATGACGACGATATCCGAAAAA 227161

RESULT 15
US-10-158-865-1/c
; Sequence 1, Application US/10158865
; Patent No. 6846651
; GENERAL INFORMATION:
;  APPLICANT: Fleischmann et al.
;  TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Frag
; Patent No. 6846651
;  TITLE OF INVENTION:  Thereof, and Uses Thereof
;  FILE REFERENCE: PB186P2C1D1
;  CURRENT APPLICATION NUMBER: US/10/158,865
;  CURRENT FILING DATE:  2002-06-03
;  PRIOR APPLICATION NUMBER: US 09/557,884
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: US 08/476,102
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: US 08/426,787
;  PRIOR FILING DATE: 1995-04-21
;  NUMBER OF SEQ ID NOS: 1
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;   LENGTH: 1830121
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;   OTHER INFORMATION: n equals a,t,c, or g
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;   NAME/KEY: misc_feature
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;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (145171)..(145171)
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;   LOCATION: (145942)..(145942)
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;   LOCATION: (150841)..(150841)
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;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (152500)..(152500)
;   OTHER INFORMATION: n equals a,t,c, or g
;   FEATURE:
;   NAME/KEY: misc_feature

Alignment Scores:
Pred. No.:              2.89e+05        Length:         1830121
Score:                  75.00           Matches:        44
Percent Similarity:     35.9%           Conservative:   25
Best Local Similarity:  22.9%           Mismatches:     81
Query Match:            8.0%            Indels:         42
DB:                     3               Gaps:           8

US-10-507-132-2 (1-172) x US-10-158-865-1 (1-1830121)

Qy         15 AspTyrLeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAsp 34
              ||||||     |||   |||       ||||||:::     |||
Db     227712 GATTATCCGCAACTTTGTACTTACTTCTATGAGTTTAATCTTTCCGATCCTGTGTTACAA 227653

Qy         35 TrpAspArgLeuArgLysValIleAlaProThrLeuArgIleAsp---------------- 49
                    :::||||||   |||         :::      :::
Db     227652 AAAAGTGCGGTAAGAAAAGCGATTGTTTCGATGATTTCTACCAATAATTTGGTTGCAGAT 227593

Qy         50 -----------------TyrArgSerPheLeuAspLys---------------------- 56
                                       :::||||||   |||
Db     227592 ATTGCTCATCTTTATCCTAACAATACTTTTTTGCCAAAATCTATGCTAGGTGAGCAAGAA 227533

Qy         57 ---LeuTrpGluAlaMetProAlaGluGluPheValGlyMetValSerSerLysGlnMet 75
                  :::||||||   :::   ||||||:::         :::   |||      |||:::
Db     227532 TCTGTTTGGGAGCCAGTTGTTGCAGAACAG---------CTCTTTTCCCAAAATCAAATT 227482

Qy         76 LeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysVal 95
                        |||:::   :::                |||::::::   :::
Db     227481 AGTGAAACTCGTCCATTGAAATTACGT---------------ATTCGTTATGATGATTTA 227437

Qy         96 SerGluAspGluValIleGlyTyr---------HisGln-----------------Leu 106
              |||   ::::::   |||               ||||||                 |||
Db     227436 TCTCTGAATCAAACCATTGCAATGCGATTAAATCATCAATTATCACAATCTGATTTATTA 227377

Qy        107 ArgValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlyHis 126
              ||||||   :::|||                   ::::::           ||||||
Db     227376 CGAGTTGAAAATCAAGGGATGAGCTGGCAAGAATTGCAAACCGCCCGCACAAAAGGCGAT 227317

Qy        127 AlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGlyValTrpLysPheAlaGly 146
                                  |||         :::         |||
Db     227316 TTTCAATTAATTCGTTCTGGCTGGTGTGCTGATTTTAATGATCCTGCAGCATTTCTAAAT 227257

Qy        147 Leu------------LysProAspIleArgTrpGly------GluPheAspPheAspArg 160
              |||               ||||||   :::   |||           :::|||||||||
Db     227256 TTATTCTATTCAAAAAGCCCAGATAACAAAAATGGCTATAAAAATGCGGAATTTGATCGT 227197

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
              :::||||||           |||      :::|||
Db     227196 TTATTTGAAAGTGCAATGACGACGATATCCGAAAAA 227161


Search completed: December  4, 2006, 19:39:17
Job time : 1182 secs
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GenCore version 5.1.9

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2006, 19:04:14 ; Search time 525 Seconds
(without alignments)
3426.362 Million cell updates/sec

Title: US-10-507-132-2
Perfect score: 942
Sequence: 1 MGSQVQKSDEITFSDYLGLM.....WGEFDFDRIFEDGRETFGDK 172

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Searched: 5244920 seqs, 3486124231 residues

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Maximum Match 100%
Listing first 45 summaries

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9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	942	100.0	516	10	ADC16590	Adc16590 Scytalone
2	938	99.6	516	10	ADC16592	Adc16592 Scytalone
3	938	99.6	600	10	ADC16602	Adc16602 Scytalone
4	938	99.6	610	10	ADC16603	Adc16603 Scytalone
5	183	19.4	697	8	ABZ52566	Abz52566 Aspergill
6	94.5	10.0	462	9	ADA28757	Ada28757 DNA encod
c 7	87.5	9.3	110000	14	AEB42401_09	Continuation (10 o
8	87	9.2	2775	10	AAD57634	Aad57634 Rice dise
c 9	86.5	9.2	48622	14	AEB39158	Aeb39158 L. pneumo
c 10	86.5	9.2	88876	14	AEB35710	Aeb35710 L. pneumo
c 11	86.5	9.2	110000	14	AEB39175_09	Continuation (10 o
c 12	86.5	9.2	110000	14	AEB42736_2	Continuation (3 of
13	85	9.0	864	2	AAX14439	Aax14439 H. pylori
14	84	8.9	850	2	AAV72504	Aav72504 Mouse SMA
15	84	8.9	1017	10	ADF00192	Adf00192 Bacterial
16	84	8.9	1454	13	ADX60282	Adx60282 Plant ful
17	84	8.9	3154	13	ADS31849	Ads31849 Mouse win
18	84	8.9	3154	13	ADU86485	Adu86485 Mouse win
19	84	8.9	3154	15	AED95374	Aed95374 Mouse Wnt
20	83	8.8	374	8	ABZ55170	Abz55170 Aspergill
21	83	8.8	2016	4	AAA54512	Aaa54512 Fructan e
22	83	8.8	3007	2	AAQ68842	Aaq68842 Plant bli
23	82.5	8.8	88232	11	ACN44980	Acn44980 Mouse gen
24	81	8.6	1047	9	ADA27222	Ada27222 Human NOV
25	81	8.6	1070	4	AAD20986	Aad20986 Human Wnt
26	81	8.6	1070	9	ADA38095	Ada38095 WNT-7B DN
27	81	8.6	1070	9	ADA27233	Ada27233 Human NOV
28	81	8.6	1350	12	ADQ79685	Adq79685 Benzoate
29	81	8.6	1853	12	ADQ79682	Adq79682 Benzoate
30	81	8.6	2160	9	ADA27231	Ada27231 Human NOV
31	81	8.6	2250	12	ADO22235	Ado22235 Human WNT
32	81	8.6	2250	13	ADU86447	Adu86447 Human win
33	81	8.6	2250	15	AED95372	Aed95372 Human Wnt
c 34	81	8.6	6312	12	ADQ79681	Adq79681 Benzoate
35	80.5	8.5	2280	6	ABZ78215	Abz78215 A. niger
36	80.5	8.5	2503	10	ADC07803	Adc07803 Rice DNA
37	80	8.5	1070	11	ADM10596	Adm10596 Human WNT
38	80	8.5	2074	4	AAA54511	Aaa54511 Fructan e
39	79.5	8.4	4041	4	ABL02973	Abl02973 Drosophil
40	79.5	8.4	20510	4	ABL02972	Abl02972 Drosophil
41	79	8.4	2109	13	ADT48723	Adt48723 Bacterial
42	79	8.4	11096	6	ABK81962	Abk81962 cDNA enco
c 43	79	8.4	349980	6	ABQ81847	Abq81847 Bifidobac
44	78.5	8.3	650	10	ADE31379	Ade31379 Human dia
45	78.5	8.3	1458	6	AAD40506	Aad40506 Infectiou

ALIGNMENTS

RESULT 1
ADC16590
ID ADC16590 standard; DNA; 516 BP.
XX
AC ADC16590;
XX
DT 18-DEC-2003 (first entry)
XX
DE Scytalone dehydrogenase gene #SEQ ID 1.
XX
KW Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor;
KW gene; ds.
XX
OS Magnaporthe grisea.
XX
FH Key Location/Qualifiers
FT CDS 1. .516
FT /*tag= a
FT /product= "scytalone dehydrogenase"
FT /partial
FT /note= "no stop codon"
XX
PN WO2003076628-A1.
XX
PD 18-SEP-2003.
XX
PF 24-FEB-2003; 2003WO-JP001980.

XX
PR 12-MAR-2002; 2002JP-00066955.
XX
PA (TSUB) KUMIAI CHEM IND CO LTD.
XX
PI Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;
XX
DR WPI; 2003-748394/70.
DR P-PSDB; ADC16591.
XX
PT Gene encoding for scytalone dehydrogenase (SCDH), useful for screening
PT for SCDH inhibitors and evaluating sensitivity to them.
XX
PS Example 2; SEQ ID NO 1; 50pp; Japanese.
XX
CC The invention relates to a gene encoding scytalone dehydrogenase (SCDH),
CC that functions in the presence of an inhibitor, comprising an optionally
CC mutated, defined amino acid sequence given in the specification. Also
CC disclosed is a method for evaluating rice blast fungus (Pyricularia
CC oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase
CC inhibitors. The gene is useful for screening for new SCDH inhibitors and
CC evaluating sensitivity to them. The current sequence represents the
CC Scytalone dehydrogenase gene sequence.
XX
SQ Sequence 516 BP; 119 A; 151 C; 155 G; 91 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.35e-107	Length:	516
Score:	942.00	Matches:	172
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	10	Gaps:	0

US-10-507-132-2 (1-172) x ADC16590 (1-516)

```
Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGATGCTGGGCGACCCCACC 240

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
              ||||||||||||||||||||||||||||||||||||
Db        481 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516
```

RESULT 2

ADC16592
ID ADC16592 standard; DNA; 516 BP.
XX
AC ADC16592;
XX
DT 18-DEC-2003 (first entry)
XX
DE Scytalone dehydrogenase gene #SEQ ID 3.
XX
KW Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor;
KW gene; ds.
XX
OS Magnaporthe grisea.
XX
FH Key Location/Qualifiers
FT CDS 1. .516
FT /*tag= a
FT /product= "scytalone dehydrogenase"
FT /partial
FT /note= "no stop codon"
XX
PN WO2003076628-A1.
XX
PD 18-SEP-2003.
XX
PF 24-FEB-2003; 2003WO-JP001980.
XX
PR 12-MAR-2002; 2002JP-00066955.
XX
PA (TSUB) KUMIAI CHEM IND CO LTD.
XX
PI Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;
XX
DR WPI; 2003-748394/70.
DR P-PSDB; ADC16593.
XX
PT Gene encoding for scytalone dehydrogenase (SCDH), useful for screening
PT for SCDH inhibitors and evaluating sensitivity to them.
XX
PS Example 2; SEQ ID NO 3; 50pp; Japanese.
XX
CC The invention relates to a gene encoding scytalone dehydrogenase (SCDH),
CC that functions in the presence of an inhibitor, comprising an optionally
CC mutated, defined amino acid sequence given in the specification. Also
CC disclosed is a method for evaluating rice blast fungus (Pyricularia
CC oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase
CC inhibitors. The gene is useful for screening for new SCDH inhibitors and
CC evaluating sensitivity to them. The current sequence represents the
CC Scytalone dehydrogenase gene sequence.
XX
SQ Sequence 516 BP; 118 A; 151 C; 156 G; 91 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.27e-107	Length:	516
Score:	938.00	Matches:	171
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	99.4%	Mismatches:	0
Query Match:	99.6%	Indels:	0
DB:	10	Gaps:	0

US-10-507-132-2 (1-172) x ADC16592 (1-516)

```
Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180
```

```
Qy          61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
               ||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db         181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 240

Qy          81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300

Qy         101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360

Qy         121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420

Qy         141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480

Qy         161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
               ||||||||||||||||||||||||||||||||||
Db         481 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516

RESULT 3
ADC16602
ID   ADC16602 standard; DNA; 600 BP.
XX
AC   ADC16602;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Scytalone dehydrogenase DNA #1.
XX
KW   Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor;
KW   gene; ds.
XX
OS   Magnaporthe grisea.
XX
PN   WO2003076628-A1.
XX
PD   18-SEP-2003.
XX
PF   24-FEB-2003; 2003WO-JP001980.
XX
PR   12-MAR-2002; 2002JP-00066955.
XX
PA   (TSUB ) KUMIAI CHEM IND CO LTD.
XX
PI   Kaku K,  Watanabe S,  Kawai K,  Shimizu T,  Nagayama K;
XX
DR   WPI; 2003-748394/70.
XX
PT   Gene encoding for scytalone dehydrogenase (SCDH), useful for screening
PT   for SCDH inhibitors and evaluating sensitivity to them.
XX
PS   Example 2; Fig 3; 50pp; Japanese.
XX
CC   The invention relates to a gene encoding scytalone dehydrogenase (SCDH),
CC   that functions in the presence of an inhibitor, comprising an optionally
CC   mutated, defined amino acid sequence given in the specification. Also
CC   disclosed is a method for evaluating rice blast fungus (Pyricularia
CC   oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase
CC   inhibitors. The gene is useful for screening for new SCDH inhibitors and
CC   evaluating sensitivity to them. The current sequence represents the
CC   Scytalone dehydrogenase DNA sequence. Note: gene sequence from this is
CC   given in ADC16590.
XX
SQ   Sequence 600 BP; 146 A; 176 C; 168 G; 110 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              5.22e-107      Length:        600
Score:                  938.00         Matches:       171
Percent Similarity:     100.0%         Conservative:  1
Best Local Similarity:  99.4%          Mismatches:    0
Query Match:            99.6%          Indels:        0
DB:                     10             Gaps:          0

US-10-507-132-2 (1-172) x ADC16602 (1-600)

Qy           1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          81 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 140

Qy          21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         141 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 200

Qy          41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         201 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 260

Qy          61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
               ||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db         261 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 320

Qy          81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         321 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 380

Qy         101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         381 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 440

Qy         121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         441 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 500

Qy         141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         501 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 560

Qy         161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
               ||||||||||||||||||||||||||||||||||
Db         561 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 596

RESULT 4
ADC16603
ID   ADC16603 standard; DNA; 610 BP.
XX
AC   ADC16603;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Scytalone dehydrogenase DNA #2.
XX
KW   Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor;
KW   gene; ds.
XX
OS   Magnaporthe grisea.
XX
PN   WO2003076628-A1.
XX
PD   18-SEP-2003.
XX
PF   24-FEB-2003; 2003WO-JP001980.
XX
PR   12-MAR-2002; 2002JP-00066955.
XX
PA   (TSUB ) KUMIAI CHEM IND CO LTD.
XX
PI   Kaku K,  Watanabe S,  Kawai K,  Shimizu T,  Nagayama K;
XX
DR   WPI; 2003-748394/70.
XX
```

```
PT   Gene encoding for scytalone dehydrogenase (SCDH), useful for screening
PT   for SCDH inhibitors and evaluating sensitivity to them.
XX
PS   Example 2; Fig 4; 50pp; Japanese.
XX
CC   The invention relates to a gene encoding scytalone dehydrogenase (SCDH),
CC   that functions in the presence of an inhibitor, comprising an optionally
CC   mutated, defined amino acid sequence given in the specification. Also
CC   disclosed is a method for evaluating rice blast fungus (Pyricularia
CC   oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase
CC   inhibitors. The gene is useful for screening for new SCDH inhibitors and
CC   evaluating sensitivity to them. The current sequence represents the
CC   Scytalone dehydrogenase DNA sequence. Note: gene sequence from this is
CC   given in ADC16592.
XX
SQ   Sequence 610 BP; 148 A; 179 C; 170 G; 113 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              5.34e-107      Length:         610
Score:                  938.00         Matches:        171
Percent Similarity:     100.0%         Conservative:   1
Best Local Similarity:  99.4%          Mismatches:     0
Query Match:            99.6%          Indels:         0
DB:                     10             Gaps:           0

US-10-507-132-2 (1-172) x ADC16603 (1-610)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 140

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 200

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 260

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||:::||||||||||||||||
Db        261 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 320

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 380

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 440

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 500

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 560

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
              ||||||||||||||||||||||||||||||||||
Db        561 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 596

RESULT 5
ABZ52566
ID   ABZ52566 standard; cDNA; 697 BP.
XX
AC   ABZ52566;
XX
DT   28-MAR-2003  (first entry)
XX
DE   Aspergillus oryzae polynucleotide SEQ ID NO 1679.
XX
KW   Aspergillus oryzae; fermentation; fungus; industrial; EST;
KW   expressed sequence tag; gene; ss.
XX
OS   Aspergillus oryzae.
XX
PN   WO200279476-A1.
XX
PD   10-OCT-2002.
XX
PF   22-MAR-2002; 2002WO-IB000890.
XX
PR   30-MAR-2001; 2001JP-00098371.
XX
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA   (NARE-) NAT RES INST BREWING.
PA   (NORQ ) NAT FOOD RES INST MIN AGRIC.
XX
PI   Machida M,  Akita O,  Kashiwagi Y,  Kitamoto K,  Horiuchi H;
PI   Takeuchi M,  Kobayashi T,  Kitamoto N,  Gomi K,  Abe K;
XX
DR   WPI; 2003-046817/04.
XX
PT   Detection of expression of specific Aspergillus genes for monitoring the
PT   fermentation and growth conditions of the fungus, using DNA probes.
XX
PS   Claim 1; SEQ ID NO 1679; 48pp + Sequence Listing; Japanese.
XX
CC   The invention relates to a polynucleotide having any of 6006 specific
CC   sequences (ABZ50888-ABZ56893), which are expressed by a fungus under
CC   specific culture conditions including one or more of eutrophic,
CC   oligotrophic, solid, early germination, alkaline, high temperature, low
CC   temperature or maltose culture or polynucleotides stringently hybridising
CC   to these sequences. The polynucleotides are useful for monitoring the
CC   progress of fermentation and the growth conditions of a fungus,
CC   especially of Aspergillus oryzae which is widely used in industrial
CC   fermentation. Also monitoring for fungal contamination. Note: The
CC   sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 697 BP; 170 A; 153 C; 180 G; 189 T; 0 U; 5 Other;

Alignment Scores:
Pred. No.:              7.33e-13       Length:         697
Score:                  183.00         Matches:        42
Percent Similarity:     47.9%          Conservative:   28
Best Local Similarity:  28.8%          Mismatches:     74
Query Match:            19.4%          Indels:         2
DB:                     8              Gaps:           1

US-10-507-132-2 (1-172) x ABZ52566 (1-697)

Qy         17 LeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAsp 36
              |||                 :::::::::||||||:::      |||:::|||   ||||||
Db        184 CTCGCATGTNAGAACCTCCTTCACGACTGGGCAAACTGCTTAGACACCAAGTCCTGGGAT 243

Qy         37 ArgLeuArgLysValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLys 56
              |||:::     :::   ||||||   :::   :::||||||   :::
Db        244 CGTATGCTGACTATATTCGCGCCCAGAATCGATGTGGATTACTCGGCGGTCGGGACACTA 303

Qy         57 LeuTrpGluAlaMetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeu 76
                  |||:::           |||:::         ||||||         |||
Db        304 AAGGCTACCGCTGTGGAGTTTTCTGTTTTTATCGAACACTACTCCAGTTCAGCACAGCTA 363

Qy         77 GlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSer 96
              |||:::|||   ::::::      ||||||||||||      :::|||   :::
Db        364 GGGAACCCCGATATCCAGTGACATCATTTTATCGGTGCCTGCAAATGGGCACGGGAACTG 423

Qy         97 GluAspGluValIleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThr 116
              |||      |||          |||:::      |||:::|||
Db        424 GAAAAAAACGTAAGGGTTGTTTTTCAAATCATGGCGGTTCATCGGAGGGCGCCAAAAGAC 483

Qy        117 ThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLys 136
```

```
                        |||      ||||||              |||        :::|||
Db        484 GGTGGTGCGGGTGTGCTGGCTAAGGGC------CAAGGGGTTAACACCATGGATTTTAAG 537

Qy        137 LysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPhe 156
              :::::::::|||      |||   |||   :::|||      :::   :::   |||
Db        538 CAGGTGGAAGGGGAGTNGAAGATCGCAGCGATTAAAGTTGGCGTNCTGTTCATGGAGGGT 597

Qy        157 AspPheAspArgIlePhe 162
              ||||||:::   :::|||
Db        598 GATTTCGAGGGCATGTTC 615
```

RESULT 6
ADA28757
ID ADA28757 standard; DNA; 462 BP.
XX
AC ADA28757;
XX
DT 20-NOV-2003 (first entry)
XX
DE DNA encoding Acinetobacter baumannii protein #44.
XX
KW ds; gene; Acinetobacter baumannii; bacterial disease; antibacterial;
KW vaccine; plant biocontrol agent.
XX
OS Acinetobacter baumannii.
XX
PN US6562958-B1.
XX
PD 13-MAY-2003.
XX
PF 04-JUN-1999;. 99US-00328352.
XX
PR 09-JUN-1998; 98US-0088701P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Breton G, Bush D;
XX
DR WPI; 2003-576092/54.
DR P-PSDB; ADA32883.
XX
PT New Acinetobacter baumanii proteins and nucleic acids, useful as reagents
PT for diagnosing a bacterial disease, as components of antibacterial
PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for
PT plants.
XX
PS Example; SEQ ID NO 44; 328pp; English.
XX
CC The invention relates to isolated Acinetobacter baumannii nucleic acids.
CC The A. baumannii nucleic acids and polypeptides are useful as reagents
CC for diagnosing a bacterial disease, as components of antibacterial
CC vaccines, as targets for antibacterial drugs, to detect the presence of
CC A. baumannii and other Acinetobacter species in a sample, in screening
CC compounds for the ability to interfere with the A. baumannii life cycle
CC or to inhibit A. baumannii infection, and as biocontrol agents for
CC plants. The present sequence represents DNA encoding an A. baumannii
CC protein.
XX
SQ Sequence 462 BP; 135 A; 76 C; 98 G; 153 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0.0447	Length:	462
Score:	94.50	Matches:	31
Percent Similarity:	43.7%	Conservative:	28
Best Local Similarity:	23.0%	Mismatches:	59
Query Match:	10.0%	Indels:	17
DB:	9	Gaps:	6

US-10-507-132-2 (1-172) x ADA28757 (1-462)

```
Qy         15 AspTyrLeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAsp 34
              ||||||      ::::::      :::      :::         :::|||   |||:::
Db         37 GACTACCATCGTATTTTAGAGGTCATTACGCGTTTTCAATTGGTTTTTGACCAGAAAAAT 96

Qy         35 TrpAspArgLeuArgLysValIleAlaProThrLeuArgIleAspTyrArgSerPheLeu 54
              .||||||          ::::::::::|||      |||   :::||||||      |||
Db         97 TGGGATGCGTTTGATGAGTTGTTAGCCGATCAACTTGAGGTGGACTATTTGCAGTTTAGA 156

Qy         55 AspLysLeuTrpGluAlaMetProAlaGluGluPheValGlyMetValSerSerLysGln 74
              :::          :::        |||:::   |||      |||   :::|||
Db        157 GGGGAGCCTTTATGTGTGGTGTCTTGTCATGAATATAAAGGT------TCACGGCAACAA 210

Qy         75 MetLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLys 94
              |||              ||||||   ||||||   :::                 :::
Db        211 GCTTTGTCACAT------TTGCGGCTACAGCACAATTTAAGCAATCCT---CTTATTCGG 261

Qy         95 ValSerGluAspGluValIleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLys 114
              :::   :::|||:::                  |||         :::|||   |||:::
Db        262 ATTGAACAAGATCAAGCA-----------TGGTTAGAATGTAATTATCAAATTTATCGT 309

Qy        115 AspThrThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrp 134
                           :::         :::   ||||||        ::::::
Db        310 -----------------TTTTCGGAAAATGATTATTTTCATTCTTTTGGTCGCTATTAT 351

Qy        135 Tyr------LysLysIleAspGlyValTrpLysPheAlaGlyLeu 147
              :::         |||      |||:::||||||      |||:::
Db        352 TTTACTTTGGCAAAACAACAGGGCATATGGAAAATTACCGGAATT 396
```

RESULT 7
AEB42401_09/c
Continuation (10 of 34) of AEB42401 from base 900001 (L. pneumophila DNA SEQ ID NO 6733.
WP Sequence split into 34 fragments LOCUS AEB42401 Accession Aeb42401

WP	Fragment Name	Begin	End
WP	AEB42401_00	1	110000
WP	AEB42401_01	100001	210000
WP	AEB42401_02	200001	310000
WP	AEB42401_03	300001	410000
WP	AEB42401_04	400001	510000
WP	AEB42401_05	500001	610000
WP	AEB42401_06	600001	710000
WP	AEB42401_07	700001	810000
WP	AEB42401_08	800001	910000
WP	AEB42401_09	900001	1010000
WP	AEB42401_10	1000001	1110000
WP	AEB42401_11	1100001	1210000
WP	AEB42401_12	1200001	1310000
WP	AEB42401_13	1300001	1410000
WP	AEB42401_14	1400001	1510000
WP	AEB42401_15	1500001	1610000
WP	AEB42401_16	1600001	1710000
WP	AEB42401_17	1700001	1810000
WP	AEB42401_18	1800001	1910000
WP	AEB42401_19	1900001	2010000
WP	AEB42401_20	2000001	2110000
WP	AEB42401_21	2100001	2210000
WP	AEB42401_22	2200001	2310000
WP	AEB42401_23	2300001	2410000
WP	AEB42401_24	2400001	2510000
WP	AEB42401_25	2500001	2610000
WP	AEB42401_26	2600001	2710000
WP	AEB42401_27	2700001	2810000
WP	AEB42401_28	2800001	2910000
WP	AEB42401_29	2900001	3010000
WP	AEB42401_30	3000001	3110000
WP	AEB42401_31	3100001	3210000
WP	AEB42401_32	3200001	3310000
WP	AEB42401_33	3300001	3345687

Alignment Scores:

Pred. No.:	522	Length:	110000
Score:	87.50	Matches:	27
Percent Similarity:	40.4%	Conservative:	19
Best Local Similarity:	23.7%	Mismatches:	51
Query Match:	9.3%	Indels:	17
DB:	14	Gaps:	2

```
US-10-507-132-2 (1-172) x AEB42401_09 (1-110000)

Qy          74 GlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArg------ 91
               |||:::|||||||||          :::        :::|||
Db       31832 CAAATACTGGGCGATGGGGCATGTCATAGTGGGAGTGAATTAGGAAACGCTTTAAAAATC 31773

Qy          92 --------------TrpGluLysValSerGluAspGluValIleGlyTyrHisGlnLeu 106
                           |||:::::::::::::::        :::|||         :::
Db       31772 AGTCGCTCAGCAGTATGGAAACAAATCAATCAGCTTAATGATTTAGGCATACCTATTATC 31713

Qy         107 ArgValProHisGlnArgTyrLys----------------------------AspThr 116
               |||:::|||||||||   |||:::                            |||
Db       31712 CGCATACCACATCAAGGATACCAATTGGAAAAGCCTTTAATCCTGCTAGACTCTGATGAA 31653

Qy         117 ThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLys 136
              |||::::::     ||||||   :::       |||||||||   :::
Db       31652 ATTACCAAGCAATTACACAGCAAAGGATTTAGCCAACCGTTTAACCTGCATTTATTTACA 31593

Qy         137 LysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPhe 156
              ||||||         ::::::              |||                 |||
Db       31592 TCGATCGACTCAACCAACCGCTACCTGAAAGATCTGCCCTTAAGCTCAGCCGTCGAAATT 31533

Qy         157 AspPheAspArgIlePheGluAspGlyArgGluThrPheGly 170
                  :::        ||||||      ||||||
Db       31532 TGCTGCACTGAAATGCAAACTCAAGGGAGAGGGCGCTTTGGA 31491

RESULT 8
AAD57634
ID   AAD57634 standard; DNA; 2775 BP.
XX
AC   AAD57634;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Rice disease resistance gene, LOX1.
XX
KW   Rice; abiotic stress tolerance; pathogen resistance; disease resistance;
KW   grain quality; nutritional content; plant yield; LOX1; plant; gene; ds.
XX
OS   Oryza sativa.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2775
FT                   /*tag=  a
FT                   /product= "Rice LOX1 protein"
XX
PN   WO2003048319-A2.
XX
PD   12-JUN-2003.
XX
PF   27-NOV-2002; 2002WO-US038359.
XX
PR   30-NOV-2001; 2001US-0334501P.
XX
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI   Sainz MB,  Salmeron J,  Weislo L;
XX
DR   WPI; 2003-505288/47.
DR   P-PSDB; AAE38266.
XX
PT   New nucleic acid from Oryza sativa, useful for altering abiotic stress
PT   tolerance, pathogen or disease resistance or the grain quality,
PT   nutritional content or yield in a plant.
XX
PS   Claim 2; Page 130-133; 223pp; English.
XX
CC   The invention relates to nucleic acid molecules from rice encoding
CC   proteins for abiotic stress tolerance, enhanced pathogen or disease
CC   resistance and altered nutritional quality. The sequences of the
CC   invention are useful for altering abiotic stress tolerance, pathogen or
CC   disease resistance or the grain quality, nutritional content or yield in
CC   a plant. The present sequence is rice disease resistance gene, LOX1
XX
SQ   Sequence 2775 BP; 526 A; 955 C; 869 G; 425 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.28          Length:          2775
Score:                  87.00         Matches:         34
Percent Similarity:     33.8%         Conservative:    16
Best Local Similarity:  23.0%         Mismatches:      44
Query Match:            9.2%          Indels:          54
DB:                     10            Gaps:            7

US-10-507-132-2 (1-172) x AAD57634 (1-2775)

Qy          55 AspLysLeuTrp-----------GluAlaMetProAlaGluGluPheValGlyMetVal 70
               ||||||||||||           ||||||:::||||||:::             :::|||
Db        1960 GACAAGCTCTGGCGCTTCGACACGGAGGCGCTCCCCGCCGAC-----------CTCGTC 2007

Qy          71 SerSerLysGlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIle--------- 87
                                    |||||||||        :::|||   :::
Db        2008 CGCCGCGGCATGGCCGAGGAGGACCCCACG------GCGGAGCACGGCCTCAAGCTCGCC 2061

Qy          88 -------------------------GlyGlyThrArgTrpGluLysVal--------- 95
                                        |||         |||:::   :::
Db        2062 ATCGAGGACTACCCGTTCGCCAACGACGGCCTCCTCATCTGGGACGCCATCAAGACCTGG 2121

Qy          96 ----------------------------SerGluAspGluValIleGlyTyrHisGln 105
                                           |||   |||   |||      :::
Db        2122 GTCCAGGCGTACGTCGCGCGGTTCTACCCCGACGCCGACAGCGTCGCCGGCGACGAGGAG 2181

Qy         106 LeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGly 125
               |||:::                                  ||||||      ||||||
Db        2182 CTCCAG-----------------------GCGTTCTGGACCGAGGTGCGCACCAAGGGG 2217

Qy         126 HisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly--------------- 140
               |||           :::      |||:::   |||:::|||
Db        2218 CACGGCGACAAGAAGGACGCCCCGTGGTGGCCGAAGTTGGACTCGCCGGAGAGCCTCGCC 2277

Qy         141 -----------------ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGly 154
                              ||||||      |||               :::   :::|||
Db        2278 CACACGCTGACCACCATCGTCTGGGTGGCGGCGGCGCACCACGCCGCCGTCAACTTCGGG 2337

Qy         155 GluPheAspPheAspArgIlePhe 162
               ::::::||||||       |||
Db        2338 CAGTACGACTTCGGCGGCTACTTC 2361

RESULT 9
AEB39158/c
ID   AEB39158 standard; DNA; 48622 BP.
XX
AC   AEB39158;
XX
DT   08-SEP-2005  (first entry)
XX
DE   L. pneumophila DNA SEQ ID NO 3490.
XX
KW   detection; infection; Antibacterial; Vaccine; ds; gene.
XX
OS   Legionella pneumophila.
XX
PN   WO2005049642-A2.
XX
PD   02-JUN-2005.
XX
PF   23-SEP-2004; 2004WO-IB003578.
XX
PR   21-NOV-2003; 2003FR-00013687.
XX
PA   (INSP ) INST PASTEUR.
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI   Buchrieser C,  Tichit M,  Etienne J,  Ma L,  Cazalet C,  Glaser P;
```

PI Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;
PI Jarraud S;
XX
DR WPI; 2005-388305/40.
XX
PT New genome of Legionella pneumophila Paris strain and derived
PT polypeptides, useful for detection or identification of the strain and
PT for treatment and prevention of infections.
XX
PS Example 9; SEQ ID NO 3490; 660pp; English.
XX
CC The invention relates to an isolated or purified nucleotide sequences (I)
CC from Legionella pneumophila Paris strain. (I), and their related
CC sequences or fragments, are useful as primers and probes for detection
CC and amplification, including differentiation between the Paris and
CC Philadelphia strains of Legionella pneumophila and to prepare recombinant
CC (hybrid) polypeptides (II). (II) are also useful for preparation of
CC specific antibodies (Ab), also used for detection/identification of
CC Legionella, and some (I), specifically those involved in synthesis of
CC surface proteins, are targets for identification of inhibitors. (II), or
CC vectors that contain (I), are useful as vaccines and immunogenic
CC compositions, for treatment and prevention of infections by L.
CC pneumophila. The present squence represents a L. pneumophila DNA.
XX
SQ Sequence 48622 BP; 15468 A; 7892 C; 9212 G; 16050 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	232	Length:	48622
Score:	86.50	Matches:	26
Percent Similarity:	40.4%	Conservative:	20
Best Local Similarity:	22.8%	Mismatches:	51
Query Match:	9.2%	Indels:	17
DB:	14	Gaps:	2

US-10-507-132-2 (1-172) x AEB39158 (1-48622)

```
Qy         74 GlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArg------ 91
              |||:::|||||||||           :::         :::|||
Db      41463 CAAATACTGGGCGATGGGGCATGTCATAGTGGGAGTGAATTAGGAAACGCTTTAAAAATC 41404

Qy         92 ---------------TrpGluLysValSerGluAspGluValIleGlyTyrHisGlnLeu 106
                          |||:::::::::::::::         :::|||          :::
Db      41403 AGTCGCTCAGCAGTATGGAAACAAATCAATCAGCTTAATGATTTAGGCATACCTATTATC 41344

Qy        107 ArgValProHisGlnArgTyrLys-----------------------------AspThr 116
              |||:::||||||||||   |||:::                             :::
Db      41343 CGCATACCACATCAAGGATACCAATTGGAAAAGCCTTTAATCCTGCTAGACTCCAATGAA 41284

Qy        117 ThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLys 136
                 |||::::::      ||||||   :::         |||||||||   :::
Db      41283 ATTACCAAGCAATTACACAGCAAAGGATTTAGCCAACCGTTTAACCTGCATTTATTTACA 41224

Qy        137 LysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPhe 156
                |||||      ::::::          |||                  |||
Db      41223 TCGATTGACTCAACCAACCGCTACCTGAAAGATCTGCCTTCAAGCTCAGCCGTCGAAATT 41164

Qy        157 AspPheAspArgIlePheGluAspGlyArgGluThrPheGly 170
                    :::         ||||||      ||||||
Db      41163 TGCTGCACTGAAATGCAAACTCAAGGGAGAGGGCGCTTTGGA 41122
```

RESULT 10
AEB35710/c
ID AEB35710 standard; DNA; 88876 BP.
XX
AC AEB35710;
XX
DT 08-SEP-2005 (first entry)
XX
DE L. pneumophila DNA SEQ ID NO 42.
XX
KW detection; infection; Antibacterial; Vaccine; ds; gene.
XX
OS Legionella pneumophila.

XX
PN WO2005049642-A2.
XX
PD 02-JUN-2005.
XX
PF 23-SEP-2004; 2004WO-IB003578.
XX
PR 21-NOV-2003; 2003FR-00013687.
XX
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;
PI Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;
PI Jarraud S;
XX
DR WPI; 2005-388305/40.
XX
PT New genome of Legionella pneumophila Paris strain and derived
PT polypeptides, useful for detection or identification of the strain and
PT for treatment and prevention of infections.
XX
PS Claim 1; SEQ ID NO 42; 660pp; English.
XX
CC The invention relates to an isolated or purified nucleotide sequences (I)
CC from Legionella pneumophila Paris strain. (I), and their related
CC sequences or fragments, are useful as primers and probes for detection
CC and amplification, including differentiation between the Paris and
CC Philadelphia strains of Legionella pneumophila and to prepare recombinant
CC (hybrid) polypeptides (II). (II) are also useful for preparation of
CC specific antibodies (Ab), also used for detection/identification of
CC Legionella, and some (I), specifically those involved in synthesis of
CC surface proteins, are targets for identification of inhibitors. (II), or
CC vectors that contain (I), are useful as vaccines and immunogenic
CC compositions, for treatment and prevention of infections by L.
CC pneumophila. The present squence represents a L. pneumophila DNA.
XX
SQ Sequence 88876 BP; 27350 A; 14957 C; 17861 G; 28707 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.:	522	Length:	88876
Score:	86.50	Matches:	26
Percent Similarity:	40.4%	Conservative:	20
Best Local Similarity:	22.8%	Mismatches:	51
Query Match:	9.2%	Indels:	17
DB:	14	Gaps:	2

US-10-507-132-2 (1-172) x AEB35710 (1-88876)

```
Qy         74 GlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArg------ 91
              |||:::|||||||||           :::         :::|||
Db      48109 CAAATACTGGGCGATGGGGCATGTCATAGTGGGAGTGAATTAGGAAACGCTTTAAAAATC 48050

Qy         92 ---------------TrpGluLysValSerGluAspGluValIleGlyTyrHisGlnLeu 106
                          |||:::::::::::::::         :::|||          :::
Db      48049 AGTCGCTCAGCAGTATGGAAACAAATCAATCAGCTTAATGATTTAGGCATACCTATTATC 47990

Qy        107 ArgValProHisGlnArgTyrLys-----------------------------AspThr 116
              |||:::||||||||||   |||:::                             :::
Db      47989 CGCATACCACATCAAGGATACCAATTGGAAAAGCCTTTAATCCTGCTAGACTCCAATGAA 47930

Qy        117 ThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLys 136
                 |||:::::::      ||||||   :::         |||||||||   :::
Db      47929 ATTACCAAGCAATTACACAGCAAAGGATTTAGCCAACCGTTTAACCTGCATTTATTTACA 47870

Qy        137 LysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPhe 156
                |||||||         ::::::          |||                  |||
Db      47869 TCGATTGACTCAACCAACCGCTACCTGAAAGATCTGCCTTCAAGCTCAGCCGTCGAAATT 47810

Qy        157 AspPheAspArgIlePheGluAspGlyArgGluThrPheGly 170
                    :::         ||||||      ||||||
```

```
Db      47809 TGCTGCACTGAAATGCAAACTCAAGGGAGAGGGCGCTTTGGA 47768

RESULT 11
AEB39175_09/c
Continuation (10 of 35) of AEB39175 from base 900001 (L. pneumophila DNA SEQ ID NO 3507.
WP Sequence split into 35 fragments  LOCUS AEB39175 Accession Aeb39175
WP     Fragment Name      Begin     End
WP     AEB39175_00            1    110000
WP     AEB39175_01       100001    210000
WP     AEB39175_02       200001    310000
WP     AEB39175_03       300001    410000
WP     AEB39175_04       400001    510000
WP     AEB39175_05       500001    610000
WP     AEB39175_06       600001    710000
WP     AEB39175_07       700001    810000
WP     AEB39175_08       800001    910000
WP     AEB39175_09       900001   1010000
WP     AEB39175_10      1000001   1110000
WP     AEB39175_11      1100001   1210000
WP     AEB39175_12      1200001   1310000
WP     AEB39175_13      1300001   1410000
WP     AEB39175_14      1400001   1510000
WP     AEB39175_15      1500001   1610000
WP     AEB39175_16      1600001   1710000
WP     AEB39175_17      1700001   1810000
WP     AEB39175_18      1800001   1910000
WP     AEB39175_19      1900001   2010000
WP     AEB39175_20      2000001   2110000
WP     AEB39175_21      2100001   2210000
WP     AEB39175_22      2200001   2310000
WP     AEB39175_23      2300001   2410000
WP     AEB39175_24      2400001   2510000
WP     AEB39175_25      2500001   2610000
WP     AEB39175_26      2600001   2710000
WP     AEB39175_27      2700001   2810000
WP     AEB39175_28      2800001   2910000
WP     AEB39175_29      2900001   3010000
WP     AEB39175_30      3000001   3110000
WP     AEB39175_31      3100001   3210000
WP     AEB39175_32      3200001   3310000
WP     AEB39175_33      3300001   3410000
WP     AEB39175_34      3400001   3503610

Alignment Scores:
Pred. No.:              696          Length:         110000
Score:                  86.50        Matches:        26
Percent Similarity:     40.4%        Conservative:   20
Best Local Similarity:  22.8%        Mismatches:     51
Query Match:            9.2%         Indels:         17
DB:                     14           Gaps:           2

US-10-507-132-2 (1-172) x AEB39175_09 (1-110000)

Qy         74 GlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArg------ 91
              |||:::|||||||||            :::         :::|||
Db      50898 CAAATACTGGGCGATGGGGCATGTCATAGTGGGAGTGAATTAGGAAACGCTTTAAAAATC 50839

Qy         92 ---------------TrpGluLysValSerGluAspGluValIleGlyTyrHisGlnLeu 106
                            |||:::::::::::::::        :::|||         :::
Db      50838 AGTCGCTCAGCAGTATGGAAACAAATCAATCAGCTTAATGATTTAGGCATACCTATTATC 50779

Qy        107 ArgValProHisGlnArgTyrLys-----------------------------AspThr 116
              |||:::|||||||||   |||:::                                :::
Db      50778 CGCATACCACATCAAGGATACCAATTGGAAAAGCCTTTAATCCTGCTAGACTCCAATGAA 50719

Qy        117 ThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLys 136
                |||::::::      ||||||   :::         |||||||||   :::
Db      50718 ATTACCAAGCAATTACACAGCAAAGGATTTAGCCAACCGTTTAACCTGCATTTATTTACA 50659

Qy        137 LysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPhe 156
              ||||||          ::::::          |||                 |||
Db      50658 TCGATTGACTCAACCAACCGCTACCTGAAAGATCTGCCTTCAAGCTCAGCCGTCGAAATT 50599
\

Qy        157 AspPheAspArgIlePheGluAspGlyArgGluThrPheGly 170
                          :::         ||||||      ||||||
Db      50598 TGCTGCACTGAAATGCAAACTCAAGGGAGAGGGCGCTTTGGA 50557

RESULT 12
AEB42736_2/c
Continuation (3 of 8) of AEB42736 from base 200001 (L. pneumophila DNA SEQ ID NO 7068. )
WP Sequence split into 8 fragments  LOCUS AEB42736 Accession Aeb42736
WP     Fragment Name      Begin     End
WP     AEB42736_0             1    110000
WP     AEB42736_1        100001    210000
WP     AEB42736_2        200001    310000
WP     AEB42736_3        300001    410000
WP     AEB42736_4        400001    510000
WP     AEB42736_5        500001    610000
WP     AEB42736_6        600001    710000
WP     AEB42736_7        700001    740626

Alignment Scores:
Pred. No.:              696          Length:         110000
Score:                  86.50        Matches:        26
Percent Similarity:     40.4%        Conservative:   20
Best Local Similarity:  22.8%        Mismatches:     51
Query Match:            9.2%         Indels:         17
DB:                     14           Gaps:           2

US-10-507-132-2 (1-172) x AEB42736_2 (1-110000)

Qy         74 GlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArg------ 91
              |||:::|||||||||            :::         :::|||
Db      42889 CAAATACTGGGCGATGGGGCATGTCATAGTGGGAGTGAATTAGGAAACGCTTTAAAAATC 42830

Qy         92 ---------------TrpGluLysValSerGluAspGluValIleGlyTyrHisGlnLeu 106
                            |||:::::::::::::::        :::|||         :::
Db      42829 AGTCGCTCAGCAGTATGGAAACAAATCAATCAGCTTAATGATTTAGGCATACCTATTATC 42770

Qy        107 ArgValProHisGlnArgTyrLys-----------------------------AspThr 116
              |||:::|||||||||   |||:::                                :::
Db      42769 CGCATACCACATCAAGGATACCAATTGGAAAAGCCTTTAATCCTGCTAGACTCCAATGAA 42710

Qy        117 ThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLys 136
                |||::::::      ||||||   :::         |||||||||   :::
Db      42709 ATTACCAAGCAATTACACAGCAAAGGATTTAGCCAACCGTTTAACCTGCATTTATTTACA 42650

Qy        137 LysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPhe 156
              ||||||          ::::::          |||                 |||
Db      42649 TCGATTGACTCAACCAACCGCTACCTGAAAGATCTGCCTTCAAGCTCAGCCGTCGAAATT 42590

Qy        157 AspPheAspArgIlePheGluAspGlyArgGluThrPheGly 170
                          :::         ||||||      ||||||
Db      42589 TGCTGCACTGAAATGCAAACTCAAGGGAGAGGGCGCTTTGGA 42548

RESULT 13
AAX14439
ID   AAX14439 standard; DNA; 864 BP.
XX
AC   AAX14439;
XX
DT   31-MAR-1999  (first entry)
XX
DE   H. pylori GHPO 811 gene.
XX
KW   GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis;
KW   peptic ulcer disease; ss.
XX
OS   Helicobacter pylori.
XX
FH   Key             Location/Qualifiers
FT   CDS             37. .834
FT                   /*tag=  a
XX
PN   WO9843478-A1.
XX
```

```
PD   08-OCT-1998.
XX
PF   01-APR-1998;   98WO-US006371.
XX
PR   01-APR-1997;   97US-00833457.
PR   24-JUN-1997;   97US-00881227.
PR   29-JUL-1997;   97US-00902615.
XX
PA   (INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Kleanthous H,  Al-Garawi A,  Miller C,  Tomb J,  Oomen RP;
XX
DR   WPI; 1998-542293/46.
DR   P-PSDB; AAW98720.
XX
PT   New isolated Helicobacter polynucleotides - used to develop products for
PT   the diagnosis, prevention and treatment of Helicobacter infections and
PT   gastrointestinal diseases.
XX
PS   Claim 1; Page 1521-1522; 2054pp; English.
XX
CC   This sequence represents a polynucleotide of the invention. It was
CC   isolated from Helicobacter pylori and encodes a H.pylori GHPO protein.
CC   The polypeptides can be used for preventing or treating Helicobacter
CC   infections, and gastroduodenal diseases associated with these infections,
CC   including acute, chronic, and atrophic gastritis, and peptic ulcer
CC   diseases, e.g. gastric and duodenal ulcers. They can also be used for the
CC   production of antibodies. The products can also be used for detection and
CC   diagnosis
XX
SQ   Sequence 864 BP; 283 A; 159 C; 198 G; 223 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:              1.58          Length:         864
Score:                  85.00         Matches:        43
Percent Similarity:     41.1%         Conservative:   31
Best Local Similarity:  23.9%         Mismatches:     54
Query Match:            9.0%          Indels:         54
DB:                     2             Gaps:           8

US-10-507-132-2 (1-172) x AAX14439 (1-864)

Qy         18 GlyLeuMetThrCysValTyrGlu---------TrpAlaAspSerTyrAspSerLysAsp 34
              |||::::::   |||   |||:::         ::::::||||||      ::::::
Db        326 GGCATTTTGAATTGTTT-TATCAGTTCGTGGGCTTTAGCGATAGCTGCAAGAACCGCCGT 384

Qy         35 TrpAspArgLeuArgLysValIleAlaProThrLeuArgIleAspTyrArgSerPheLeu 54
                ||||::::::   |||:::   |||         :::|||      |||||||||
Db        385 AGGNTGCGCGTGAAGTGCGTTTTGTTGCCTAATGAGAGCGTGGATTCTTTGAGTTTTTTA 444

Qy         55 AspLysLeu------TrpGluAlaMetProAlaGluGluPheValGlyMetValSerSer 72
                 :::         |||             |||   :::   :::|||:::|||
Db        445 TACCGATCGGCTAATTGGAGCGAAAGGGAAGCGTATGACATGCTTGGTATTGTGTTTGAC 504

Qy         73 Lys---------------------------------GlnMetLeuGlyAspProThrLeu 81
              |||                                       :::|||   |||   |||
Db        505 AAACACCCCTATTTGAAACGCCTTATTATGCCGCATGATTGGGTAGGCCACCCATTATTG 564

Qy         82 ArgThrGlnHisPheIleGlyGly------ThrArgTrpGluLysValSerGlu------ 97
              |||:::          |||           :::|||   :::|||   :::
Db        565 CGCTCTTACCCGCTCAAAGGCGATGAATTCGCCCAATGGTATGAAGTGGATAAAATTTTT 624

Qy         98 -----------AspGluValIleGlyTyrHisGln----------------------- 105
                         ||||||:::|||      |||
Db        625 GGTAAAGAATACCGAGAAGTGGTGGGTAAAGAGCAGAGAGACAGCGCAAGAGTGGATGAA 684

Qy        106 -----------------LeuArgValProHisGlnArgTyrLysAspThrThrMetLys 119
                             ::::::   :::::::::   |||         :::|||
Db        685 AAAGACACTTTCAATTTTGCAAAAATTGGCTATGAACAGGGCAAGGGCGAAGAATTAAAA 744

Qy        120 GluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAsp 139
              ||||||      |||                         |||   :::|||||||||
```

```
Db        745 GAAGTAGAAGAAAAG----------------------CATGCGTTTAAGAAAATCCCT 780

Qy        140 GlyValTrpLysPheAlaGlyLeuLysProAsp----------------IleArgTrp 153
                 |||   :::||||||      :::|||                  |||:::|||
Db        781 TTTGTCAA-AGATTTGCACAAAATCGCCCCCACTATCTTAAAAAAGAGGCTATAAAATGG 839

RESULT 14
AAV72504
ID   AAV72504 standard; cDNA; 850 BP.
XX
AC   AAV72504;
XX
DT   20-MAR-2003  (revised)
DT   01-MAR-1999  (first entry)
XX
DE   Mouse SMAD interacting protein SIP7 cDNA clone Th74.
XX
KW   SIP7; SMAD interacting protein 1; mouse; embryogenesis; differentiation;
KW   cancer; neural disease; immune disease; therapy; diagnosis; ds.
XX
OS   Mus sp.
XX
PN   WO9855512-A2.
XX
PD   10-DEC-1998.
XX
PF   28-MAY-1998;   98WO-EP003193.
XX
PR   02-JUN-1997;   97EP-00201645.
XX
PA   (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI   Verschueren K,  Remacle J,  Huylebroeck D;
XX
DR   WPI; 1999-045732/04.
XX
PT   New SMAD interacting proteins obtained by a two hybrid screening assay -
PT   useful for diagnosing developmental disorders and e.g. cancer, immune and
PT   neural disease.
XX
PS   Claim 18; Page 38; 48pp; English.
XX
CC   This cDNA clone (Th74) comprises a novel SMAD interacting protein partial
CC   cDNA, designated SIP7. By using Smad1 C-domain fused to GAL4 DNA-binding
CC   domain and a mouse embryo cDNA as bait and prey, respectively, in a two-
CC   hybrid screen, a partial Smad4 and Smad interacting protein cDNAs (see
CC   AAV72502-05 and AAV72512-25), were obtained, including SIP1 (see
CC   AAW83318). The invention also provides recombinant expression vectors,
CC   transfected or transduced cells, a method of screening for compounds
CC   which affect the interaction between SMAD and SMAD interacting protein,
CC   transgenic animals useful for testing medicaments and as therapy models,
CC   and a method for post-transcriptional regulation of gene expression by
CC   members of the TGF-beta superfamily by manipulation or modulation of the
CC   interaction between Smad function and/or activity and mRNA stability.
CC   SIPs and nucleic acids encoding them are useful therapeutically and in
CC   claimed kits for diagnosing diseases or disorders related to cancer,
CC   malformation, immune or neural disease, bone metabolism related diseases
CC   or disorders and diseases affecting organs such as skin, lung, kidney,
CC   pancreas, stomach, gonad, muscle or intestine. (Updated on 20-MAR-2003 to
CC   correct PA field.)
XX
SQ   Sequence 850 BP; 155 A; 293 C; 264 G; 138 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.06          Length:         850
Score:                  84.00         Matches:        32
Percent Similarity:     41.7%         Conservative:   11
Best Local Similarity:  31.1%         Mismatches:     36
Query Match:            8.9%          Indels:         24
DB:                     2             Gaps:           7

US-10-507-132-2 (1-172) x AAV72504 (1-850)
```

```
Qy          84 GlnHisPheIleGlyGlyThrArgTrp------GluLysValSerGluAspGluValIle 101
               ||||||                ||||||           :::   |||      |||
Db         536 CAGCACCAGTTCCGATTCGGCCGCTGGAACTGCTCCGCCCTGGGCGAGAAGACCGTCTTC 595

Qy         102 GlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluVal 121
               |||      :::|||||||||      :::           |||           :::
Db         596 GGG---CAAGAACTCCGAGTAGGGAGTCGAGAGGCTGCCTTCACC------TATGCCATC 646

Qy         122 ThrMetLysGlyHisAlaHisSer--------------------AlaAsnLeuHis--- 133
               |||      |||   ||||||:::                   ||||||
Db         647 ACGGCGGCGGGCGTGGCGCATGCTGTCACCGCTGCCTGCAGCCAGGGCAATCTGAGCAAT 706

Qy         134 --------------------------TrpTyrLysLysIleAspGlyValTrpLysPhe 144
                                        :::|||   :::   :::|||   ||||||:::
Db         707 TGTGGCTGTGACCGGGAGAAGCAAGGCTACTACAACCAGGCGGAAGGC---TGGAAGTGG 763

Qy         145 AlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArgIlePheGluAsp 164
                  |||         |||:::|||:::|||      ||||||   |||   |||   |||
Db         764 GGGGGCTGCTCAGCGGACGTCCGCTACGGC---ATCGACTTTTCTCGTCGCTTTGTGGAT 820

Qy         165 GlyArgGlu 167
                  ||||||
Db         821 GCCCGTGAG 829
```

```
RESULT 15
ADF00192
ID   ADF00192 standard; DNA; 1017 BP.
XX
AC   ADF00192;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Bacterial polynucleotide #477.
XX
KW   Proteus mirabilis infection; bacterial infection; antibacterial;
KW   immunostimulant; gene; ds.
XX
OS   Proteus mirabilis.
XX
PN   US6605709-B1.
XX
PD   12-AUG-2003.
XX
PF   05-APR-2000; 2000US-00543681.
XX
PR   09-APR-1999;   99US-0128706P.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
XX
PI   Breton GL;
XX
DR   WPI; 2003-895291/82.
DR   P-PSDB; ADF04364.
XX
PT   New Proteus mirabilis polypeptides and polynucleotides, useful as
PT   reagents for diagnosis of bacterial disease, as components of
PT   antibacterial vaccines, as targets for antibacterial drugs, or as
PT   biocontrol agents for plants.
XX
PS   Disclosure; SEQ ID NO 477; 870pp; English.
XX
CC   The invention relates to new Proteus mirabilis polypeptides and
CC   polynucleotides. The invention also relates to antibodies against the
CC   polypeptides, methods for producing the polypeptides, a method of
CC   generating vaccines for immunising an individual against P. mirabilis, a
CC   method for evaluating a compound for the ability to bind a P. mirabilis
CC   polypeptide and a method for screening test compounds for anti-bacterial
CC   activity. The polypeptides and polynucleotides are useful as molecular
CC   targets for diagnosing, preventing and treating pathological conditions
CC   resulting from bacterial infection, as reagents for diagnosis of
CC   bacterial diseases, as components of antibacterial vaccines, as targets
CC   for antibacterial drugs or as bio-control agents for plants. This
CC   sequence represents a Proteus mirabilis polynucleotide of the invention.
```

```
XX
SQ   Sequence 1017 BP; 290 A; 186 C; 254 G; 287 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.63          Length:         1017
Score:                  84.00         Matches:        39
Percent Similarity:     37.3%         Conservative:   18
Best Local Similarity:  25.5%         Mismatches:     42
Query Match:            8.9%          Indels:         54
DB:                     10            Gaps:           10

US-10-507-132-2 (1-172) x ADF00192 (1-1017)

Qy          35 TrpAspArgLeuArgLysValIleAlaProThrLeuArgIleAspTyrArgSerPheLeu 54
               ||||||:::   ::::::                                        |||
Db         280 TGGGATAAAGCACAACGA----------------------------GAAGATGTGCTT 309

Qy          55 AspLysLeuTrpGluAlaMetProAlaGluGluPheValGlyMetValSerSerLysGln 74
               ||||||:::::::|||      |||   :::   ||||||
Db         310 GATAAAATGTTTGAAACAGCGCCA---CAGTCTTTCGTG-------------------- 345

Qy          75 MetLeuGlyAspProThrLeuArg---ThrGlnHisPheIleGlyGlyThrArgTrpGlu 93
               ||||||   |||       ||||||      :::|||   :::       |||   ||||||
Db         346 ATGCTTGCAGATCTTTGTTTAAGAGGGGCTAAACACACATTACAGCGTACCTCTTGGGAA 405

Qy          94 LysValSerGluAspGluValIleGlyTyrHisGlnLeuArg------------------ 107
                  :::         |||:::|||         :::|||:::
Db         406 GGGATA---------GAGATTATA------GAGCGCTTAAAAGCACAAGGGCGTAATGTT 450

Qy         108 ---------ValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLys 124
                        |||||||||           |||                 :::       |||
Db         451 ATTTTTATGGTACCGCATGGATGGGCTGTTGATGTACCTGCCATGTTATTGGCTGCTAAA 510

Qy         125 GlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLys------IleAspGlyValTrp 142
               |||         :::|||      |||      |||            |||   :::|||
Db         511 GGGCAAAAAATGGCAGCAATGTTTCACCACCAAAAAGATCCGGTGACTGATTATTTATGG 570

Qy         143 ------------------------------------LysPheAlaGlyLeuLysPro 149
                                                   :::   ||||||:::||||||
Db         571 AATAAAGCACGTTACCATTTCGGCGGACGTTTACACTCGCGCGAAGCGGGGATAAAACCT 630

Qy         150 AspIleArg-----------------TrpGlyGluPhe 156
                  |||                  ||||||   :::
Db         631 TTTATTTCAACGGTGCGCCAAGGGTTTTGGGGGTATTAT 669


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Job time : 599 secs
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GenCore version 5.1.9

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2006, 19:08:15 ; Search time 5106 Seconds
(without alignments)
3231.186 Million cell updates/sec

Title: US-10-507-132-2
Perfect score: 942
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss07
-USER=US10507132_@CGN_1_1_5548_@runat_04122006_143856_11163 -NCPU=6 -ICPU=3
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
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2: gb_pat:*
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8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	938	99.6	807	4	AB004741	AB004741 Magnaport
2	653	69.3	770	4	AB100172	AB100172 Bipolaris
3	652.5	69.3	1477	4	AF316575	AF316575 Ophiostom
4	641	68.0	1215	4	AY214004	AY214004 Ceratocys
5	633	67.2	1151	4	COGSCD1	D86079 Colletotric
6	499	53.0	427	4	AY098656	AY098656 Ophiostom
7	499	53.0	1447	4	AFU95042	U95042 Aspergillus
8	495	52.5	424	4	AY098657	AY098657 Ophiostom
9	494.5	52.5	423	4	AY098660	AY098660 Ophiostom
10	493	52.3	432	4	AY098654	AY098654 Ceratocys
11	489.5	52.0	428	4	AY098659	AY098659 Ophiostom
12	489	51.9	421	4	AY098661	AY098661 Ophiostom
13	489	51.9	433	4	AY098655	AY098655 Ceratocys
14	487	51.7	414	4	AY098663	AY098663 Ophiostom
15	487	51.7	414	4	AY098664	AY098664 Ophiostom
16	486	51.6	415	4	AY098662	AY098662 Ophiostom
17	484.5	51.4	423	4	AY098666	AY098666 Ophiostom
18	484.5	51.4	573	4	SMA575152	AJ575152 Sordaria
19	472	50.1	433	4	AY098658	AY098658 Ophiostom
20	465.5	49.4	422	4	AY098665	AY098665 Ophiostom
c 21	208	22.1	110000	4	AP007161_08	Continuation (9 of
22	99.5	10.6	186614	15	AP003602	AP003602 Nostoc sp
23	94.5	10.0	462	2	AR317494	AR317494 Sequence
c 24	93.5	9.9	250093	12	AC114058	AC114058 Rattus no
25	92	9.8	110000	15	AP006618_50	Continuation (51 o
26	91.5	9.7	246255	12	AC158089	AC158089 Bos tauru
27	91	9.7	9158	15	AF210152	AF210152 Clostridi
c 28	90	9.6	75898	10	AY190604	AY190604 Halovirus
c 29	90	9.6	110000	15	CP000096_20	Continuation (21 o
30	90	9.6	110000	15	CR954246_09	Continuation (10 o
31	89.5	9.5	110000	4	CR382135_03	Continuation (4 of
c 32	88.5	9.4	110000	4	AP007150_09	Continuation (10 o
33	88.5	9.4	177466	15	AE001826	AE001826 Deinococc
34	88	9.3	9742	15	ESU57489	U57489 Eubacterium
35	88	9.3	40679	3	AY052766	AY052766 Salmonell
36	88	9.3	110000	15	CP000091_14	Continuation (15 o
c 37	88	9.3	230569	12	AC096163	AC096163 Rattus no
38	88	9.3	273650	12	AC096020	AC096020 Rattus no
c 39	87.5	9.3	110000	15	CR628337_09	Continuation (10 o
c 40	87.5	9.3	143840	6	AC121929	AC121929 Mus muscu
c 41	87.5	9.3	219269	6	AC133519	AC133519 Mus muscu
42	87	9.2	2232	4	AF095896	AF095896 Oryza sat
43	87	9.2	2664	4	AF095895	AF095895 Oryza sat
44	87	9.2	3196	4	AK066825	AK066825 Oryza sat
45	87	9.2	92928	11	AC140789	AC140789 Gallus ga

ALIGNMENTS

RESULT 1
AB004741
LOCUS AB004741 807 bp mRNA linear PLN 13-NOV-1998
DEFINITION Magnaporthe grisea mRNA for scytalone dehydratase, complete cds.
ACCESSION AB004741
VERSION AB004741.1 GI:3798733
KEYWORDS scytalone dehydratase; sdh1.
SOURCE Magnaporthe grisea
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE 1 (sites)
AUTHORS Motoyama,T., Imanishi,K. and Yamaguchi,I.
TITLE cDNA cloning, expression, and mutagenesis of scytalone dehydratase needed for pathogenicity of the rice blast fungus, Pyricularia oryzae
JOURNAL Biosci. Biotechnol. Biochem. 62 (3), 564-566 (1998)
PUBMED 9571787
REFERENCE 2 (bases 1 to 807)
AUTHORS Motoyama,T.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-1997) Takayuki Motoyama, The Institute of Physical and Chemical Research (RIKEN), Miclobial Toxicology Lab.; 2-1 Hirosawa, Wako-shi, Saitama 351-0198, Japan
(E-mail:tmotoyam@postman.riken.go.jp, Tel:+81-48-467-9518)
COMMENT Sequence updated (27-Oct-1998).
FEATURES Location/Qualifiers

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     source          1. .807
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /db_xref="taxon:148305"
                     /note="sequence obtained from anamorph Pyricularia oryzae
                     whose telemorphic form is unknown"
     gene            1. .807
                     /gene="Sdh1"
     CDS             81. .599
                     /gene="Sdh1"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="BAA34046.1"
                     /db_xref="GI:3798734"
                     /translation="MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAP
                     TLRIDYRSFLDKLWEAMPAEEFVGMVSSKQVLGDPTLRTQHFIGGTRWEKVSEDEVIG
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                     IFEDGRETFGDK"
ORIGIN

Alignment Scores:
Pred. No.:              6.61e-108       Length:         807
Score:                  938.00          Matches:        171
Percent Similarity:     100.0%          Conservative:   1
Best Local Similarity:  99.4%           Mismatches:     0
Query Match:            99.6%           Indels:         0
DB:                     4               Gaps:           0

US-10-507-132-2 (1-172) x AB004741 (1-807)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 140

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 200

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 260

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db        261 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 320

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 380

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 440

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 500

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 560

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
              ||||||||||||||||||||||||||||||||||||
Db        561 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 596

RESULT 2
AB100172
LOCUS       AB100172                770 bp    DNA     linear   PLN 01-APR-2004
DEFINITION  Bipolaris oryzae BSCD1gene for scytalone dehydratase, complete cds.
ACCESSION   AB100172
VERSION     AB100172.1  GI:32879676
KEYWORDS    .
SOURCE      Bipolaris oryzae
  ORGANISM  Bipolaris oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
            Pleosporales; Pleosporaceae; mitosporic Cochliobolus; Bipolaris.
REFERENCE   1
  AUTHORS   Kihara,J., Moriwaki,A., Ueno,M., Tokunaga,T., Arase,S. and Honda,Y.
  TITLE     Cloning, functional analysis and expression of a scytalone
            dehydratase gene (SCD1) involved in melanin biosynthesis of the
            phytopathogenic fungus Bipolaris oryzae
  JOURNAL   Curr. Genet. 45 (4), 197-204 (2004)
   PUBMED   14716498
REFERENCE   2  (bases 1 to 770)
  AUTHORS   Kihara,J. and Moriwaki,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JAN-2003) Junichi Kihara, Shimane University, Faculty
            of Life and Environmental Science; Nishikawatsu 1060, Matsue,
            Shimane 690-8504, Japan (E-mail:j-kihara@life.shimane-u.ac.jp,
            Tel:81-852-32-6520, Fax:81-852-32-6597)
FEATURES             Location/Qualifiers
     source          1. .770
                     /organism="Bipolaris oryzae"
                     /mol_type="genomic DNA"
                     /strain="D9/F6-69"
                     /db_xref="taxon:33195"
     gene            join(34. .70,125. .645)
                     /gene="BSCD1"
     CDS             join(34. .70,125. .645)
                     /gene="BSCD1"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="BAC79365.1"
                     /db_xref="GI:32879677"
                     /translation="MFEKKELQPTFEEVMGCQSACYEWADSYDSKDWERLRKCVAPTL
                     KIDYRSFLDKIWEAMPADEFVAMASDPAVLGNPLLKTQHFIGGTRWEKTAEDEITGYH
                     QLRVPHQRYTDESRATVAVKGHAHSFNTHWYKKIDGEWKFAGLNPDIRWYEYDFDKVF
                     AEGREQLGEAKAAAGIPETAPGQAV"
ORIGIN

Alignment Scores:
Pred. No.:              4.53e-72        Length:         770
Score:                  653.00          Matches:        114
Percent Similarity:     79.8%           Conservative:   24
Best Local Similarity:  65.9%           Mismatches:     31
Query Match:            69.3%           Indels:         4
DB:                     4               Gaps:           1

US-10-507-132-2 (1-172) x AB100172 (1-770)

Qy          3 SerGlnValGlnLysSerAspGluIleThrPheSerAspTyr----------LeuGly 18
              |||   ||||||   ||||||   :::   ::::::::::          :::|||
Db         76 TCATGTGTGCAGTAAAGTGACTCTCTCTGGTGGGCTAACTGGGTAGCAGAGGTCATGGGC 135

Qy         19 LeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeu 38
                 :::      ||||||||||||||||||||||||||||||||||:::||||||
Db        136 TGTCAATCGGCATGCTACGAATGGGCAGACAGCTACGACAGCAAGGACTGGGAGCGTCTG 195

Qy         39 ArgLysValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrp 58
              ||||||   :::|||||||||||:::|||||||||||||||||||||||:::|||
Db        196 CGCAAGTGCGTCGCTCCGACTCTGAAGATTGACTACCGGTCCTTCTTGGACAAGATATGG 255

Qy         59 GluAlaMetProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAsp 78
              ||||||||||||||:::|||||||||   |||   |||          :::||||||:::
Db        256 GAGGCGATGCCAGCGGATGAGTTTGTGGGCCATGGCCTCTGACCCTGCGGTGCTCGGCAAC 315

Qy         79 ProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAsp 98
              |||   |||:::||||||||||||||||||||||||||||||||||   :::||||||
Db        316 CCCCTCCTCAAGACACAGCACTTCATCGGCGGAACACGGTGGGAGAAGACGGCCGAGGAT 375

Qy         99 GluValIleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMet 118
              |||:::   ||||||||||||||||||||||||||||||||||   |||   :::
Db        376 GAGATTACGGGATACCACCAGCTGCGAGTGCCTCACCAGCGATACACGGATGAGTCACGG 435

Qy        119 LysGluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIle 138
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Db        436 GCGACGGTGGCAGTCAAGGGCCACGCCCACAGCTTCAACACGCACTGGTACAAAAAGATT 495

Qy        139 AspGlyValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPhe 158

Db        496 GACGGCGAGTGGAAGTTTGCCGGGCTGAACCCGGACATTAGGTGGTACGAGTATGACTTT 555

Qy        159 AspArgIlePheGluAspGlyArgGluThrPheGlyAsp 171

Db        556 GACAAGGTGTTTGCAGAGGGCCGCGAGCAGCTGGGCGAG 594
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RESULT 3
AF316575
LOCUS AF316575 1477 bp DNA linear PLN 22-MAY-2002
DEFINITION Ophiostoma floccosum strain 387N scytalone dehydratase (OSD1) gene, complete cds.
ACCESSION AF316575
VERSION AF316575.1 GI:12964737
KEYWORDS .
SOURCE Ophiostoma floccosum
ORGANISM Ophiostoma floccosum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE 1 (bases 1 to 1477)
AUTHORS Wang,H.L., Kim,S.H. and Breuil,C.
TITLE A scytalone dehydratase gene from Ophiostoma floccosum restores the melanization and pathogenicity phenotypes of a melanin-deficient Colletotrichum lagenarium mutant
JOURNAL Mol. Genet. Genomics 266 (1), 126-132 (2001)
PUBMED 11589570
REFERENCE 2 (bases 1 to 1477)
AUTHORS Wang,H. and Breuil,C.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-2000) Wood Science, University of British Columbia, 2424 Main Mall, Vancouver, BC V6T 1Z4, Canada
FEATURES Location/Qualifiers
source 1. .1477
/organism="Ophiostoma floccosum"
/mol_type="genomic DNA"
/strain="387N"
/db_xref="taxon:104300"
gene <316. .>1105
/gene="OSD1"
mRNA join(<316. .394,471. .571,635. .>1105)
/gene="OSD1"
/product="scytalone dehydratase"
CDS join(316. .394,471. .571,635. .1105)
/gene="OSD1"
/codon_start=1
/product="scytalone dehydratase"
/protein_id="AAK11296.1"
/db_xref="GI:12964738"
/translation="MGLNISSLTSTTSSAPKTTGSDISFEDYMGLCSAAYEWADSYDS
KDWDRLRKCIAPTLRIDYRSFLNKLWEAMPAEEFIGMISDPSVLGNPLLRTQHFFGAS
RWERISDTEVVGYHQLRVPHQVYTDTTLTQVAVKGHAHSANTHWYRKVDGVWKFAGLD
PKIRWFEYDFDKVFASGRDQFGTEEKAAATAGPELLAKDKVQSAIASAQRAVAVSA"
ORIGIN

Alignment Scores:

Pred. No.:	1.16e-71	Length:	1477
Score:	652.50	Matches:	113
Percent Similarity:	75.7%	Conservative:	21
Best Local Similarity:	63.8%	Mismatches:	22
Query Match:	69.3%	Indels:	21
DB:	4	Gaps:	1

US-10-507-132-2 (1-172) x AF316575 (1-1477)

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Qy         15 AspTyrLeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAsp 34

Db        470 GACTACATGGGCCTCTGCAGTGCCGCCTACGAGTGGGCCGACAGCTATGATTCCAAGGAC 529

Qy         35 TrpAspArgLeuArgLysValIleAlaProThrLeuArgIle---------------- 48

Db        530 TGGGACCGTCTGCGCAAGTGCATTGCTCCCACTCTGCGAATCGTACGTCTTATACAACCC 589

Qy         49 -----------------------------------------AspTyrArgSerPhe 53

Db        590 TGCTTTCTCTATTAACCCATAAAGATCTTCTTTGCTAACAGACAGGACTACCGCTCGTTC 649

Qy         54 LeuAspLysLeuTrpGluAlaMetProAlaGluGluPheValGlyMetValSerSerLys 73

Db        650 CTGAACAAGCTGTGGGAGGCCATGCCGGCCGAAGAGTTTATCGGCATGATCTCCGACCCC 709

Qy         74 GlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrpGlu 93

Db        710 AGCGTTCTCGGCAACCCCCTGCTGCGCACACAACACTTCTTCGGCGCCTCGCGCTGGGAG 769

Qy         94 LysValSerGluAspGluValIleGlyTyrHisGlnLeuArgValProHisGlnArgTyr 113

Db        770 CGCATCTCCGACACCGAGGTCGTGGGCTACCATCAGCTGCGCGTCCCCCACCAGGTCTAC 829

Qy        114 LysAspThrThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHis 133

Db        830 ACAGATACCACTCTCACACAAGTTGCCGTCAAGGGCCACGCCCACTCGGCCAACACCCAC 889

Qy        134 TrpTyrLysLysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIleArgTrp 153

Db        890 TGGTACCGCAAGGTCGACGGCGTCTGGAAGTTTGCCGGCCTCGATCCCAAGATCCGCTGG 949

Qy        154 GlyGluPheAspPheAspArgIlePheGluAspGlyArgGluThrPheGly 170

Db        950 TTCGAATACGATTTTGATAAGGTGTTTGCCAGCGGCCGCGACCAGTTTGGC 1000
```

RESULT 4
AY214004
LOCUS AY214004 1215 bp DNA linear PLN 10-MAR-2004
DEFINITION Ceratocystis resinifera syctalone dehydratase I (SD1) gene, complete cds.
ACCESSION AY214004
VERSION AY214004.1 GI:37787189
KEYWORDS .
SOURCE Ceratocystis resinifera
ORGANISM Ceratocystis resinifera
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Microascales; Microascales incertae sedis; Ceratocystis.
REFERENCE 1 (bases 1 to 1215)
AUTHORS Loppnau,P.A.
TITLE Canadian Populations and Melanin Biosynthesis Genes of Ceratocystis resinifera
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1215)
AUTHORS Loppnau,P.A.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Wood Science, University of British Columbia, 4041-2424 Main Mall, Vancouver, BC V6T 1Z4, Canada
FEATURES Location/Qualifiers
source 1. .1215
/organism="Ceratocystis resinifera"
/mol_type="genomic DNA"
/isolate="EL3-21"
/specific_host="Pinus contorta"
/db_xref="taxon:95837"
/country="Canada: Alberta, Edson"
gene <233. .>934
/gene="SD1"
mRNA join(<233. .305,379. .476,545. .>934)
/gene="SD1"
/product="syctalone dehydratase I"
CDS join(233. .305,379. .476,545. .934)
/gene="SD1"
/codon_start=1
/product="syctalone dehydratase I"
/protein_id="AAO60167.1"
/db_xref="GI:37787190"

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                     /translation="MVAGSSDSTQVTASTVNPKTISFEDYCGLNTALYEWADSYDSKD
                     WDRLRRTIAPTLRIDYRSFLDKLWEAMPAEDFIKMISDPNVLGDPLLKTQHFVGASRW
                     ERVSDDEVVGWHQLRVPHQRYTDATKTTVKVKGHAHSANKHWYKKVDGVWKFAGLYPE
                     IRWSEYDFDKVFASGREEFGDEDIDV"
     exon            233. .305
                     /gene="SD1"
                     /number=1
     exon            379. .476
                     /gene="SD1"
                     /number=2
     exon            545. .934
                     /gene="SD1"
                     /number=3
ORIGIN

Alignment Scores:
Pred. No.:              2.56e-70        Length:         1215
Score:                  641.00          Matches:        115
Percent Similarity:     74.7%           Conservative:   21
Best Local Similarity:  63.2%           Mismatches:     23
Query Match:            68.0%           Indels:         24
DB:                     4               Gaps:           1

US-10-507-132-2 (1-172) x AY214004 (1-1215)

Qy         14 SerAspTyrLeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerLys 33
              :::||||||   ||||||   |||   :::||||||||||||||||||||||||||||||
Db        375 GCAGATTATTGTGGTCTTAACACTGCCTTATACGAGTGGGCTGATAGCTACGACAGCAAG 434

Qy         34 AspTrpAspArgLeuArgLysValIleAlaProThrLeu---------------------- 46
              ||||||||||||||||:::   ||||||||||||||
Db        435 GATTGGGACCGTCTGCGTCGTACCATTGCCCCAACACTAAGAGTGAGCATCTCTCGCTGA 494

Qy         47 ----------------------------------------------------ArgIleAspTyr 50
                                                                   |||   ||||||
Db        495 TATAGCAGAATATATCTTAGTTCTTACTAACAACATATATGTTTTGCTAGATC-GACTAC 553

Qy         51 ArgSerPheLeuAspLysLeuTrpGluAlaMetProAlaGluGluPheValGlyMetVal 70
              ||||||||||||||||||||||||||||||||||||||||:::|||:::   |||:::
Db        554 CGCTCGTTCCTGGATAAGCTATGGGAAGCAATGCCTGCCGAGGACTTTATTAAGATGATC 613

Qy         71 SerSerLysGlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThr 90
              |||         :::||||||||||||    |||:::||||||||||||:::|||   :::
Db        614 TCCGACCCCAACGTTCTCGGCGACCCTCTACTAAAGACCCAGCACTTCGTCGGCGCTTCG 673

Qy         91 ArgTrpGluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgValProHis 110
              ||||||||||:::||||||:::||||||||||:::|||:::||||||||||||||||||||
Db        674 CGCTGGGAGCGTGTTAGTGACGATGAAGTCGTTGGCTGGCACCAGCTACGTGTGCCCCAC 733

Qy        111 GlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlyHisAlaHisSerAla 130
              |||||||||   |||   |||          |||   :::||||||||||||||||||||
Db        734 CAGCGCTACACTGATGCTACGAAGACCACCGTCAAGGTCAAAGGCCACGCCCACTCAGCC 793

Qy        131 AsnLeuHisTrpTyrLysLysIleAspGlyValTrpLysPheAlaGlyLeuLysProAsp 150
              |||  ||||||||||||||:::||||||||||||||||||||||||||   |||:::
Db        794 AACAAGCACTGGTACAAGAAGGTAGATGGCGTGTGGAAATTTGCCGGTCTCTATCCGGAG 853

Qy        151 IleArgTrpGlyGluPheAspPheAspArgIlePheGluAspGlyArgGluThrPheGly 170
              |||||||||   |||:::|||||||||::::::|||      |||||||||   ||||||
Db        854 ATCCGCTGGTCAGAGTACGATTTCGACAAGGTGTTTGCTAGCGGCCGTGAAGAGTTTGGT 913

Qy        171 AspLys 172
              |||:::
Db        914 GATGAG 919

RESULT 5
COGSCD1
LOCUS       COGSCD1                 1151 bp    DNA     linear   PLN 25-DEC-2002
DEFINITION  Colletotrichum lagenarium DNA for scytalone dehydratase, complete
            cds.
ACCESSION   D86079
VERSION     D86079.1  GI:1395159
KEYWORDS    melanin biosynthesis; scytalone dehydratase.
SOURCE      Colletotrichum lagenarium
  ORGANISM  Colletotrichum lagenarium
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
            mitosporic Phyllachoraceae; Colletotrichum.
REFERENCE   1
  AUTHORS   Kubo,Y., Takano,Y., Endo,N., Yasuda,N., Tajima,S. and Furusawa,I.
  TITLE     Cloning and structural analysis of the melanin biosynthesis gene
            SCD1 encoding scytalone dehydratase in Colletotrichum lagenarium
  JOURNAL   Appl. Environ. Microbiol. 62 (12), 4340-4344 (1996)
   PUBMED   8953707
REFERENCE   2  (bases 1 to 1151)
  AUTHORS   Kubo,Y., Takano,Y., Noriko,E., Yasuda,N., Tajima,S. and Furusawa,I.
  TITLE     Cloning and structural analysis of the melanin biosynthesis gene
            encoding scytalone dehydratase of Colletotrichum lagenarium
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1151)
  AUTHORS   Kubo,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-JUN-1996) Yasuyuki Kubo, Laboratory of Plant
            Pathology, Faculty of Agriculture, Kyoto Prefectural University;
            Shimogamo, Kyoto, Kyoto 606, Japan (E-mail:y_kubo@kpu.ac.jp,
            Tel:075-702-0957, Fax:075-702-0957)
FEATURES             Location/Qualifiers
     source          1. .1151
                     /organism="Colletotrichum lagenarium"
                     /mol_type="genomic DNA"
                     /isolate="104-T"
                     /db_xref="taxon:5462"
     TATA_signal     117. .121
     gene            join(233. .266,324. .421,489. .923)
                     /gene="SCD1"
     CDS             join(233. .266,324. .421,489. .923)
                     /gene="SCD1"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="BAA13009.1"
                     /db_xref="GI:1395160"
                     /translation="MASPAGNITFEDYLGLNAALFEWADSYDSKDWDRLRKCIAPELR
                     IDYRSFLDKIWEAMPAEEFIAMISDKSVLGNPLLKTQHFIGGSRWEKVSDTEVIGHHQ
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                     DGRDSYGTEDQKTDVKVVEKEIKFAAAH"
     exon            <233. .266
                     /gene="SCD1"
                     /number=1
     intron          267. .323
                     /gene="SCD1"
                     /number=1
     exon            324. .421
                     /gene="SCD1"
                     /number=2
     intron          422. .488
                     /gene="SCD1"
                     /number=2
     exon            489. .923
                     /gene="SCD1"
                     /number=3
     polyA_signal    1054. .1057
     polyA_site      1073
ORIGIN

Alignment Scores:
Pred. No.:              2.44e-69        Length:         1151
Score:                  633.00          Matches:        112
Percent Similarity:     76.0%           Conservative:   24
Best Local Similarity:  62.6%           Mismatches:     20
Query Match:            67.2%           Indels:         23
DB:                     4               Gaps:           1

US-10-507-132-2 (1-172) x COGSCD1 (1-1151)

Qy         15 AspTyrLeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAsp 34
              ||||||||||||||||         ::::::||||||||||||||||||||||||||||||
```

```
Db        323 GACTACCTCGGTCTCAACGCCGCTCTCTTCGAGTGGGCCGACTCCTACGACTCCAAGGAC 382

Qy         35 TrpAspArgLeuArgLysValIleAlaProThrLeuArg---------------------- 47
              ||||||||||||||||   |||||||||   ||||||
Db        383 TGGGACCGTCTCCGCAAGTGCATCGCCCCCGAGCTCCGCGTAAGTCTCTTCCCCCAAATA 442

Qy         48 ----------------------------------------------IleAspTyrArgSe 52
                                                            ||||||||||||||
Db        443 CACGCAAACAGAAACCGTCGTCCACCGGTATTAACCCGAACGCAAGATCGACTACCGCTC 502

Qy         52 rPheLeuAspLysLeuTrpGluAlaMetProAlaGluGluPheValGlyMetValSerSe 72
              |||||||||||||:::|||||||||||||||||||||||||:::   |||:::|||
Db        503 CTTCCTCGACAAGATCTGGGAGGCCATGCCCGCCGAGGAGTTCATCGCCATGATCTCGGA 562

Qy         72 rLysGlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTr 92
              |||   :::||||||:::|||   |||:::||||||||||||||||||:::||||||
Db        563 CAAGTCCGTCCTCGGCAACCCGCTCCTCAAGACGCAGCACTTCATCGGCGGCTCCCGCTG 622

Qy         92 pGluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgValProHisGlnAr 112
              ||||||||||||:::   |||||||||||:::||||||||||||||||||||||::
Db        623 GGAAAAGGTCTCGGACACGGAGGTCATCGGCCACCACCAGCTGCGCGTGCCGCACCAAAA 682

Qy        112 gTyrLysAspThrThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaAsnLe 132
              :|||   |||   :::      ||||||   :::||||||||||||||||||   |||::
Db        683 GTACACCGACGCCTCGCGCACCGAGGTCGCCGTCAAGGGCCACGCCCACAGCTACAACAT 742

Qy        132 uHisTrpTyrLysLysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIleAr 152
              :||||||||:::|||::::::||||||||||||||||||||||||   |||:::|||||
Db        743 GCACTGGTACCGCAAGGTCAACGGCGTGTGGAAGTTCGCCGGTCTGAACCCCGAGATCCG 802

Qy        152 gTrpGlyGluPheAspPheAspArgIlePheGluAspGlyArgGluThrPheGly 170
              ||||   |||:::|||||||||   :::|||   |||||||||:::::::::|||
Db        803 GTGGTCCGAGTACGACTTTGACGCCGTCTTCGCCGACGGCCGCGACTCGTACGGC 857
```

RESULT 6
AY098656
LOCUS AY098656 427 bp DNA linear PLN 16-JAN-2003
DEFINITION Ophiostoma piceae isolate AU1 scytalone dehydratase (SD) gene, partial cds.
ACCESSION AY098656
VERSION AY098656.1 GI:21238821
KEYWORDS .
SOURCE Ophiostoma piceae
ORGANISM Ophiostoma piceae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE 1 (bases 1 to 427)
AUTHORS Fleet,C. and Breuil,C.
TITLE Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi
JOURNAL Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE 2 (bases 1 to 427)
AUTHORS Fleet,C. and Breuil,C.
TITLE Direct Submission
JOURNAL Submitted (22-APR-2002) Wood Science, University of British Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES Location/Qualifiers
source 1. .427
/organism="Ophiostoma piceae"
/mol_type="genomic DNA"
/isolate="AU1"
/db_xref="taxon:61273"
/country="Canada"
gene <1. .>427
/gene="SD"
mRNA join(<1. .69,132. .>427)
/gene="SD"
/product="scytalone dehydratase"
CDS join(<1. .69,132. .>427)
/gene="SD"
/codon_start=1
/product="scytalone dehydratase"
/protein_id="AAM34802.1"
/db_xref="GI:21238822"
/translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPAEEFIG MISDPSVLGNPLLRTQHFFGASRWERISDTEVVGYHQLRVPHQVYTDTTLTQVAVKGH AHSANTHWYRKVDGVWKFAG"
ORIGIN

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Alignment Scores:
Pred. No.:                5.24e-53        Length:          427
Score:                    499.00          Matches:         91
Percent Similarity:       74.6%           Conservative:    15
Best Local Similarity:    64.1%           Mismatches:      15
Query Match:              53.0%           Indels:          22
DB:                       4               Gaps:            1

US-10-507-132-2 (1-172) x AY098656 (1-427)

Qy         25 GluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLysValIleAlaPro 44
              ||||||||||||   ||||||||||||||||||||||||||||||||   |||||||||
Db          1 GAGTGGGCGGACAGGTACGATTCCAAGGACTGGGACCGTCTGCGCAAGTGCATTGCTCCC 60

Qy         45 ThrLeu---------------------------------------------------- 46
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Db         61 ACTCTGCGAGTACGTCTTATACAACCCTGCTTTCTCTATTAACCCATAAAGATCTTCTTG 120

Qy         47 ---------ArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetProAla 63
                        |||   |||||||||||||||||:::|||||||||||||||||||||||
Db        121 CTAACAGACAGATC-GACTACCGCTCGTTCCTGAACAAGCTGTGGGAGGCCATGCCGGCC 179

Qy         64 GluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThrLeuArgThr 83
              |||||||||:::||||||:::|||          :::||||||::|||   |||||||||
Db        180 GAAGAGTTTATCGGCATGATCTCCGACCCCAGCGTTCTCGGCAACCCCCTGCTGCGCACA 239

Qy         84 GlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluValIleGlyTyr 103
              |||||||||   |||   :::|||||||||:::::::|||:::   ||||||:::||||||
Db        240 CAACACTTCTTCGGCGCCTCGCGCTGGGAGCGCATCTCCGACACCGAGGTCGTGGGCTAC 299

Qy        104 HisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMet 123
              ||||||||||||||||||||||||   |||   |||||||||:::   :::|||   :::
Db        300 CATCAGCTGCGCGTCCCCCACCAGGTCTACACAGATACCACTCTCACACAAGTTGCCGTC 359

Qy        124 LysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGlyValTrpLys 143
              ||||||||||||||||||||||   |||||||||:::|||:::|||||||||||||||||
Db        360 AAGGGCCACGCCCACTCGGCCAACACCCACTGGTACCGCAAGGTCGACGGCGTCTGGAAG 419

Qy        144 PheAla 145
              ||||||
Db        420 TTCGCC 425
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RESULT 7
AFU95042
LOCUS AFU95042 1447 bp DNA linear PLN 12-NOV-1999
DEFINITION Aspergillus fumigatus scytalone dehydratase (arp1) gene, complete cds.
ACCESSION U95042
VERSION U95042.1 GI:2555059
KEYWORDS .
SOURCE Aspergillus fumigatus
ORGANISM Aspergillus fumigatus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE 1 (bases 1 to 1447)
AUTHORS Tsai,H.F., Washburn,R.G., Chang,Y.C. and Kwon-Chung,K.J.
TITLE Aspergillus fumigatus arp1 modulates conidial pigmentation and complement deposition
JOURNAL Mol. Microbiol. 26 (1), 175-183 (1997)
PUBMED 9383199
REFERENCE 2 (bases 1 to 1447)
AUTHORS Tsai,H.F., Wheeler,M.H., Chang,Y.C. and Kwon-Chung,K.J.
TITLE A developmentally regulated gene cluster involved in conidial pigment biosynthesis in Aspergillus fumigatus
JOURNAL J. Bacteriol. 181 (20), 6469-6477 (1999)
PUBMED 10515939
REFERENCE 3 (bases 1 to 1447)

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  AUTHORS   Tsai,H.-F., Washburn,R.G., Chang,Y.C. and Kwon-Chung,K.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-MAR-1997) LCI/MMS, NIH/NIAID, 10 Center Drive,
            MSC1882, Bldg 10/Rm 11C304, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .1447
                     /organism="Aspergillus fumigatus"
                     /mol_type="genomic DNA"
                     /strain="B-5233"
                     /db_xref="taxon:5085"
     gene            <331. .>939
                     /gene="arp1"
     mRNA            join(<331. .370,419. .474,529. .>939)
                     /gene="arp1"
                     /product="scytalone dehydratase"
     CDS             join(331. .370,419. .474,529. .939)
                     /gene="arp1"
                     /function="modulates conidial pigmentation and complement
                     deposition"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAC49843.1"
                     /db_xref="GI:2555060"
                     /translation="MVEKKPNLTLEFHDYLALKKVLFDWADSYDAKDWDRLRSIIAPT
                     LTVDYRQIGLRKWDDMPAEDYMAMISDMDFLGDPTVKTQHLLGESWWEKISDTEVIGH
                     HQLRAAHQVYTDSTLQTVKLKGHGHATNEHYYRKVDGVWKFAGLKPTVRWNEYQFEDV
                     FRAAKPSV"
     exon            <331. .370
                     /gene="arp1"
                     /number=1
     intron          371. .418
                     /gene="arp1"
                     /number=1
     exon            419. .474
                     /gene="arp1"
                     /number=2
     intron          475. .528
                     /gene="arp1"
                     /number=2
     exon            529. .>939
                     /gene="arp1"
                     /number=3
ORIGIN

Alignment Scores:
Pred. No.:              2.34e-52        Length:         1447
Score:                  499.00          Matches:        84
Percent Similarity:     68.2%           Conservative:   32
Best Local Similarity:  49.4%           Mismatches:     36
Query Match:            53.0%           Indels:         18
DB:                     4               Gaps:           1

US-10-507-132-2 (1-172) x AFU95042 (1-1447)

Qy          11 IleThrPheSerAspTyrLeuGlyLeuMetThrCysValTyrGluTrpAlaAspSerTyr 30
               :::|||      |||||||||   |||         :::::::::|||||||||||||||
Db         406 CTAACCCGGCCAGACTATCTTGCCCTAAAAAAAGTCCTCTTTGACTGGGCAGACAGCTAT 465

Qy          31 AspSerLys------------------------------------------------------ 33
               |||:::|||
Db         466 GACGCCAAGGTAAGTTCAACGTCCCGTCCCCGCGAGCGGGAAAACCATATTCACCCAGGG 525

Qy          34 ---AspTrpAspArgLeuArgLysValIleAlaProThrLeuArgIleAspTyrArgSer 52
                  ||||||||||||||||   :::|||||||||||||||   :::|||||||||
Db         526 TAGGACTGGGATCGACTTCGAAGCATCATCGCCCCGACCCTTACCGTGGACTACAGGCAG 585

Qy          53 PheLeuAspLysLeuTrpGluAlaMetProAlaGluGluPheValGlyMetValSerSer 72
                  :::   |||:::   ||||||||||||:::::::::   |||:::|||
Db         586 ATCGGACTGCGAAAGTGGGATGACATGCCTGCGGAAGACTACATGGCCATGATTTCTGAC 645

Qy          73 LysGlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrp 92
                  ||||||||||||||:::::|||||||||   :::|||   :::   |||
Db         646 ATGGACTTCTTGGGTGACCCCACCGTCAAGACCCAGCATCTGCTGGGCGAGTCCTGGTGG 705

Qy          93 GluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgValProHisGlnArg 112
               ||||||:::|||:::   ||||||||||||:::|||||||||||      ||||||
Db         706 GAAAAGATCTCCGATACCGAGGTCATTGGCCACCATCAGCTGCGCGCCGCCCATCAGGTC 765

Qy         113 TyrLysAspThrThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaAsnLeu 132
               |||   |||:::|||::::::   |||   :::|||||||||   |||:::   |||
Db         766 TACACGGACAGCACCTTGCAAACTGTCAAGCTCAAGGGGCACGGGCATGCCACCAATGAG 825

Qy         133 HisTrpTyrLysLysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIleArg 152
               |||:::|||:::|||:::||||||||||||||||||||||||||||||||   :::|||
Db         826 CACTACTACCGCAAGGTCGACGGCGTGTGGAAGTTTGCCGGCCTGAAACCTACCGTGCGG 885

Qy         153 TrpGlyGluPheAspPheAspArgIlePhe 162
               |||   |||:::   |||:::   :::|||
Db         886 TGGAATGAGTATCAATTCGAGGATGTCTTC 915

RESULT 8
AY098657
LOCUS       AY098657                424 bp    DNA     linear   PLN 16-JAN-2003
DEFINITION  Ophiostoma floccosum isolate GR10 scytalone dehydratase (SD) gene,
            partial cds.
ACCESSION   AY098657
VERSION     AY098657.1  GI:21238823
KEYWORDS    .
SOURCE      Ophiostoma floccosum
  ORGANISM  Ophiostoma floccosum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE   1  (bases 1 to 424)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Inhibitors and genetic analysis of scytalone dehydratase confirm
            the presence of DHN-melanin pathway in sapstain fungi
  JOURNAL   Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE   2  (bases 1 to 424)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2002) Wood Science, University of British
            Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .424
                     /organism="Ophiostoma floccosum"
                     /mol_type="genomic DNA"
                     /isolate="GR10"
                     /db_xref="taxon:104300"
                     /country="United Kingdom"
     gene            <1. .>424
                     /gene="SD"
     mRNA            join(<1. .69,132. .>424)
                     /gene="SD"
                     /product="scytalone dehydratase"
     CDS             join(<1. .69,132. .>424)
                     /gene="SD"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAM34803.1"
                     /db_xref="GI:21238824"
                     /translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPAEEFIG
                     MISDPSVLGNPLLRTQHFFGASRWERISDTEVVGYHQLRVPHQVYTDTTLTQVAVKGH
                     AHSANTHWYRKVDGVWKFA"
ORIGIN

Alignment Scores:
Pred. No.:              1.66e-52        Length:         424
Score:                  495.00          Matches:        90
Percent Similarity:     74.5%           Conservative:   15
Best Local Similarity:  63.8%           Mismatches:     15
Query Match:            52.5%           Indels:         22
DB:                     4               Gaps:           1

US-10-507-132-2 (1-172) x AY098657 (1-424)

Qy          25 GluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLysValIleAlaPro 44
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Db          1 GAGTGGGCGGACAGGTACGATTCCAAGGACTGGGACCGTCTGCGCAAGTGCATTGCTCCC 60

Qy         45 ThrLeu---------------------------------------------------------- 46
              ||||||
Db         61 ACTCTGCGAGTACGTCTTATACAACCCTGCTTTCTCTATTAACCCATAAAGATCTTCTTG 120

Qy         47 ---------ArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetProAla 63
                      |||   |||||||||||||||||:::|||||||||||||||||||||||
Db        121 CTAACAGACAGATC-GACTACCGCTCGTTCCTGAACAAGCTGTGGGAGGCCATGCCGGCC 179

Qy         64 GluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThrLeuArgThr 83
              |||||||||:::||||||:::|||          :::||||||:::|||   |||||||||
Db        180 GAAGAGTTTATCGGCATGATCTCCGACCCCAGCGTTCTCGGCAACCCCCTGCTGCGCACA 239

Qy         84 GlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluValIleGlyTyr 103
              |||||||||   |||   :::|||||||||:::::|||:::   |||||||:::||||||
Db        240 CAACACTTCTTCGGCGCCTCGCGCTGGGAGCGCATCTCCGACACCGAGGTCGTGGGCTAC 299

Qy        104 HisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMet 123
              ||||||||||||||||||||||    |||   |||||||||:::   :::|||   :::
Db        300 CATCAGCTGCGCGTCCCCCACCAGGTCTACACAGATACCACTCTCACACAAGTTGCCGTC 359

Qy        124 LysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGlyValTrpLys 143
              ||||||||||||||||||||||   |||||||||:::|||:::|||||||||||||||
Db        360 AAGGGCCACGCCCACTCGGCCAACACCCACTGGTACCGCAAGGTCGACGGCGTCTGGAAG 419

Qy        144 Phe 144
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Db        420 TTC 422
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RESULT 9
AY098660
LOCUS AY098660 423 bp DNA linear PLN 16-JAN-2003
DEFINITION Ophiostoma piceae isolate 187-1 scytalone dehydratase (SD) gene, partial cds.
ACCESSION AY098660
VERSION AY098660.1 GI:21238829
KEYWORDS .
SOURCE Ophiostoma piceae
ORGANISM Ophiostoma piceae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE 1 (bases 1 to 423)
AUTHORS Fleet,C. and Breuil,C.
TITLE Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi
JOURNAL Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE 2 (bases 1 to 423)
AUTHORS Fleet,C. and Breuil,C.
TITLE Direct Submission
JOURNAL Submitted (22-APR-2002) Wood Science, University of British Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES Location/Qualifiers
source 1. .423
/organism="Ophiostoma piceae"
/mol_type="genomic DNA"
/isolate="187-1"
/db_xref="taxon:61273"
/country="Canada"
gene <1. .>423
/gene="SD"
mRNA join(<1. .69,128. .>423)
/gene="SD"
/product="scytalone dehydratase"
CDS join(<1. .69,128. .>423)
/gene="SD"
/codon_start=1
/product="scytalone dehydratase"
/protein_id="AAM34806.1"
/db_xref="GI:21238830"
/translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIG
MISDPNVLGNPLLRTQHFFGASRWERVSDTEVIGYHQLRVPHQVYTDASLSTVAVKGH
AHSANQHWYRKVDGVWKFAG"
ORIGIN

Alignment Scores:

Pred. No.:	1.91e-52	Length:	423
Score:	494.50	Matches:	91
Percent Similarity:	74.5%	Conservative:	14
Best Local Similarity:	64.5%	Mismatches:	16
Query Match:	52.5%	Indels:	20
DB:	4	Gaps:	1

US-10-507-132-2 (1-172) x AY098660 (1-423)

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Qy         25 GluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLysValIleAlaPro 44
              ||||||||||||   ||||||||||||||||||||||||||||||||   |||||||||
Db          1 GAGTGGGCGGACAGGTACGACTCCAAGGACTGGGACCGCCTGCGCAAGTGCATTGCCCCG 60

Qy         45 ThrLeuArg------------------------------------------------------ 47
              |||||||||
Db         61 ACGCTGCGGGTATGTGCAATTTCACCTGGGAGACAAGACACAGAGCCACAATAACTAACA 120

Qy         48 -------IleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetProAlaGluGl 65
                    ||||||||||||||||||||:::|||||||||||||||||||||||||:::||
Db        121 CTCACAGATCGATTACCGGTCGTTTCTGAACAAGCTCTGGGAGGCCATGCCGGCAGATGA 180

Qy         65 uPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThrLeuArgThrGlnHi 85
              ||||:::|||||:::|||          :::||||||:::|||   ||||||||||||||
Db        181 GTTTATCGGCATGATCTCGGACCCCAACGTCCTCGGCAACCCCCTGCTACGGACACAACA 240

Qy         85 sPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluValIleGlyTyrHisGl 105
              ||||   |||   :::|||||||||:::||||||:::   |||||||||||||||||||
Db        241 CTTCTTTGGCGCCTCGCGCTGGGAACGCGTCTCCGATACGGAGGTTATTGGCTACCACCA 300

Qy        105 nLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGl 125
              ||||||||||||||||||   |||   |||   ::::::      |||   :::|||||
Db        301 GCTGCGCGTCCCCCACCAGGTCTACACCGACGCCTCCCTGTCGACCGTTGCCGTCAAGGG 360

Qy        125 yHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGlyValTrpLysPheAl 145
              ||||||||||||||||||   |||||||||:::|||:::|||||||||||||||||||||
Db        361 CCACGCACACTCGGCCAACCAGCACTGGTACCGCAAGGTTGACGGCGTCTGGAAGTTCGC 420

Qy        145 a 145
              |
Db        421 C 421
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RESULT 10
AY098654
LOCUS AY098654 432 bp DNA linear PLN 16-JAN-2003
DEFINITION Ceratocystis pinicola scytalone dehydratase (SD) gene, partial cds.
ACCESSION AY098654
VERSION AY098654.1 GI:21238817
KEYWORDS .
SOURCE Ceratocystis pinicola
ORGANISM Ceratocystis pinicola
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Microascales; Microascales incertae sedis; Ceratocystis.
REFERENCE 1 (bases 1 to 432)
AUTHORS Fleet,C. and Breuil,C.
TITLE Inhibitors and genetic analysis of scytalone dehydratase confirm the presence of DHN-melanin pathway in sapstain fungi
JOURNAL Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE 2 (bases 1 to 432)
AUTHORS Fleet,C. and Breuil,C.
TITLE Direct Submission
JOURNAL Submitted (22-APR-2002) Wood Science, University of British Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES Location/Qualifiers
source 1. .432
/organism="Ceratocystis pinicola"
/mol_type="genomic DNA"
/isolate="0901"
/db_xref="taxon:72031"

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                     /country="United Kingdom"
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     mRNA            join(<1. .69,138. .>432)
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                     /product="scytalone dehydratase"
     CDS             join(<1. .69,138. .>432)
                     /gene="SD"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAM34800.1"
                     /db_xref="GI:21238818"
                     /translation="EWADWYDSKDWDRLRRTIAPTLRIDYRSFLDKLWEAMPAEDFIK
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                     AHSANKHWYKKVDGVWKFA"
ORIGIN

Alignment Scores:
Pred. No.:              3.03e-52        Length:         432
Score:                  493.00          Matches:        91
Percent Similarity:     72.9%           Conservative:   14
Best Local Similarity:  63.2%           Mismatches:     16
Query Match:            52.3%           Indels:         24
DB:                     4               Gaps:           1

US-10-507-132-2 (1-172) x AY098654 (1-432)

Qy         25 GluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLysValIleAlaPro 44
              ||||||||||||   ||||||||||||||||||||||||||||:::   ||||||||||
Db          1 GAGTGGGCGGACTGGTACGATAGCAAAGACTGGGACCGTCTGCGTCGTACTATTGCCCCA 60

Qy         45 ThrLeu---------------------------------------------------- 46
              ||||||
Db         61 ACATTAAGAGTAAGCATCCCTCGCCAGTACAGGAGAATATATATCAGTTCTTACTAACAA 120

Qy         47 --------------ArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMet 61
                           |||   ||||||||||||||||||||||||||||||||||||||
Db        121 CATATATGTTTTGCTAGATC-GACTATCGCTCGTTCCTGGATAAGCTGTGGGAAGCCATG 179

Qy         62 ProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThrLeu 81
              |||||||||:::|||:::   |||:::|||         :::||||||||||||   |||
Db        180 CCTGCCGAGGACTTCATCAAGATGATTTCCGACCCCAACGTCCTCGGCGACCCTCTACTG 239

Qy         82 ArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluValIle 101
              :::|||||||||||||:::|||   :::|||||||||:::|||||||:::|||||||||:::
Db        240 AAGACCCAGCACTTCGTCGGTGCTTCGCGCTGGGAGCGTGTTAGTGATGACGAGGTCGTT 299

Qy        102 GlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluVal 121
              |||:::||||||||||||||||||||||||||||||   |||   |||         |||
Db        300 GGCTGGCACCAGCTACGTGTGCCCCACCAACGCTACACCGATGCTACAAAGACCACTGTC 359

Qy        122 ThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGlyVal 141
                 :::|||||||||||||||||||||||   ||||||||||||||:::|||||||||
Db        360 AAGGTCAAGGGCCACGCCCACTCGGCTAACAAGCACTGGTATAAGAAGGTAGATGGCGTC 419

Qy        142 TrpLysPheAla 145
              ||||||||||||
Db        420 TGGAAATTTGCG 431

RESULT 11
AY098659
LOCUS       AY098659                 428 bp    DNA     linear   PLN 16-JAN-2003
DEFINITION  Ophiostoma minus isolate OM3 scytalone dehydratase (SD) gene,
            partial cds.
ACCESSION   AY098659
VERSION     AY098659.1  GI:21238827
KEYWORDS    .
SOURCE      Ophiostoma minus
  ORGANISM  Ophiostoma minus
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE   1  (bases 1 to 428)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Inhibitors and genetic analysis of scytalone dehydratase confirm
            the presence of DHN-melanin pathway in sapstain fungi
  JOURNAL   Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE   2  (bases 1 to 428)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2002) Wood Science, University of British
            Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .428
                     /organism="Ophiostoma minus"
                     /mol_type="genomic DNA"
                     /isolate="OM3"
                     /db_xref="taxon:150568"
                     /country="United Kingdom"
     gene            <1. .>428
                     /gene="SD"
     mRNA            join(<1. .69,133. .>428)
                     /gene="SD"
                     /product="scytalone dehydratase"
     CDS             join(<1. .69,133. .>428)
                     /gene="SD"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAM34805.1"
                     /db_xref="GI:21238828"
                     /translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIS
                     MISDPSVLGNPLLRTQHSFGASRWGRVSDTEVIGYHQLRVPHQVYTDASLSTVAVKGH
                     AHSANQHWYRKVDGVWKFAG"
ORIGIN

Alignment Scores:
Pred. No.:              8.25e-52        Length:         428
Score:                  489.50          Matches:        88
Percent Similarity:     71.8%           Conservative:   14
Best Local Similarity:  62.0%           Mismatches:     19
Query Match:            52.0%           Indels:         21
DB:                     4               Gaps:           1

US-10-507-132-2 (1-172) x AY098659 (1-428)

Qy         25 GluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLysValIleAlaPro 44
              ||||||||||||   ||||||||||||||||||||||||||||||||||   ||||||||||
Db          1 GAGTGGGCGGACAGGTACGACTCCAAGGACTGGGACCGCCTGCGCAAGTGCATTGCACCG 60

Qy         45 ThrLeuArg------------------------------------------------- 47
              ||||||||
Db         61 ACTCTGCGGGTATGCACATTACATCTCTTGGGACATGCAGACGCACAGACCGACTGACTG 120

Qy         48 ------------IleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetProAla 63
                         |||||||||||||||||||:::|||||||||||||||||||||||||
Db        121 ACTGACTGACAGATCGACTACCGCTCGTTTCTAAACAAGCTCTGGGAGGCCATGCCGGCA 180

Qy         64 GluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThrLeuArgThr 83
              :::||||||:::   |||:::|||         :::||||||:::|||   ||||||||||
Db        181 GACGAGTTTATCAGCATGATCTCGGACCCCAGCGTCCTCGGCAACCCCCTGCTGCGCACA 240

Qy         84 GlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluValIleGlyTyr 103
              ||||||      |||   :::||||||   :::||||||:::   ||||||||||||||||
Db        241 CAGCACTCTTTTGGCGCCTCGCGCTGGGGACGCGTCTCCGACACCGAGGTCATTGGCTAC 300

Qy        104 HisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMet 123
              ||||||||||||||||||||||   |||   |||   ::::::      |||   :::
Db        301 CACCAGCTGCGCGTCCCCCACCAGGTCTACACCGACGCCTCCCTGTCGACCGTGGCCGTC 360

Qy        124 LysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGlyValTrpLys 143
              ||||||||||||||||||||||   ||||||||:::|||:::||||||||||||||||||
Db        361 AAGGGCCACGCACACTCGGCCAACCAGCACTGGTACCGCAAGGTCGACGGCGTCTGGAAG 420

Qy        144 PheAla 145
              ||||||
Db        421 TTCGCC 426
```

```
RESULT 12
AY098661
LOCUS       AY098661                 421 bp    DNA     linear   PLN 16-JAN-2003
DEFINITION  Ophiostoma piceae isolate W5 scytalone dehydratase (SD) gene,
            partial cds.
ACCESSION   AY098661
VERSION     AY098661.1  GI:21238831
KEYWORDS    .
SOURCE      Ophiostoma piceae
  ORGANISM  Ophiostoma piceae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE   1  (bases 1 to 421)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Inhibitors and genetic analysis of scytalone dehydratase confirm
            the presence of DHN-melanin pathway in sapstain fungi
  JOURNAL   Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE   2  (bases 1 to 421)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2002) Wood Science, University of British
            Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .421
                     /organism="Ophiostoma piceae"
                     /mol_type="genomic DNA"
                     /isolate="W5"
                     /db_xref="taxon:61273"
                     /country="Austria"
     gene            <1. .>421
                     /gene="SD"
     mRNA            join(<1. .69,126. .>421)
                     /gene="SD"
                     /product="scytalone dehydratase"
     CDS             join(<1. .69,126. .>421)
                     /gene="SD"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAM34807.1"
                     /db_xref="GI:21238832"
                     /translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIG
                     MISDPNVLGNPLLRTQHFFGASRWERVSDTEVIGYHQLRVPHQVYTDASLSTVAVKGH
                     AHSANQHWYRKVDGVWKFAG"
ORIGIN

Alignment Scores:
Pred. No.:              9.34e-52        Length:         421
Score:                  489.00          Matches:        90
Percent Similarity:     74.3%           Conservative:   14
Best Local Similarity:  64.3%           Mismatches:     17
Query Match:            51.9%           Indels:         20
DB:                     4               Gaps:           1

US-10-507-132-2 (1-172) x AY098661 (1-421)

Qy         25 GluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLysValIleAlaPro 44
              ||||||||||||   ||||||||||||||||||||||||||||||||   |||||||||
Db          1 GAGTGGGCGGACAGGTACGACTCTAAGGACTGGGACCGCCTGCGCAAGTGCATTGCCCCG 60

Qy         45 ThrLeu---------------------------------------------------------- 46
              ||||||
Db         61 ACGCTGCGGGTATGTGCGATTTCACCTGGGAGACAAGACAGAGCCACAATAACTAACAAT 120

Qy         47 ---ArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetProAlaGluGlu 65
                  |||   ||||||||||||||||||:::|||||||||||||||||||||||||:::|||
Db        121 AACAGATC-GATTACCGGTCGTTTCTGAACAAGCTCTGGGAGGCCATGCCGGCAGATGAG 179

Qy         66 PheValGlyMetValSerSerLysGlnMetLeuGlyAspProThrLeuArgThrGlnHis 85
              |||:::||||||:::|||          :::||||||:::|||   ||||||||||||||
Db        180 TTTATCGGCATGATCTCGGACCCCAACGTCCTCGGCAACCCCCTGCTACGCACACAACAC 239

Qy         86 PheIleGlyGlyThrArgTrpGluLysValSerGluAspGluValIleGlyTyrHisGln 105
              |||   |||   :::||||||||||:::|||||||:::   ||||||||||||||||||||

Db        240 TTCTTTGGCGCCTCACGCTGGGAACGCGTCTCCGATACGGAGGTCATTGGCTACCACCAG 299

Qy        106 LeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGly 125
              ||||||||||||||||||   |||   |||   ::::::      |||   :::||||||
Db        300 CTGCGCGTCCCCCACCAGGTCTACACCGACGCCTCCCTGTCGACCGTTGCCGTCAAGGGC 359

Qy        126 HisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGlyValTrpLysPheAla 145
              ||||||||||||||||||   |||||||||:::|||:::||||||||||||||||||||
Db        360 CACGCACACTCGGCCAACCAGCACTGGTACCGCAAGGTTGACGGCGTCTGGAAGTTTGCC 419

RESULT 13
AY098655
LOCUS       AY098655                 433 bp    DNA     linear   PLN 16-JAN-2003
DEFINITION  Ceratocystis resinifera scytalone dehydratase (SD) gene, partial
            cds.
ACCESSION   AY098655
VERSION     AY098655.1  GI:21238819
KEYWORDS    .
SOURCE      Ceratocystis resinifera
  ORGANISM  Ceratocystis resinifera
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Microascales; Microascales incertae sedis;
            Ceratocystis.
REFERENCE   1  (bases 1 to 433)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Inhibitors and genetic analysis of scytalone dehydratase confirm
            the presence of DHN-melanin pathway in sapstain fungi
  JOURNAL   Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE   2  (bases 1 to 433)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2002) Wood Science, University of British
            Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .433
                     /organism="Ceratocystis resinifera"
                     /mol_type="genomic DNA"
                     /isolate="125-214"
                     /db_xref="taxon:95837"
                     /country="Canada"
     gene            <1. .>433
                     /gene="SD"
     mRNA            join(<1. .69,138. .>433)
                     /gene="SD"
                     /product="scytalone dehydratase"
     CDS             join(<1. .69,138. .>433)
                     /gene="SD"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAM34801.1"
                     /db_xref="GI:21238820"
                     /translation="EWADRYDSKDWDRLXRTIAPTLRIDYRSFLDKLWEAMPAEDFIK
                     MISDPNVLGDPLLKTQHFVGASRWERVSDDEVVGWHQLRVPHQRYTDATKTTVKVKGH
                     AHSANKHWYKKVDGVWKFAG"
ORIGIN

Alignment Scores:
Pred. No.:              9.67e-52        Length:         433
Score:                  489.00          Matches:        90
Percent Similarity:     72.2%           Conservative:   14
Best Local Similarity:  62.5%           Mismatches:     17
Query Match:            51.9%           Indels:         24
DB:                     4               Gaps:           1

US-10-507-132-2 (1-172) x AY098655 (1-433)

Qy         25 GluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLysValIleAlaPro 44
              ||||||||||||   ||||||||||||||||||||||||||||||||   :::   |||||||||
Db          1 GAGTGGGCGGACAGGTATGACAGCAAGGATTGGGACCGTCTGNGTCGTACCATTGCCCCA 60

Qy         45 ThrLeu---------------------------------------------------------- 46
              ||||||
Db         61 ACACTAAGAGTGAGCATCTCTCGCTGATATAGCAGAATATATCTTAGTTCTTACTAACAA 120
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```
Qy         47 --------------ArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMet 61
                            |||  ||||||||||||||||||||||||||||||||||||||
Db        121 CATATATGTTTTGCTAGATC-GACTACCGCTCGTTCCTGGATAAGCTATGGGAAGCAATG 179

Qy         62 ProAlaGluGluPheValGlyMetValSerSerLysGlnMetLeuGlyAspProThrLeu 81
              |||||||||:::|||:::   |||:::|||         :::||||||||||||   |||
Db        180 CCTGCCGAGGACTTTATTAAGATGATCTCCGACCCCAACGTTCTCGGCGACCCTCTACTA 239

Qy         82 ArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluValIle 101
              :::|||||||||||:::|||   :::|||||||||:::|||||||:::|||||||||::: 
Db        240 AAGACCCAGCACTTCGTCGGCGCTTCGCGCTGGGAGCGTGTTAGTGACGATGAAGTCGTT 299

Qy        102 GlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGluVal 121
              |||:::|||||||||||||||||||||||||||||   |||   |||         |||
Db        300 GGCTGGCACCAGCTACGTGTGCCCCACCAGCGCTACACTGATGCTACGAAGACCACCGTC 359
                .
Qy        122 ThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGlyVal 141
                 :::|||||||||||||||||||||||   ||||||||||||||:::|||||||||
Db        360 AAGGTCAAAGGCCACGCCCACTCAGCCAACAAGCACTGGTACAAGAAGGTAGATGGCGTC 419

Qy        142 TrpLysPheAla 145
              ||||||||||||
Db        420 TGGAAGTTTGCC 431
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```
RESULT 14
AY098663
LOCUS       AY098663                414 bp    DNA     linear   PLN 16-JAN-2003
DEFINITION  Ophiostoma piliferum isolate 198-2GF scytalone dehydratase (SD)
            gene, partial cds.
ACCESSION   AY098663
VERSION     AY098663.1  GI:21238835
KEYWORDS    .
SOURCE      Ophiostoma piliferum
  ORGANISM  Ophiostoma piliferum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE   1  (bases 1 to 414)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Inhibitors and genetic analysis of scytalone dehydratase confirm
            the presence of DHN-melanin pathway in sapstain fungi
  JOURNAL   Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE   2  (bases 1 to 414)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2002) Wood Science, University of British
            Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .414
                     /organism="Ophiostoma piliferum"
                     /mol_type="genomic DNA"
                     /isolate="198-2GF"
                     /db_xref="taxon:38032"
                     /country="United Kingdom"
     gene            <1. .>414
                     /gene="SD"
     mRNA            join(<1. .69,119. .>414)
                     /gene="SD"
                     /product="scytalone dehydratase"
     CDS             join(<1. .69,119. .>414)
                     /gene="SD"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAM34809.1"
                     /db_xref="GI:21238836"
                     /translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIG
                     MISDPSVLGNPLLRTQHFFGASRWERISDTEVVGHRQLRVPHQVYTDATLSQVAVKGH
                     AHSANTHWYRKVDGVWKFAG"
ORIGIN

Alignment Scores:
Pred. No.:              1.63e-51        Length:         414
Score:                  487.00          Matches:        88
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Percent Similarity:     76.1%           Conservative:   17
Best Local Similarity:  63.8%           Mismatches:     16
Query Match:            51.7%           Indels:         17
DB:                     4               Gaps:           1

US-10-507-132-2 (1-172) x AY098663 (1-414)

Qy         25 GluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLysValIleAlaPro 44
              ||||||||||||   ||||||||||||||||||||||||||||||||   |||||||||
Db          1 GAGTGGGCGGACAGGTACGACTCCAAGGACTGGGACCGTCTGCGCAAGTGCATCGCTCCC 60

Qy         45 ThrLeuArg----------------------------------------------------Il 48
              ||||||||                                                    ||
Db         61 ACCCTCCGTGTAAGCACCCTCCCCTTCACTATGCTGCCCGACGGCTGCTGACCGACAGAT 120

Qy         48 eAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetProAlaGluGluPheValGl 68
              ||||||||||||||||||:::|||||||||||||||||||||||:::|||||||:::||
Db        121 CGACTACCGCTCGTTCCTCAACAAGCTGTGGGAGGCCATGCCGGCCGACGAGTTCATCGG 180

Qy         68 yMetValSerSerLysGlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIleGl 88
              ||||:::|||         :::||||||:::|||   ||||||||||||||||   ||
Db        181 CATGATCTCCGACCCCAGCGTGCTCGGCAACCCGCTGCTGCGCACCCAGCACTTCTTCGG 240

Qy         88 yGlyThrArgTrpGluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgVa 108
              |  :::|||||||||:::::|||:::   ||||||:::|||:::   ||||||||||||
Db        241 CGCCTCGCGCTGGGAGCGCATCTCCGACACCGAGGTCGTCGGCCACCGCCAGCTGCGCGT 300

Qy        108 lProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlyHisAlaHi 128
              ||||||||||  |||   |||:::   :::|||  :::||||||||||||||||
Db        301 CCCCCACCAGGTCTACACCGATGCAACCCTCTCACAGGTCGCCGTCAAGGGCCACGCCCA 360

Qy        128 sSerAlaAsnLeuHisTrpTyrLysLysIleAspGlyValTrpLysPheAla 145
              ||||||||||   |||||||||:::|||:::||||||||||||||||||||
Db        361 CTCGGCCAACACCCACTGGTACCGCAAGGTCGACGGCGTCTGGAAGTTTGCC 412
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```
RESULT 15
AY098664
LOCUS       AY098664                414 bp    DNA     linear   PLN 16-JAN-2003
DEFINITION  Ophiostoma piliferum isolate 201-1A scytalone dehydratase (SD)
            gene, partial cds.
ACCESSION   AY098664
VERSION     AY098664.1  GI:21238837
KEYWORDS    .
SOURCE      Ophiostoma piliferum
  ORGANISM  Ophiostoma piliferum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE   1  (bases 1 to 414)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Inhibitors and genetic analysis of scytalone dehydratase confirm
            the presence of DHN-melanin pathway in sapstain fungi
  JOURNAL   Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE   2  (bases 1 to 414)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2002) Wood Science, University of British
            Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .414
                     /organism="Ophiostoma piliferum"
                     /mol_type="genomic DNA"
                     /isolate="201-1A"
                     /db_xref="taxon:38032"
                     /country="Austria"
     gene            <1. .>414
                     /gene="SD"
     mRNA            join(<1. .69,120. .>414)
                     /gene="SD"
                     /product="scytalone dehydratase"
     CDS             join(<1. .69,120. .>414)
                     /gene="SD"
                     /codon_start=1
                     /product="scytalone dehydratase"
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                     /protein_id="AAM34810.1"
                     /db_xref="GI:21238838"
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                     MISDPSVLGNPLLRTQHFFGASRWERISDTEVVGHHQLRVPHQVYTDATLSQVAVKGH
                     AHSANTHWYRKVDGVWKFA"
ORIGIN

Alignment Scores:
Pred. No.:              1.63e-51        Length:         414
Score:                  487.00          Matches:        88
Percent Similarity:     76.1%           Conservative:   17
Best Local Similarity:  63.8%           Mismatches:     16
Query Match:            51.7%           Indels:         18
DB:                     4               Gaps:           1

US-10-507-132-2 (1-172) x AY098664 (1-414)

Qy         25 GluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLysValIleAlaPro 44
              ||||||||||||   ||||||||||||||||||||||||||||||   |||||||||
Db          1 GAGTGGGCGGATAGGTACGACTCCAAGGACTGGGACCGTCTGCGCAAGTGCATCGCTCCC 60

Qy         45 ThrLeu----------------------------------------------------Arg 47
              ||||||                                                    |||
Db         61 ACCCTCCGTGTAAGCACCCTCCCCTTCACTATGCTGCACCGACAGCTGCTGACCGACAGA 120

Qy         48 IleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetProAlaGluGluPheVal 67
                ||||||||||||||||:::||||||||||||||||||||||:::||||||:::
Db        121 TC-GACTACCGCTCGTTCCTCAACAAGCTGTGGGAGGCCATGCCGGCCGACGAGTTCATC 179

Qy         68 GlyMetValSerSerLysGlnMetLeuGlyAspProThrLeuArgThrGlnHisPheIle 87
              ||||||:::|||         :::||||||:::|||   ||||||||||||||||||
Db        180 GGCATGATCTCCGACCCCAGCGTGCTCGGCAACCCGCTGCTGCGCACCCAGCACTTCTTC 239

Qy         88 GlyGlyThrArgTrpGluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArg 107
              |||   :::|||||||||:::::|||:::   ||||||:::|||:::||||||||||||
Db        240 GGCGCCTCGCGCTGGGAGCGCATCTCCGACACCGAGGTCGTCGGCCACCACCAGCTGCGC 299

Qy        108 ValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlyHisAla 127
              ||||||||||||   |||   |||   |||:::   :::|||   :::||||||||||||
Db        300 GTCCCCCACCAGGTCTACACCGATGCAACCCTCTCACAGGTCGCCGTCAAGGGCCACGCC 359

Qy        128 HisSerAlaAsnLeuHisTrpTyrLysLysIleAspGlyValTrpLysPheAla 145
              ||||||||||||   |||||||||:::|||:::||||||||||||||||||||
Db        360 CACTCGGCCAACACCCACTGGTACCGCAAGGTCGACGGCGTCTGGAAGTTTGCC 413


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Job time : 5111 secs
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: December 5, 2006, 01:03:51 ; Search time 200 Seconds
(without alignments)
393.206 Million cell updates/sec

Title: US-10-507-132-4
Perfect score: 172
Sequence: 1 MGSQVQKSDEITFSDYLGLM.....WGEFDFDRIFEDGRETFGDK 172

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2589342

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
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7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	172	100.0	172	7	ADC16593	Adc16593 Scytalone
2	97	56.4	172	7	ADC16591	Adc16591 Scytalone
3	7	4.1	98	4	AAG98943	Aag98943 E. coli g
4	7	4.1	132	5	ABP02041	Abp02041 Human ORF
5	7	4.1	187	8	ADS43113	Ads43113 Bacterial
6	7	4.1	191	10	AEE60274	Aee60274 Cat chlam
7	7	4.1	198	7	ADM04932	Adm04932 Human pro
8	7	4.1	198	9	AEC87862	Aec87862 Human cDN
9	7	4.1	225	8	ADX91359	Adx91359 Plant ful
10	7	4.1	251	7	ABO62543	Abo62543 Klebsiell
11	7	4.1	255	4	AAU21761	Aau21761 Novel hum
12	7	4.1	255	4	AAM83837	Aam83837 Human imm
13	7	4.1	255	7	ADC46402	Adc46402 Human neo
14	7	4.1	255	8	ADX79742	Adx79742 Plant ful
15	7	4.1	258	8	ADO02033	Ado02033 Thalecres
16	7	4.1	258	9	AEB92523	Aeb92523 Phenyl pr
17	7	4.1	258	10	AEF35108	Aef35108 A. thalia
18	7	4.1	286	2	AAW61477	Aaw61477 A. fumiga
19	7	4.1	287	9	ABM93344	Abm93344 M. xanthu
20	7	4.1	293	8	ADS22785	Ads22785 Bacterial
21	7	4.1	296	8	ADP45467	Adp45467 Human col
22	7	4.1	385	4	AAB98083	Aab98083 Human bra
23	7	4.1	385	5	AAU80276	Aau80276 Human KIA
24	7	4.1	388	4	ABB65417	Abb65417 Drosophil
25	7	4.1	429	7	ADM26078	Adm26078 Hyperther
26	7	4.1	450	4	AAU15851	Aau15851 Human nov
27	7	4.1	450	6	ABU54920	Abu54920 Human nov
28	7	4.1	463	7	ADB64726	Adb64726 Human pro
29	7	4.1	470	8	ADT71318	Adt71318 PUFA PKS
30	7	4.1	472	4	AAB98084	Aab98084 Human pro
31	7	4.1	472	5	AAU80277	Aau80277 Human CLZ
32	7	4.1	472	5	ABP43682	Abp43682 Human pro
33	7	4.1	489	6	ABU23300	Abu23300 Protein e
34	7	4.1	509	3	AAY91965	Aay91965 PMWaV-1 h
35	7	4.1	600	4	ABG07764	Abg07764 Novel hum
36	7	4.1	606	8	ABM80136	Abm80136 Tumour-as
37	7	4.1	619	4	AAU45500	Aau45500 Propionib
38	7	4.1	619	6	ABM42019	Abm42019 Propionib
39	7	4.1	626	2	AAW41501	Aaw41501 Human DP.
40	7	4.1	626	3	AAB07495	Aab07495 A T-cell
41	7	4.1	626	3	AAB07494	Aab07494 A T-cell
42	7	4.1	681	9	AEA21009	Aea21009 Novel hum
43	7	4.1	716	8	ADS23909	Ads23909 Bacterial
44	7	4.1	719	4	AAU21607	Aau21607 Novel hum
45	7	4.1	719	7	ADC46248	Adc46248 Human neo

ALIGNMENTS

RESULT 1
ADC16593
ID ADC16593 standard; protein; 172 AA.
XX
AC ADC16593;
XX
DT 18-DEC-2003 (first entry)
XX
DE Scytalone dehydrogenase #SEQ ID 4.
XX
KW Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor.
XX
OS Magnaporthe grisea.
XX
PN WO2003076628-A1.
XX
PD 18-SEP-2003.
XX
PF 24-FEB-2003; 2003WO-JP001980.
XX
PR 12-MAR-2002; 2002JP-00066955.
XX
PA (TSUB) KUMIAI CHEM IND CO LTD.
XX
PI Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;
XX
DR WPI; 2003-748394/70.
DR N-PSDB; ADC16592.
XX
PT Gene encoding for scytalone dehydrogenase (SCDH), useful for screening
PT for SCDH inhibitors and evaluating sensitivity to them.
XX
PS Claim 7; SEQ ID NO 4; 50pp; Japanese.
XX
CC The invention relates to a gene encoding scytalone dehydrogenase (SCDH),
CC that functions in the presence of an inhibitor, comprising an optionally
CC mutated, defined amino acid sequence given in the specification. Also
CC disclosed is a method for evaluating rice blast fungus (Pyricularia
CC oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase
CC inhibitors. The gene is useful for screening for new SCDH inhibitors and
CC evaluating sensitivity to them. The current sequence represents the
CC Scytalone dehydrogenase amino acid sequence.
XX
SQ Sequence 172 AA;

Query Match 100.0%; Score 172; DB 7; Length 172;

```
  Best Local Similarity   100.0%;  Pred. No. 3.3e-179;
  Matches  172;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60

Qy         61 MPAEEFVGMVSSKQVLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MPAEEFVGMVSSKQVLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE 120

Qy        121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172


RESULT 2
ADC16591
ID   ADC16591 standard; protein; 172 AA.
XX
AC   ADC16591;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Scytalone dehydrogenase #SEQ ID 2.
XX
KW   Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor.
XX
OS   Magnaporthe grisea.
XX
PN   WO2003076628-A1.
XX
PD   18-SEP-2003.
XX
PF   24-FEB-2003; 2003WO-JP001980.
XX
PR   12-MAR-2002; 2002JP-00066955.
XX
PA   (TSUB ) KUMIAI CHEM IND CO LTD.
XX
PI   Kaku K,  Watanabe S,  Kawai K,  Shimizu T,  Nagayama K;
XX
DR   WPI; 2003-748394/70.
DR   N-PSDB; ADC16590.
XX
PT   Gene encoding for scytalone dehydrogenase (SCDH), useful for screening
PT   for SCDH inhibitors and evaluating sensitivity to them.
XX
PS   Claim 1; SEQ ID NO 2; 50pp; Japanese.
XX
CC   The invention relates to a gene encoding scytalone dehydrogenase (SCDH),
CC   that functions in the presence of an inhibitor, comprising an optionally
CC   mutated, defined amino acid sequence given in the specification. Also
CC   disclosed is a method for evaluating rice blast fungus (Pyricularia
CC   oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase
CC   inhibitors. The gene is useful for screening for new SCDH inhibitors and
CC   evaluating sensitivity to them. The current sequence represents the
CC   Scytalone dehydrogenase amino acid sequence.
XX
SQ   Sequence 172 AA;

  Query Match             56.4%;  Score 97;  DB 7;  Length 172;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-97;
  Matches   97;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         76 LGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWY 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 LGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWY 135

Qy        136 KKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172
              ||||||||||||||||||||||||||||||||||||||
Db        136 KKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172


RESULT 3
AAG98943
ID   AAG98943 standard; protein; 98 AA.
XX
AC   AAG98943;
XX
DT   26-SEP-2001  (first entry)
XX
DE   E. coli growth and proliferation related protein sequence SEQ ID NO:413.
XX
KW   Escherichia coli; growth; proliferation; microbial; antimicrobial;
KW   bacterial infection; microorganism.
XX
OS   Escherichia coli.
XX
PN   WO200134810-A2.
XX
PD   17-MAY-2001.
XX
PF   09-NOV-2000; 2000WO-US030950.
XX
PR   09-NOV-1999;   99US-0164415P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Forsyth RA,  Ohlsen K,  Zyskind J;
XX
DR   WPI; 2001-335933/35.
DR   N-PSDB; AAH84614.
XX
PT   Novel nucleic acids that inhibit Escherichia coli proliferation, useful
PT   for screening for homologous genes and for designing expression vectors.
XX
PS   Claim 19; Page 476; 522pp; English.
XX
CC   AAH84373 to AAH84499 represent Escherichia coli growth and proliferation
CC   related DNA sequences (I). AAH84500 to AAH84670 encode the E. coli growth
CC   and proliferation related proteins given in AAG99078 and AAG98830 to
CC   AAG98999. (I) can be used as potential targets for the generation of new
CC   antimicrobial agents, and for identification of compounds which interact
CC   with the gene products of (I). In addition the expression of (I) and the
CC   purification of the proteins, the purified proteins can be used to
CC   generate reagents and screen small molecule libraries or other candidate
CC   compound libraries for compounds that can be further developed to yield
CC   novel antimicrobial compounds. In addition, nucleic acid probes
CC   complementary to (I) that are specific for particular species of
CC   microorganisms can be used to identify particular microorganism species
CC   in clinical specimens, therefore, providing a rapid and dependable method
CC   by which to identify the causative agents of a bacterial infection. Also,
CC   antibodies generated against proteins translated from mRNA transcribed
CC   from proliferation-required sequences can also be used to screen for
CC   specific microorganisms that produce such proteins in a species-specific
CC   manner. AAH84371 and AAH84670 represent sequencing primers used in the
CC   isolation of E. coli growth and proliferation related sequence, which are
CC   used in an example from the present invention
XX
SQ   Sequence 98 AA;

  Query Match              4.1%;  Score 7;  DB 4;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 44;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         46 LRIDYRS 52
              |||||||
Db         59 LRIDYRS 65


RESULT 4
ABP02041
ID   ABP02041 standard; protein; 132 AA.
XX
AC   ABP02041;
```

XX
DT 25-JUN-2002 (first entry)
XX
DE Human ORFX protein sequence SEQ ID NO:4064.
XX
KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis.
XX
OS Homo sapiens.
XX
PN WO200192523-A2.
XX
PD 06-DEC-2001.
XX
PF 29-MAY-2001; 2001WO-US010836.
XX
PR 30-MAY-2000; 2000US-0206132P.
PR 29-AUG-2000; 2000US-0228716P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach MD;
XX
DR WPI; 2002-106308/14.
DR N-PSDB; ABN17793.
XX
PT Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders.
XX
PS Disclosure; SEQ ID NO 4064; 1037pp; English.
XX
CC The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC disorder in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative disorders, disorders related to organ
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC storage disease, various immune deficiencies and disorders, infectious
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage. N.B. The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 132 AA;

Query Match 4.1%; Score 7; DB 5; Length 132;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 RLRKVIA 43
|||||||
Db 117 RLRKVIA 123

RESULT 5
ADS43113
ID ADS43113 standard; protein; 187 AA.
XX
AC ADS43113;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #21543.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 21543; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 187 AA;

Query Match 4.1%; Score 7; DB 8; Length 187;

```
  Best Local Similarity   100.0%;  Pred. No. 80;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          96 SEDEVIG 102
               |||||||
Db         154 SEDEVIG 160


RESULT 6
AEE60274
ID   AEE60274 standard; protein; 191 AA.
XX
AC   AEE60274;
XX
DT   09-FEB-2006  (first entry)
XX
DE   Cat chlamydia outer membrane protein SEQ ID NO: 69.
XX
KW   chlamydia infection; antibacterial; conjunctivitis; ophthalmological;
KW   pneumonia; antiinflammatory; respiratory-gen.; bronchitis; diagnostic;
KW   vaccine; outer membrane protein.
XX
OS   Chlamydia sp.
XX
PN   JP2005333964-A.
XX
PD   08-DEC-2005.
XX
PF   25-MAY-2004; 2004JP-00183135.
XX
PR   25-MAY-2004; 2004JP-00183135.
XX
PA   (UYYA-) UNIV YAMAGUCHI.
XX
PI   Shirai M,  Azuma Y,  Kuhara S,  Hattori S,  Fukushi H;
XX
DR   WPI; 2006-004059/01.
XX
PT   Novel nucleic acid derived from cat Chlamydia, useful as probe in
PT   detecting conjunctivitis, pneumonia or bronchitis.
XX
PS   Claim 6; SEQ ID NO 69; 19pp; Japanese.
XX
CC   The present sequence is one of a series of outer membrane proteins
CC   (AEE60274-AEE60310) derived from cat Chlamydia. The present invention
CC   relates to a 1166239 base nucleic acid sequence comprising the genome of
CC   cat Chlamydia (AEE60206) or a 7552 base sequence comprising a Chlamydia
CC   plasmid (AEE60207). Also claimed are cat Chlamydia proteins comprising:
CC   inclusion body membrane proteins (AEE60208-AEE60273); outer membrane
CC   proteins (AEE60274-AEE60310); type-3 secretion proteins (AEE60311-
CC   AEE60330); highly antigenic proteins (AEE60331-AEE60334); pathogenicity
CC   related proteins (AEE60335-AEE60392); heat shock proteins (AEE60393-
CC   AEE60400); and proteins which do not exist in pneumonia Chlamydia
CC   (AEE60401-AEE60526). Probes which target these nucleic acid or protein
CC   sequences are useful in screening methods, involving nucleic acid
CC   hybridization or base sequence determination, where the nucleic acid
CC   hybridization process is in situ hybridization or Southern hybridization
CC   process. Such screening methods are useful for detecting conjunctivitis,
CC   pneumonia and bronchitis, based on the presence or absence of a
CC   alteration in a gene (presence or absence of deletion or the point
CC   mutation). The disclosed sequences are also useful in producing vaccines
CC   for preventing infection of Chlamydia.
XX
SQ   Sequence 191 AA;

  Query Match             4.1%;  Score 7;  DB 10;  Length 191;
  Best Local Similarity   100.0%;  Pred. No. 82;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          27 ADSYDSK 33
               |||||||
Db          62 ADSYDSK 68


RESULT 7
ADM04932
ID   ADM04932 standard; protein; 198 AA.
XX
AC   ADM04932;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Human protein of the invention SEQ ID NO:3617.
XX
KW   human; gene therapy; diagnostic marker; pharmaceutical.
XX
OS   Homo sapiens.
XX
PN   EP1347046-A1.
XX
PD   24-SEP-2003.
XX
PF   12-APR-2002; 2002EP-00008400.
XX
PR   22-MAR-2002; 2002JP-00137785.
XX
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI   Isogai T,  Sugiyama T,  Otsuki T,  Wakamatsu A,  Sato H,  Ishii S;
PI   Yamamoto J,  Isono Y,  Hio Y,  Otsuka K,  Nagai K,  Irie R,  Tamechika I;
PI   Seki N,  Yoshikawa T,  Otsuka M,  Nagahari K,  Masuho Y;
XX
DR   WPI; 2003-723558/69.
DR   N-PSDB; ADM02489.
XX
PT   New polynucleotides and polypeptides are useful in gene therapy, for
PT   developing a diagnostic marker or medicines for regulating their
PT   expression and activity, or as a target of gene therapy.
XX
PS   Claim 1; SEQ ID NO 3617; 305pp; English.
XX
CC   The invention relates to a novel human polynucleotide and the encoded
CC   polypeptide. A polynucleotide of the invention may have a use in gene
CC   therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
CC   as a primer for synthesizing the polynucleotide or as a probe for
CC   detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC   useful in gene therapy, for developing a diagnostic marker or medicines
CC   for regulating their expression and activity, or as a target of gene
CC   therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC   are useful as pharmaceutical agents. The present sequence represents a
CC   protein sequence of the invention.
XX
SQ   Sequence 198 AA;

  Query Match             4.1%;  Score 7;  DB 7;  Length 198;
  Best Local Similarity   100.0%;  Pred. No. 85;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          76 LGDPTLR 82
               |||||||
Db           2 LGDPTLR 8


RESULT 8
AEC87862
ID   AEC87862 standard; protein; 198 AA.
XX
AC   AEC87862;
XX
DT   01-DEC-2005  (first entry)
XX
DE   Human cDNA clone protein NT2NE20159740, SEQ ID 3617.
XX
KW   Osteopathic; Cytostatic; Antiinflammatory; Gastrointestinal-Gen.;
KW   Antiulcer; Gene Therapy; Osteoporosis; cancer; inflammation; gastritis;
KW   stomach ulcer; gastrointestinal ulcer.
```

XX
OS Homo sapiens.
XX
PN EP1580263-A1.
XX
PD 28-SEP-2005.
XX
PF 12-APR-2002; 2004EP-00027348.
XX
PR 22-MAR-2002; 2002JP-00137785.
PR 12-APR-2002; 2002EP-00008400.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2005-667421/69.
DR N-PSDB; AEC85419.
XX
PT New full-length cDNA sequences, useful for treating diseases, e.g.
PT osteoporosis, cancer, inflammation, gastritis, or gastroduodenal ulcer.
XX
PS Example 3; SEQ ID NO 3617; 296pp; English.
XX
CC The present invention relates to novel human cDNAs (AEC84246-AEC86688)
CC encoding proteins AEC86689-AEC89131. The cDNAs are useful for analyzing
CC the functions of the proteins, and for developing medicines for diseases
CC e.g. osteoporosis, cancer, inflammation, gastritis, or gastroduodenal
CC ulcer. Note: The sequence data for this patent did not form part of the
CC printed specification but was obtained in electronic format directly from
CC EPO.
XX
SQ Sequence 198 AA;

Query Match 4.1%; Score 7; DB 9; Length 198;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         76 LGDPTLR 82
              |||||||
Db          2 LGDPTLR 8
```

RESULT 9
ADX91359
ID ADX91359 standard; protein; 225 AA.
XX
AC ADX91359;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polypeptide seqid 54023.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
DR WPI; 2004-180133/17.
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 54023; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 225 AA;

Query Match 4.1%; Score 7; DB 8; Length 225;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 QVQKSDE 10
              |||||||
Db         20 QVQKSDE 26
```

RESULT 10
ABO62543
ID ABO62543 standard; protein; 251 AA.
XX
AC ABO62543;
XX
DT 29-JUL-2004 (first entry)
XX
DE Klebsiella pneumoniae polypeptide seqid 9060.
XX
KW Recombinant expression vector; transcription regulatory element;
KW Klebsiella pneumoniae protein; antibacterial; Vaccine.
XX
OS Klebsiella pneumoniae.
XX
PN US6610836-B1.
XX
PD 26-AUG-2003.
XX
PF 27-JAN-2000; 2000US-00489039.
XX
PR 29-JAN-1999; 99US-0117747P.
XX

PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Breton GL, Osborne M;
XX
DR WPI; 2003-895346/82.
DR N-PSDB; ACH96094.
XX
PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
PT preparing a vaccine composition against Klebsiella pneumoniae.
XX
PS Disclosure; SEQ ID NO 9060; 932pp; English.
XX
CC The invention describes a new isolated nucleic acid encoding a Klebsiella
CC pneumoniae polypeptide. Also described are: a recombinant expression
CC vector comprising the nucleic acid, operably linked to a transcription
CC regulatory element; and a cell comprising the recombinant expression
CC vector. The nucleic acid is useful for preparing a vaccine composition
CC against Klebsiella pneumoniae. This is the amino acid sequence of a
CC Klebsiella pneumoniae polypeptide of the invention
XX
SQ Sequence 251 AA;

Query Match 4.1%; Score 7; DB 7; Length 251;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 140 GVWKFAG 146
|||||||
Db 212 GVWKFAG 218

RESULT 11
AAU21761
ID AAU21761 standard; protein; 255 AA.
XX
AC AAU21761;
XX
DT 06-DEC-2001 (first entry)
XX
DE Novel human neoplastic disease associated polypeptide #194.
XX
KW Human; neoplastic disease associated polypeptide; cancer;
KW hyperproliferative disorder; neural disorder; immune system disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW neuroprotective; cytostatic; anti inflammatory; vasotropic.
XX
OS Homo sapiens.
XX
PN WO200155163-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001358.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
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PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465558/50.
DR N-PSDB; AAS34960.
XX
PT Novel polypeptides and polynucleotides useful as diagnostic reagents to
PT diagnose diseases or disorders associated with aberrant expression or
PT activity of polypeptides, and for treating cancers, rheumatoid arthritis.
XX
PS Claim 11; SEQ ID NO 488; 687pp; English.
XX
CC The present invention relates to the isolation of novel human neoplastic
CC disease associated polypeptides, and cDNA (AAS34767-AAS35050) and DNA
CC sequences encoding for these polypeptides. The sequences of the invention
CC are useful in the diagnosis, treatment, prevention and/or prognosis of
CC disorders involving neoplastic disease such as hyperproliferative
CC disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem
CC glioma, adult liver cancer, childhood cerebellar astrocytoma, or
CC Hodgkin's lymphoma). The sequences of the invention may also be useful
CC for treating other disorders such as neural disorders, immune system
CC disorders, muscular disorders, reproductive disorders, gastrointestinal
CC disorders, pulmonary disorders, cardiovascular disorders and renal
CC disorders. The polynucleotide sequences of the invention are also useful
CC in gene therapy. AAU21568-AAU21851 represent the novel human neoplastic
CC disease associated polypeptides of the invention. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 255 AA;

Query Match 4.1%; Score 7; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 DRLRKVI 42
|||||||
Db 116 DRLRKVI 122

RESULT 12
AAM83837
ID AAM83837 standard; protein; 255 AA.
XX
AC AAM83837;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen SEQ ID NO:11430.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
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PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
DR N-PSDB; AAK56618.
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
PS Claim 11; SEQ ID NO 11430; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 255 AA;

Query Match 4.1%; Score 7; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 DRLRKVI 42
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Db 116 DRLRKVI 122

RESULT 13
ADC46402
ID ADC46402 standard; protein; 255 AA.
XX
AC ADC46402;

XX
DT 18-DEC-2003 (first entry)
XX
DE Human neoplastic disease-associated gene 40 protein #2.
XX
KW Neoplastic disease-associated polypeptide; gene therapy;
KW hyperproliferative disease; cancer; autoimmune disorder; diabetes;
KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;
KW autoimmune thyroiditis; haemolytic anaemia; haematopoietic disorder;
KW haematologic disorder; anaemia; thrombocytopaenia; allergic reaction;
KW asthma; eczema; inflammatory disorder; ischaemia-reperfusion injury;
KW inflammatory bowel disease; Crohn's disease; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; renal disorder;
KW acute glomerulonephritis; end-stage renal disease;
KW cardiovascular disorder; atherosclerosis; myocarditis;
KW infectious disease; AIDS; cachexia; anorexia; wound healing;
KW epithelial cell proliferation; Human.
XX
OS Homo sapiens.
XX
PN US2003082758-A1.
XX
PD 01-MAY-2003.
XX
PF 22-MAR-2002; 2002US-00103313.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
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PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.

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PR   17-NOV-2000; 2000US-0249297P.
PR   17-NOV-2000; 2000US-0249299P.
PR   17-NOV-2000; 2000US-0249300P.
PR   01-DEC-2000; 2000US-0250160P.
PR   01-DEC-2000; 2000US-0250391P.
PR   05-DEC-2000; 2000US-0251030P.
PR   05-DEC-2000; 2000US-0251988P.
PR   05-DEC-2000; 2000US-0256719P.
PR   06-DEC-2000; 2000US-0251479P.
PR   08-DEC-2000; 2000US-0251856P.
PR   08-DEC-2000; 2000US-0251868P.
PR   08-DEC-2000; 2000US-0251869P.
PR   08-DEC-2000; 2000US-0251989P.
PR   08-DEC-2000; 2000US-0251990P.
PR   11-DEC-2000; 2000US-0254097P.
PR   05-JAN-2001; 2001US-0259678P.
PR   17-JAN-2001; 2001US-00764854.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM,  Barash SC;
XX
DR   WPI; 2003-786918/74.
DR   N-PSDB; ADC46118.
XX
PT   New isolated human neoplastic disease-associated polypeptides and
PT   polynucleotides, useful for diagnosing, preventing, prognosticating or
PT   treating medical conditions such as cancer, AIDS, diabetes or Parkinson's
PT   disease.
XX
PS   Claim 11; SEQ ID NO 488; 302pp; English.
XX
CC   The invention relates to one of 238 disclosed human neoplastic disease-
CC   associated polypeptides encoded by 171 disclosed cDNA sequences
CC   (including their domains, epitopes, full-length proteins,allelic variants
CC   or species homologues). Also included are there encoding nucleic acids, a
CC   recombinant vector comprising the nucleic acid, a recombinant host cell
CC   comprising the nucleic acid (expressing the protein), an isolated
CC   antibody that binds specifically to the isolated polypeptide, preventing,
CC   treating or ameliorating a medical condition, diagnosing a pathological
CC   condition or a susceptibility to a pathological condition in a subject,
CC   identifying a binding partner to the polypeptide, identifying an activity
CC   in a biological assay, and the gene corresponding to the cDNA sequence.
CC   The polypeptides, polynucleotides and antibodies are useful for
CC   detecting, preventing, diagnosing, prognosticating, treating or
CC   ameliorating medical conditions such as hyperproliferative diseases or
CC   cancer, autoimmune disorders (e.g. diabetes, rheumatoid arthritis,
CC   systemic lupus erythematosus, multiple sclerosis, autoimmune thyroiditis
CC   or haemolytic anaemia), haematopoietic or haematologic disorders (e.g.
CC   anaemia or thrombocytopaenia), allergic reactions including asthma or
CC   eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury,

  Query Match             4.1%;  Score 7;  DB 7;  Length 255;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         36 DRLRKVI 42
              |||||||
Db        116 DRLRKVI 122


RESULT 14
ADX79742
ID   ADX79742 standard; protein; 255 AA.
XX
AC   ADX79742;
XX
DT   23-MAR-2006  (revised)
DT   21-APR-2005  (first entry)
XX
DE   Plant full length insert polypeptide seqid 49108.
XX
KW   plant protectant; plant growth regulant; gene therapy; plant;
KW   recombinant DNA construct; physical array; plant breeding marker;
KW   cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW   extreme osmotic condition; pathogen tolerance; pest tolerance;
KW   growth rate; cell cycle pathway; disease resistance;
KW   galactomannan production; lignin production; plant growth regulator;
KW   yield; plant growth; plant development; seed oil; protein yield;
KW   protein content.
XX
OS   Zea mays.
XX
PN   US2004034888-A1.
XX
PD   19-FEB-2004.
XX
PF   28-APR-2003; 2003US-00425114.
XX
PR   06-MAY-1999;   99US-00304517.
PR   05-NOV-2001; 2001US-00985678.
XX
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
XX
PI   Liu J,  Zhou Y,  Kovalic DK,  Screen SE,  Tabaska JE,  Cao Y;
XX
DR   WPI; 2004-180133/17.
XX
PT   New recombinant DNA construct, useful for improving plant tolerance to
PT   cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT   pests, for conferring increased resistance to plant disease, or for
PT   improving yield.
XX
PS   Claim 1; SEQ ID NO 49108; 15pp; English.
XX
CC   The invention describes a recombinant DNA construct comprising a
CC   polynucleotide consisting of a sequence encoding an amino acid sequence
CC   available in electronic form from the US patent office at
CC   ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC   of the invention are also useful in physical arrays of molecules and as
CC   plant breeding markers. The recombinant DNA construct is useful for
CC   improving plant tolerance to cold, heat, drought, herbicides, extreme
CC   osmotic conditions, pathogens or pests, for manipulating growth rate in
CC   plant cells by modification of the cell cycle pathway, for conferring
CC   increased resistance to plant disease, for producing galactomannan,
CC   lignin or plant growth regulators, for increasing the rate of homologous
CC   recombination in plants, for improving yield by modification of
CC   photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC   or by providing improved plant growth and development under at least one
CC   stress condition or for modifying seed oil or protein yield and/or
CC   content. This is the amino acid sequence of a plant full length insert
CC   polypeptide that can be used in the recombinant DNA construct of the
CC   invention.
CC
CC   Revised record issued on 23-MAR-2006 : Corrected organism line
XX
SQ   Sequence 255 AA;

  Query Match             4.1%;  Score 7;  DB 8;  Length 255;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GSQVQKS 8
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Db        115 GSQVQKS 121


RESULT 15
ADO02033
ID   ADO02033 standard; protein; 258 AA.
XX
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AC ADO02033;
XX
DT 01-JUL-2004 (first entry)
XX
DE Thalecress transcription factor protein #223.
XX
KW Thalecress; transcription factor; plant; transgenic; abiotic stress;
KW cold tolerance; heat tolerance; drought; osmotic stress;
KW phosphate limitation; potassium limitation; nitrogen limitation;
KW hormone sensitivity; disease resistance; sugar sensing; seed germination;
KW flowering; inflorescence architectural change;
KW meristem cell differentiation; phyllotaxy; apical dominance;
KW trichome development; seed development; premature senescence;
KW delayed senescence; lethality; necrosis; plant size; leaf morphology;
KW seed morphology; secondary metabolism; light response; shade avoidance.
XX
OS Arabidopsis thaliana.
XX
PN US2004045049-A1.
XX
PD 04-MAR-2004.
XX
PF 10-APR-2003; 2003US-00412699.
XX
PR 13-SEP-1999; 99US-00394519.
PR 21-JAN-2000; 2000US-00489376.
PR 17-FEB-2000; 2000US-00506720.
PR 22-MAR-2000; 2000US-00532591.
PR 22-MAR-2000; 2000US-00533029.
PR 22-MAR-2000; 2000US-00533030.
PR 22-MAR-2000; 2000US-00533392.
PR 22-MAR-2000; 2000US-00533648.
PR 06-APR-2000; 2000WO-US009448.
PR 16-NOV-2000; 2000US-00713994.
PR 27-MAR-2001; 2001US-00819142.
PR 17-APR-2001; 2001US-00837444.
PR 30-JAN-2002; 2002US-00958131.
PR 14-JUN-2002; 2002US-00171468.
PR 09-AUG-2002; 2002US-00225066.
PR 09-AUG-2002; 2002US-00225067.
PR 09-AUG-2002; 2002US-00225068.
PR 17-DEC-2002; 2002US-0434166P.
PR 25-FEB-2003; 2003US-00374780.
XX
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMAHA R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
XX
PI Zhang J, Fromm ME, Heard JE, Riechmann JL, Adam LJ, Broun PE;
PI Pineda O, Reuber TL, Keddie JS, Yu G, Jiang C, Samaha RS;
PI Pilgrim ML, Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R;
PI Sherman BK;
XX
DR WPI; 2004-225755/21.
DR N-PSDB; ADO02032.
XX
PT New transgenic plant, useful in developing phenotypes with altered or
PT improved characteristics or traits.
XX
PS Claim 1; SEQ ID NO 446; 213pp; English.
XX
CC The invention relates to a transgenic plant comprises a recombinant
CC polynucleotide having a polynucleotide sequence or its complementary
CC sequence comprising a sequence encoding a polypeptide, that initiates
CC transcription (i.e. a transcription factor) from Arabidopsis, Soybean,
CC Rice, Rape or Corn, comprising any of the sequences appearing as ADO01588
CC -ADO03527 or ADO03530-ADO03559. Also included are using a transgenic
CC plant to grow a progeny plant, an expression cassette (comprising a
CC constitutive, inducible or tissue-specific promoter and a recombinant
CC polynucleotide described above), a host cell comprising the expression
CC cassette, producing a modified plant having a modified trait, identifying
CC a factor that is modulated by or interacts with a polypeptide encoded by
CC the polynucleotide sequence and identifying at least one downstream
CC polynucleotide sequence that is subject to a regulatory effect of any of
CC the polypeptides encoded by the polynucleotide described above. The
CC transgenic plant is useful for producing a plant that has an altered
CC trait e.g. an enhanced tolerance to abiotic stress (increased tolerance
CC to chilling, germination in cold conditions,freezing tolerance, tolerance
CC to heat, tolerance to drought, tolerance to osmotic stress, tolerance to
CC salt, tolerance to phosphate limitation, tolerance to potassium
CC limitation, decreased sensitivity to nitrogen limitation), altered
CC hormone sensitivity, reduced sensitivity to abscisic acid, an altered
CC response to ethylene, disease resistance, altered susceptibility to
CC Botrytis, altered susceptibility to Fusarium, altered susceptibility to
CC Erysiphe, altered susceptibility to Pseudomonas syringae, altered
CC susceptibility to Sclerotinia, altered sugar sensing, improved seed
CC germination and seedling vigor, early flowering, late flowering, extended
CC period of flowering, an inflorescence architectural change, a change in
CC stem bifurcations, a lack of a shoot meristem, reduced meristem cell
CC differentiation, altered phyllotaxy, altered branching pattern, reduced
CC apical dominance, reduced trichome density, ectopic trichome development,
CC altered trichome development, altered stem morphology, increased root
CC growth, increased root hairs, altered seed development, altered cell
CC proliferation/cell differentiation, premature senescence, delayed
CC senescence, lethality, increased necrosis, an increase in seedling or
CC plant size, decreased plant size, a change in leaf morphology, increased
CC altered leaf development, increased leaf size and mass, glossy leaves,
CC leaf cell expansion, change in seed morphology, altered seed coloration,
CC increased seed size, decreased seed size, altered seed shape, change in
CC leaf biochemistry, increased leaf wax, an alteration in leaf prenyl lipid
CC content, increased leaf insoluble sugars, decreased leaf insoluble
CC sugars, increased leaf anthocyanins, an alteration of leaf fatty acid
CC content, an alteration of leaf glucosinolate content, change in seed
CC biochemistry, an increase in seed oil content, decrease in seed oil
CC content, increase in seed fatty acid content, decrease in seed fatty acid
CC content, increase in seed protein content, decrease in seed protein
CC content, alteration in seed prenyl lipid content, increase in seed
CC sterols, upregulation of genes involved in secondary metabolism, increase
CC in root anthocyanins, increase in plant anthocyanins, and alteration in
CC light response or shade avoidance. The present sequence represents a
CC thalecress transcription factor of the invention.
XX
SQ Sequence 258 AA;

Query Match 4.1%; Score 7; DB 8; Length 258;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 155 EFDFDRI 161
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Db 188 EFDFDRI 194

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Job time : 203 secs

OM protein - protein search, using sw model

Run on: December 5, 2006, 01:13:16 ; Search time 53 Seconds
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284.062 Million cell updates/sec

Title: US-10-507-132-4
Perfect score: 172
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 650591 seqs, 87530628 residues

Word size : 1

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7	4.1	64	2	US-09-270-767-41287	Sequence 41287, A
2	7	4.1	64	2	US-09-270-767-56503	Sequence 56503, A
3	7	4.1	98	2	US-09-711-164-413	Sequence 413, App
4	7	4.1	251	2	US-09-489-039A-9060	Sequence 9060, Ap
5	7	4.1	259	1	US-08-629-291A-30	Sequence 30, Appl
6	7	4.1	259	1	US-08-658-335B-30	Sequence 30, Appl
7	7	4.1	259	2	US-09-406-640-30	Sequence 30, Appl
8	7	4.1	286	2	US-09-319-806-4	Sequence 4, Appli
9	7	4.1	287	2	US-09-902-540-12543	Sequence 12543, A
10	7	4.1	294	2	US-09-230-637-31	Sequence 31, Appl
11	7	4.1	361	2	US-09-270-767-42397	Sequence 42397, A
12	7	4.1	463	2	US-10-104-047-2880	Sequence 2880, Ap
13	7	4.1	626	2	US-09-155-770-7	Sequence 7, Appli
14	7	4.1	806	2	US-09-949-016-8753	Sequence 8753, Ap
15	7	4.1	883	1	US-07-718-575-4	Sequence 4, Appli
16	7	4.1	883	1	US-08-481-206-4	Sequence 4, Appli
17	7	4.1	883	1	US-08-687-379-6	Sequence 6, Appli
18	7	4.1	883	1	US-08-687-379-8	Sequence 8, Appli
19	7	4.1	883	1	US-08-486-269A-4	Sequence 4, Appli
20	7	4.1	883	2	US-08-483-327-2	Sequence 2, Appli
21	7	4.1	883	2	US-08-666-221B-2	Sequence 2, Appli
22	7	4.1	883	2	US-08-666-221B-8	Sequence 8, Appli
23	7	4.1	883	2	US-08-400-067-1	Sequence 1, Appli
24	7	4.1	883	2	US-08-439-946-2	Sequence 2, Appli
25	7	4.1	883	2	US-08-242-344-2	Sequence 2, Appli
26	7	4.1	1323	1	US-08-026-138E-4	Sequence 4, Appli
27	7	4.1	1336	1	US-08-231-193A-58	Sequence 58, Appl
28	7	4.1	1336	1	US-08-486-273A-58	Sequence 58, Appl
29	7	4.1	1336	2	US-08-940-086A-58	Sequence 58, Appl
30	7	4.1	1336	2	US-08-940-035A-58	Sequence 58, Appl
31	7	4.1	1336	2	US-08-935-105A-58	Sequence 58, Appl
32	7	4.1	1336	2	US-09-648-797-58	Sequence 58, Appl
33	7	4.1	1336	2	US-09-386-123-58	Sequence 58, Appl
34	7	4.1	1336	2	US-10-038-937-58	Sequence 58, Appl
35	7	4.1	1336	2	US-10-007-747-58	Sequence 58, Appl
36	7	4.1	1336	2	US-09-945-901-58	Sequence 58, Appl
37	7	4.1	1345	2	US-09-949-016-11209	Sequence 11209, A
38	6	3.5	17	2	US-09-461-325-305	Sequence 305, App
39	6	3.5	17	2	US-10-012-542-305	Sequence 305, App
40	6	3.5	17	2	US-10-115-123-305	Sequence 305, App
41	6	3.5	18	1	US-08-640-847C-36	Sequence 36, Appl
42	6	3.5	37	1	US-08-448-481-5	Sequence 5, Appli
43	6	3.5	42	1	US-08-377-687-39	Sequence 39, Appl
44	6	3.5	42	1	US-08-777-192-39	Sequence 39, Appl
45	6	3.5	42	2	US-08-971-982-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-09-270-767-41287
; Sequence 41287, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41287
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-41287

Query Match 4.1%; Score 7; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 YRSFLDK 56
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Db 35 YRSFLDK 41

RESULT 2
US-09-270-767-56503
; Sequence 56503, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56503
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-56503

Query Match 4.1%; Score 7; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          50 YRSFLDK 56
               |||||||
Db          35 YRSFLDK 41


RESULT 3
US-09-711-164-413
; Sequence 413, Application US/09711164
; Patent No. 6589738
; GENERAL INFORMATION:
;  APPLICANT:  Forsyth, R. Allyn
;  APPLICANT:  Ohlsen, Kari
;  APPLICANT:  Zyskind, Judith
;  TITLE OF INVENTION:  GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERET
;  FILE REFERENCE:  ELITRA.008A
;  CURRENT APPLICATION NUMBER: US/09/711,164
;  CURRENT FILING DATE:  2000-11-09
;  PRIOR APPLICATION NUMBER:  US 60/164415
;  PRIOR FILING DATE:  1999-11-9
;  NUMBER OF SEQ ID NOS:  469
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 413
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Escherichia coli
US-09-711-164-413

  Query Match             4.1%;  Score 7;  DB 2;  Length 98;
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  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          46 LRIDYRS 52
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Db          59 LRIDYRS 65


RESULT 4
US-09-489-039A-9060
; Sequence 9060, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 9060
;   LENGTH: 251
;   TYPE: PRT
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9060

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Qy         140 GVWKFAG 146
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Db         212 GVWKFAG 218


RESULT 5
US-08-629-291A-30
; Sequence 30, Application US/08629291A
; Patent No. 5959174
;  GENERAL INFORMATION:
;    APPLICANT:  Coruzzi, Gloria
;    APPLICANT:  Oliveira, Igor
;    APPLICANT:  Lam, Hon-Ming
;    APPLICANT:  Hsieh, Ming-Hsuin
;    TITLE OF INVENTION:  PLANT GLUTAMATE RECEPTORS
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/629,291A
;      FILING DATE:  08-APR-1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  5914-050
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  259 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-629-291A-30

  Query Match             4.1%;  Score 7;  DB 1;  Length 259;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         162 FEDGRET 168
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Db          48 FEDGRET 54


RESULT 6
US-08-658-335B-30
; Sequence 30, Application US/08658335B
; Patent No. 5981703
;  GENERAL INFORMATION:
;    APPLICANT:  Coruzzi, Gloria
;    APPLICANT:  Oliveira, Igor
;    APPLICANT:  Lam, Hon-Ming
;    APPLICANT:  Hsieh, Ming-Hsiun
;    TITLE OF INVENTION:  PLANT GLUTAMATE RECEPTORS
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/658,335B
;      FILING DATE:  05-JUN-1996
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
```

```
;       NAME:  Coruzzi, Laura A.
;       REGISTRATION NUMBER:  30,742
;       REFERENCE/DOCKET NUMBER:  5914-052
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 790-9090
;       TELEFAX:  (212) 869-9741/8864
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  30:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  259 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-658-335B-30
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Query Match 4.1%; Score 7; DB 1; Length 259;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        162 FEDGRET 168
              |||||||
Db         48 FEDGRET 54
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RESULT 7
US-09-406-640-30
; Sequence 30, Application US/09406640
; Patent No. 6451546
;  GENERAL INFORMATION:
;       APPLICANT: Coruzzi, Gloria
;                  Oliveira, Igor
;                  Lam, Hon-Ming
;                  Hsieh, Ming-Hsiun
;       TITLE OF INVENTION: PLANT GLUTAMATE RECEPTORS
;       NUMBER OF SEQUENCES: 36
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: U.S.A.
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/406,640
;            FILING DATE: 27-Sep-1999
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Coruzzi, Laura A.
;            REGISTRATION NUMBER: 30,742
;            REFERENCE/DOCKET NUMBER: 5914-082
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-9741/8864
;            TELEX: 66141 PENNIE
;  INFORMATION FOR SEQ ID NO: 30:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 259 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-406-640-30
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Query Match 4.1%; Score 7; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        162 FEDGRET 168
              |||||||
Db         48 FEDGRET 54
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RESULT 8
US-09-319-806-4
; Sequence 4, Application US/09319806
; Patent No. 6830891
; GENERAL INFORMATION:
;  APPLICANT:  Crameri, Reto
;  APPLICANT:  Hemman, Stefanie
;  APPLICANT:  Blaser, Kurt
;  TITLE OF INVENTION:  Methods for Diagnosis of Allergic Bronchopulmonary
;  TITLE OF INVENTION:  Aspergillosis
;  FILE REFERENCE:  10806-93
;  CURRENT APPLICATION NUMBER: US/09/319,806
;  CURRENT FILING DATE:  1999-08-19
;  PRIOR APPLICATION NUMBER:  SE9604815-2
;  PRIOR FILING DATE:  1996-12-20
;  PRIOR APPLICATION NUMBER:  PCT/SE97/02171
;  PRIOR FILING DATE:  1997-12-19
;  NUMBER OF SEQ ID NOS:  8
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 286
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: recombinant
;   OTHER INFORMATION: allergan rAsp f4
US-09-319-806-4
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Query Match 4.1%; Score 7; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        153 WGEFDFD 159
              |||||||
Db        200 WGEFDFD 206
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```
RESULT 9
US-09-902-540-12543
; Sequence 12543, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 12543
;   LENGTH: 287
;   TYPE: PRT
;   ORGANISM: Myxococcus xanthus
US-09-902-540-12543
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Query Match 4.1%; Score 7; DB 2; Length 287;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         44 PTLRIDY 50
              |||||||
Db        232 PTLRIDY 238
```

```
RESULT 10
US-09-230-637-31
; Sequence 31, Application US/09230637
; Patent No. 6264958
; GENERAL INFORMATION:
;  APPLICANT:  Hayward, Gary
;  APPLICANT:  Nicholas, John
;  APPLICANT:  Hardwick, J. Marie
;  APPLICANT:  Reitz, Marvin
;  TITLE OF INVENTION:  No. 6264958el Genes of Kaposi's Sarcoma
;  TITLE OF INVENTION:  Associated Herpesvirus
;  FILE REFERENCE:  1107.78372
;  CURRENT APPLICATION NUMBER: US/09/230,637
;  CURRENT FILING DATE:  1999-11-23
;  PRIOR APPLICATION NUMBER:  60/022,591
;  PRIOR FILING DATE:  1996-07-25
;  PRIOR APPLICATION NUMBER:  PCT US 97/12931
;  PRIOR FILING DATE:  1997-07-24
;  NUMBER OF SEQ ID NOS:  62
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 31
;   LENGTH: 294
;   TYPE: PRT
;   ORGANISM: Herpes simplex
US-09-230-637-31

  Query Match             4.1%;  Score 7;  DB 2;  Length 294;
  Best Local Similarity   100.0%;  Pred. No. 36;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         51 RSFLDKL 57
              |||||||
Db         96 RSFLDKL 102


RESULT 11
US-09-270-767-42397
; Sequence 42397, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42397
;   LENGTH: 361
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-270-767-42397

  Query Match             4.1%;  Score 7;  DB 2;  Length 361;
  Best Local Similarity   100.0%;  Pred. No. 44;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         51 RSFLDKL 57
              |||||||
Db        270 RSFLDKL 276


RESULT 12
US-10-104-047-2880
; Sequence 2880, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: No. 6943241el full length cDNA
;  FILE REFERENCE: H1-A0105
;  CURRENT APPLICATION NUMBER: US/10/104,047
;  CURRENT FILING DATE:  2002-03-25
;  PRIOR APPLICATION NUMBER:
;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 4096
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2880
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-104-047-2880

  Query Match             4.1%;  Score 7;  DB 2;  Length 463;
  Best Local Similarity   100.0%;  Pred. No. 55;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         51 RSFLDKL 57
              |||||||
Db        177 RSFLDKL 183


RESULT 13
US-09-155-770-7
; Sequence 7, Application US/09155770A
; Patent No. 6300484
; GENERAL INFORMATION:
;  APPLICANT: Duhl, David
;  TITLE OF INVENTION: DNA ENCODING DP-75 AND A PROCESS FOR ITS USE
;  FILE REFERENCE: 200130.418
;  CURRENT APPLICATION NUMBER: US/09/155,770A
;  CURRENT FILING DATE: 1998-09-30
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 626
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-155-770-7

  Query Match             4.1%;  Score 7;  DB 2;  Length 626;
  Best Local Similarity   100.0%;  Pred. No. 72;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         36 DRLRKVI 42
              |||||||
Db         23 DRLRKVI 29


RESULT 14
US-09-949-016-8753
; Sequence 8753, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8753
;   LENGTH: 806
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-8753

  Query Match             4.1%;  Score 7;  DB 2;  Length 806;
  Best Local Similarity   100.0%;  Pred. No. 90;
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  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        162 FEDGRET 168
              |||||||
Db        615 FEDGRET 621


RESULT 15
US-07-718-575-4
; Sequence 4, Application US/07718575
; Patent No. 5202257
;  GENERAL INFORMATION:
;    APPLICANT:  Heinemann Ph.D., Stephen F.
;    APPLICANT:  Boulter Ph.D., James R.
;    APPLICANT:  Hollmann Ph.D., Michael NMN
;    APPLICANT:  Bettler Ph.D., Bernhard NMN
;    APPLICANT:  Jensen Ph.D., Jan E.
;    TITLE OF INVENTION:  GLUTAMATE RECEPTOR COMPOSITIONS AND
;    TITLE OF INVENTION:  METHODS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pretty, Schroeder, Brueggemann & Clark
;      STREET:  444 So. Flower St., Suite 2000
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  90071-2921
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/718,575
;      FILING DATE:  19910813
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Reiter Ph.D., Stephen E.
;      REGISTRATION NUMBER:  31192
;      REFERENCE/DOCKET NUMBER:  P31 8962
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619)535-8949
;      TELEX:  9103330318
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  883 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-718-575-4

  Query Match             4.1%;  Score 7;  DB 1;  Length 883;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        162 FEDGRET 168
              |||||||
Db        577 FEDGRET 583


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Job time : 55 secs
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: December 5, 2006, 01:14:01 ; Search time 187 Seconds
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426.059 Million cell updates/sec

Title: US-10-507-132-4
Perfect score: 172
Sequence: 1 MGSQVQKSDEITFSDYLGLM.....WGEFDFDRIFEDGRETFGDK 172

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2097797 seqs, 463214858 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2096646

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7	4.1	75	4	US-10-425-115-186523	Sequence 186523,
2	7	4.1	98	4	US-10-287-274-413	Sequence 413, App
3	7	4.1	139	4	US-10-424-599-187642	Sequence 187642,
4	7	4.1	187	4	US-10-369-493-21543	Sequence 21543, A
5	7	4.1	198	4	US-10-108-260A-3617	Sequence 3617, Ap
6	7	4.1	219	4	US-10-425-115-335717	Sequence 335717,
7	7	4.1	225	4	US-10-425-114-54023	Sequence 54023, A
8	7	4.1	228	4	US-10-424-599-167826	Sequence 167826,
9	7	4.1	236	4	US-10-425-115-232623	Sequence 232623,
10	7	4.1	255	4	US-10-103-313-488	Sequence 488, App
11	7	4.1	255	4	US-10-425-114-49108	Sequence 49108, A
12	7	4.1	258	4	US-10-412-699B-446	Sequence 446, App
13	7	4.1	259	4	US-10-223-047-30	Sequence 30, Appl
14	7	4.1	286	5	US-10-612-358-4	Sequence 4, Appli
15	7	4.1	293	4	US-10-369-493-11818	Sequence 11818, A
16	7	4.1	312	4	US-10-437-963-185545	Sequence 185545,
17	7	4.1	327	4	US-10-424-599-209185	Sequence 209185,
18	7	4.1	388	6	US-11-097-143-23043	Sequence 23043, A
19	7	4.1	429	5	US-10-506-454-684	Sequence 684, App
20	7	4.1	450	3	US-09-764-864-804	Sequence 804, App
21	7	4.1	463	4	US-10-104-047-2880	Sequence 2880, Ap
22	7	4.1	463	6	US-11-072-512-2880	Sequence 2880, Ap
23	7	4.1	470	5	US-10-810-352-68	Sequence 68, Appl
24	7	4.1	486	6	US-11-079-463-7267	Sequence 7267, Ap
25	7	4.1	489	4	US-10-282-122A-51224	Sequence 51224, A
26	7	4.1	491	4	US-10-437-963-195742	Sequence 195742,
27	7	4.1	504	4	US-10-437-963-182249	Sequence 182249,
28	7	4.1	528	6	US-11-188-298-8025	Sequence 8025, Ap
29	7	4.1	533	4	US-10-437-963-108161	Sequence 108161,
30	7	4.1	600	5	US-10-450-763-38123	Sequence 38123, A
31	7	4.1	626	4	US-10-310-671-7	Sequence 7, Appli
32	7	4.1	626	4	US-10-310-671-11	Sequence 11, Appl
33	7	4.1	716	4	US-10-369-493-12942	Sequence 12942, A
34	7	4.1	719	4	US-10-103-313-334	Sequence 334, App
35	7	4.1	750	4	US-10-437-963-185546	Sequence 185546,
36	7	4.1	762	6	US-11-097-143-10509	Sequence 10509, A
37	7	4.1	807	4	US-10-367-094-185	Sequence 185, App
38	7	4.1	847	4	US-10-478-245-7	Sequence 7, Appli
39	7	4.1	875	4	US-10-367-094-178	Sequence 178, App
40	7	4.1	877	4	US-10-367-094-183	Sequence 183, App
41	7	4.1	883	4	US-10-177-293-190	Sequence 190, App
42	7	4.1	883	5	US-10-482-029-301	Sequence 301, App
43	7	4.1	883	5	US-10-753-267-102	Sequence 102, App
44	7	4.1	883	5	US-10-936-626-141	Sequence 141, App
45	7	4.1	883	5	US-10-938-061-141	Sequence 141, App

ALIGNMENTS

RESULT 1
US-10-425-115-186523
; Sequence 186523, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 186523
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_10169C.1.pep
US-10-425-115-186523

Query Match 4.1%; Score 7; DB 4; Length 75;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 143 KFAGLKP 149
|||||||
Db 61 KFAGLKP 67

RESULT 2
US-10-287-274-413
; Sequence 413, Application US/10287274
; Publication No. US20030181408A1
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETO
; FILE REFERENCE: ELITRA.008DV1
; CURRENT APPLICATION NUMBER: US/10/287,274
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/164415
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: US 09/711164
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSEQ for Windows Version 4.0

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; SEQ ID NO 413
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Escherichia coli
US-10-287-274-413

  Query Match             4.1%;  Score 7;  DB 4;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 60;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         46 LRIDYRS 52
              |||||||
Db         59 LRIDYRS 65


RESULT 3
US-10-424-599-187642
; Sequence 187642, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 187642
;   LENGTH: 139
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(139)
;   OTHER INFORMATION: unsure at all Xaa locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_140454C.1.pep
US-10-424-599-187642

  Query Match             4.1%;  Score 7;  DB 4;  Length 139;
  Best Local Similarity   100.0%;  Pred. No. 81;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        146 GLKPDIR 152
              |||||||
Db        124 GLKPDIR 130


RESULT 4
US-10-369-493-21543
; Sequence 21543, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
;  APPLICANT: Cao, Yongwei
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Goldman, Barry S.
;  APPLICANT:  Chen, Xianfeng
;  TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
;  TITLE OF INVENTION:  PLANTS WITH IMPROVED PROPERTIES
;  FILE REFERENCE: 38-10(52052)B
;  CURRENT APPLICATION NUMBER: US/10/369,493
;  CURRENT FILING DATE:  2003-02-28
;  PRIOR APPLICATION NUMBER: US 60/360,039
;  PRIOR FILING DATE: 2002-02-21
;  NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 21543
;   LENGTH: 187
;   TYPE: PRT
;   ORGANISM: Methanobacterium thermoautotrophicum
US-10-369-493-21543

  Query Match             4.1%;  Score 7;  DB 4;  Length 187;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         96 SEDEVIG 102
              |||||||
Db        154 SEDEVIG 160


RESULT 5
US-10-108-260A-3617
; Sequence 3617, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: No. US20040005560A1el full length cDNA
;  FILE REFERENCE: H1-A0106
;  CURRENT APPLICATION NUMBER: US/10/108,260A
;  CURRENT FILING DATE:  2002-03-27
;  NUMBER OF SEQ ID NOS: 5458
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3617
;   LENGTH: 198
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-108-260A-3617

  Query Match             4.1%;  Score 7;  DB 4;  Length 198;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         76 LGDPTLR 82
              |||||||
Db          2 LGDPTLR 8


RESULT 6
US-10-425-115-335717
; Sequence 335717, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 335717
;   LENGTH: 219
;   TYPE: PRT
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_6927C.1.pep
US-10-425-115-335717

  Query Match             4.1%;  Score 7;  DB 4;  Length 219;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GSQVQKS 8
              |||||||
Db         79 GSQVQKS 85


RESULT 7
US-10-425-114-54023
; Sequence 54023, Application US/10425114
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; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54023
;   LENGTH: 225
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 701068004_FLI.pep
US-10-425-114-54023

  Query Match             4.1%;  Score 7;  DB 4;  Length 225;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 QVQKSDE 10
              |||||||
Db         20 QVQKSDE 26


RESULT 8
US-10-424-599-167826
; Sequence 167826, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 167826
;   LENGTH: 228
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_122563C.1.pep
US-10-424-599-167826

  Query Match             4.1%;  Score 7;  DB 4;  Length 228;
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  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 QVQKSDE 10
              |||||||
Db         23 QVQKSDE 29


RESULT 9
US-10-425-115-232623
; Sequence 232623, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 232623
;   LENGTH: 236
;   TYPE: PRT
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(236)
;   OTHER INFORMATION: unsure at all Xaa locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_143745C.1.pep
US-10-425-115-232623

  Query Match             4.1%;  Score 7;  DB 4;  Length 236;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         94 KVSEDEV 100
              |||||||
Db        126 KVSEDEV 132


RESULT 10
US-10-103-313-488
; Sequence 488, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PJZ07C1
;  CURRENT APPLICATION NUMBER: US/10/103,313
;  CURRENT FILING DATE:  2002-03-12
;  NUMBER OF SEQ ID NOS: 653
;      Prior Application removed - See File Wrapper or Palm
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 488
;   LENGTH: 255
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: misc_feature
;   LOCATION: (223)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;   NAME/KEY: misc_feature
;   LOCATION: (232)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-103-313-488

  Query Match             4.1%;  Score 7;  DB 4;  Length 255;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         36 DRLRKVI 42
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Db        116 DRLRKVI 122


RESULT 11
US-10-425-114-49108
; Sequence 49108, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
;  APPLICANT: Liu, Jingdong
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Screen, Steven E
```

```
;  APPLICANT:  Tabaska, Jack E
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53313)B
;  CURRENT APPLICATION NUMBER: US/10/425,114
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 49108
;   LENGTH: 255
;   TYPE: PRT
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: 700048791_FLI.pep
US-10-425-114-49108

  Query Match             4.1%;  Score 7;  DB 4;  Length 255;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GSQVQKS 8
              |||||||
Db        115 GSQVQKS 121


RESULT 12
US-10-412-699B-446
; Sequence 446, Application US/10412699B
; Publication No. US20040045049A1
; GENERAL INFORMATION:
;  APPLICANT: Mendel Biotechnology, Inc.
;  APPLICANT:  Zhang, James
;  APPLICANT:  Fromm, Michael E.
;  APPLICANT:  Heard, Jacqueline E.
;  APPLICANT:  Riechmann, Jose Luis
;  APPLICANT:  Adam, Luc J.
;  APPLICANT:  Broun, Pierre E.
;  APPLICANT:  Pineda, Omaira
;  APPLICANT:  Reuber, T. Lynne
;  APPLICANT:  Keddie, James S.
;  APPLICANT:  Yu, Guo-Liang
;  APPLICANT:  Jiang, Cai-Zhong
;  APPLICANT:  Samaha, Raymond R.
;  APPLICANT:  Pilgrim, Marsha L.
;  APPLICANT:  Creelman, Robert A.
;  APPLICANT:  DuBell, Arnold N.
;  APPLICANT:  Ratcliffe, Oliver
;  APPLICANT:  Kumimoto, Roderick
;  APPLICANT:  Sherman, Bradley K.
;  TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
;  FILE REFERENCE: MBI-0048CIP
;  CURRENT APPLICATION NUMBER: US/10/412,699B
;  CURRENT FILING DATE:  2003-04-10
;  PRIOR APPLICATION NUMBER: 09/394,519
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: 09/489,376
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: 09/506,720
;  PRIOR FILING DATE: 2000-02-17
;  PRIOR APPLICATION NUMBER: 09/533,030
;  PRIOR FILING DATE: 2000-03-22
;  PRIOR APPLICATION NUMBER: 09/533,392
;  PRIOR FILING DATE: 2000-03-22
;  PRIOR APPLICATION NUMBER: 09/533,029
;  PRIOR FILING DATE: 2000-03-22
;  PRIOR APPLICATION NUMBER: 09/532,591
;  PRIOR FILING DATE: 2000-03-22
;  PRIOR APPLICATION NUMBER: 09/533,648
;  PRIOR FILING DATE: 2000-03-22
;  PRIOR APPLICATION NUMBER: 09/713,994
;  PRIOR FILING DATE: 2000-11-16
;  PRIOR APPLICATION NUMBER: 09/819,142
;  PRIOR FILING DATE: 2001-03-27
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2011
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 446
;   LENGTH: 258
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   OTHER INFORMATION: G669
US-10-412-699B-446

  Query Match             4.1%;  Score 7;  DB 4;  Length 258;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        155 EFDFDRI 161
              |||||||
Db        188 EFDFDRI 194


RESULT 13
US-10-223-047-30
; Sequence 30, Application US/10223047
; Publication No. US20030022305A1
;   GENERAL INFORMATION:
;        APPLICANT: Coruzzi, Gloria
;                   Oliveira, Igor
;                   Lam, Hon-Ming
;                   Hsieh, Ming-Hsiun
;        TITLE OF INVENTION: PLANT GLUTAMATE RECEPTORS
;        NUMBER OF SEQUENCES: 36
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: U.S.A.
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/223,047
;             FILING DATE: 16-Aug-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/406,640
;             FILING DATE: 27-Sep-1999
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Coruzzi, Laura A.
;             REGISTRATION NUMBER: 30,742
;             REFERENCE/DOCKET NUMBER: 5914-082
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 790-9090
;             TELEFAX: (212) 869-9741/8864
;             TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 30:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 259 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-223-047-30

  Query Match             4.1%;  Score 7;  DB 4;  Length 259;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        162 FEDGRET 168
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Db         48 FEDGRET 54


RESULT 14
US-10-612-358-4
; Sequence 4, Application US/10612358
; Publication No. US20050074410A1
; GENERAL INFORMATION:
;  APPLICANT: Crameri, Reto
;  APPLICANT:  Hemman, Stefanie
;  APPLICANT:  Blaser, Kurt
;  TITLE OF INVENTION: Methods for Diagnosis of Allergic Bronchopulmonary
;  TITLE OF INVENTION:  Aspergillosis
;  FILE REFERENCE: 10806-93
;  CURRENT APPLICATION NUMBER: US/10/612,358
;  CURRENT FILING DATE:  2003-07-02
;  PRIOR APPLICATION NUMBER: SE9604815-2
;  PRIOR FILING DATE: 1996-12-20
;  PRIOR APPLICATION NUMBER: PCT/SE97/02171
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: US09/319806
;  PRIOR FILING DATE: 1999-08-19
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 286
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: recombinant
;   OTHER INFORMATION: allergan rAsp f4
US-10-612-358-4

  Query Match             4.1%;  Score 7;  DB 5;  Length 286;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        153 WGEFDFD 159
              |||||||
Db        200 WGEFDFD 206


RESULT 15
US-10-369-493-11818
; Sequence 11818, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
;  APPLICANT: Cao, Yongwei
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Goldman, Barry S.
;  APPLICANT:  Chen, Xianfeng
;  TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
;  TITLE OF INVENTION:  PLANTS WITH IMPROVED PROPERTIES
;  FILE REFERENCE: 38-10(52052)B
;  CURRENT APPLICATION NUMBER: US/10/369,493
;  CURRENT FILING DATE:  2003-02-28
;  PRIOR APPLICATION NUMBER: US 60/360,039
;  PRIOR FILING DATE: 2002-02-21
;  NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 11818
;   LENGTH: 293
;   TYPE: PRT
;   ORGANISM: Mesorhizobium loti
US-10-369-493-11818

  Query Match             4.1%;  Score 7;  DB 4;  Length 293;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         36 DRLRKVI 42
              |||||||
Db        218 DRLRKVI 224

Search completed: December  5, 2006, 01:17:56
Job time : 188 secs
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GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: December 5, 2006, 01:14:56 ; Search time 45 Seconds
(without alignments)
340.946 Million cell updates/sec

Title: US-10-507-132-4
Perfect score: 172
Sequence: 1 MGSQVQKSDEITFSDYLGLM.....WGEFDFDRIFEDGRETFGDK 172

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 351643 seqs, 89200972 residues

Word size : 1

Total number of hits satisfying chosen parameters: 351006

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA_New:*
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2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	172	100.0	172	6	US-10-507-132-4	Sequence 4, Appli
2	97	56.4	172	6	US-10-507-132-2	Sequence 2, Appli
3	9	5.2	33	6	US-10-507-132-19	Sequence 19, Appl
4	7	4.1	198	7	US-11-293-697-3617	Sequence 3617, Ap
5	7	4.1	258	7	US-11-179-064B-76	Sequence 76, Appl
6	7	4.1	258	7	US-11-056-355B-81940	Sequence 81940, A
7	7	4.1	264	6	US-10-953-349-17570	Sequence 17570, A
8	7	4.1	264	7	US-11-056-355B-52964	Sequence 52964, A
9	7	4.1	279	7	US-11-056-355B-81939	Sequence 81939, A
10	7	4.1	280	6	US-10-953-349-17569	Sequence 17569, A
11	7	4.1	280	7	US-11-174-307B-4558	Sequence 4558, Ap
12	7	4.1	280	7	US-11-056-355B-52963	Sequence 52963, A
13	7	4.1	292	6	US-10-953-349-17568	Sequence 17568, A
14	7	4.1	292	7	US-11-056-355B-52962	Sequence 52962, A
15	7	4.1	357	6	US-10-953-349-16815	Sequence 16815, A
16	7	4.1	357	7	US-11-056-355B-59499	Sequence 59499, A
17	7	4.1	369	6	US-10-953-349-16814	Sequence 16814, A
18	7	4.1	369	7	US-11-056-355B-59498	Sequence 59498, A
19	7	4.1	373	6	US-10-953-349-16813	Sequence 16813, A
20	7	4.1	373	7	US-11-174-307B-4610	Sequence 4610, Ap
21	7	4.1	373	7	US-11-056-355B-59497	Sequence 59497, A
22	7	4.1	419	7	US-11-330-403-5226	Sequence 5226, Ap
23	7	4.1	491	6	US-10-449-902-31790	Sequence 31790, A
24	7	4.1	602	7	US-11-330-403-2140	Sequence 2140, Ap
25	7	4.1	712	7	US-11-056-355B-87051	Sequence 87051, A
26	7	4.1	713	7	US-11-056-355B-87050	Sequence 87050, A
27	7	4.1	765	7	US-11-330-403-12624	Sequence 12624, A
28	7	4.1	817	7	US-11-056-355B-76258	Sequence 76258, A
29	7	4.1	817	7	US-11-056-355B-87049	Sequence 87049, A
30	7	4.1	832	7	US-11-056-355B-88920	Sequence 88920, A
31	7	4.1	832	7	US-11-056-355B-92676	Sequence 92676, A
32	7	4.1	833	7	US-11-056-355B-88919	Sequence 88919, A
33	7	4.1	833	7	US-11-056-355B-92675	Sequence 92675, A
34	7	4.1	879	7	US-11-056-355B-76257	Sequence 76257, A
35	7	4.1	883	7	US-11-056-355B-79947	Sequence 79947, A
36	7	4.1	883	7	US-11-226-554-141	Sequence 141, App
37	7	4.1	883	7	US-11-248-718-141	Sequence 141, App
38	7	4.1	884	7	US-11-056-355B-79946	Sequence 79946, A
39	7	4.1	887	7	US-11-056-355B-76256	Sequence 76256, A
40	7	4.1	889	7	US-11-221-332-100	Sequence 100, App
41	7	4.1	937	7	US-11-056-355B-88918	Sequence 88918, A
42	7	4.1	937	7	US-11-056-355B-92674	Sequence 92674, A
43	7	4.1	988	7	US-11-056-355B-79945	Sequence 79945, A
44	6	3.5	18	6	US-10-520-521-8	Sequence 8, Appli
45	6	3.5	41	7	US-11-434-137-2676	Sequence 2676, Ap

ALIGNMENTS

RESULT 1
US-10-507-132-4
; Sequence 4, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
; APPLICANT: Koichiro KAKU et al.
; TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
; TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
; FILE REFERENCE: 1254-0258PUS1
; CURRENT APPLICATION NUMBER: US/10/507,132
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: JP 2002-66955
; PRIOR FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Pyricularia oryzae
US-10-507-132-4

Query Match 100.0%; Score 172; DB 6; Length 172;
Best Local Similarity 100.0%; Pred. No. 9.2e-178;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60
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Db          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60

Qy         61 MPAEEFVGMVSSKQVLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE 120
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Db         61 MPAEEFVGMVSSKQVLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE 120

Qy        121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172
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Db        121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172
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RESULT 2
US-10-507-132-2
; Sequence 2, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
; APPLICANT: Koichiro KAKU et al.
; TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
; TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
; FILE REFERENCE: 1254-0258PUS1
; CURRENT APPLICATION NUMBER: US/10/507,132

; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: JP 2002-66955
; PRIOR FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Pyricularia oryzae
US-10-507-132-2

Query Match 56.4%; Score 97; DB 6; Length 172;
Best Local Similarity 100.0%; Pred. No. 9e-97;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 76 LGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWY 135
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 76 LGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWY 135

Qy 136 KKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172
||||||||||||||||||||||||||||||||||||
Db 136 KKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172

RESULT 3
US-10-507-132-19
; Sequence 19, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
; APPLICANT: Koichiro KAKU et al.
; TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
; TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
; FILE REFERENCE: 1254-0258PUS1
; CURRENT APPLICATION NUMBER: US/10/507,132
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: JP 2002-66955
; PRIOR FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide derived fro
; OTHER INFORMATION: Pyricularia oryzae
US-10-507-132-19

Query Match 5.2%; Score 9; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGSQVQKSD 9
|||||||||
Db 25 MGSQVQKSD 33

RESULT 4
US-11-293-697-3617
; Sequence 3617, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3617
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3617

Query Match 4.1%; Score 7; DB 7; Length 198;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 76 LGDPTLR 82
|||||||
Db 2 LGDPTLR 8

RESULT 5
US-11-179-064B-76
; Sequence 76, Application US/11179064B
; Publication No. US20060123508A1
; GENERAL INFORMATION:
; APPLICANT: DIXON, RICHARD A.
; APPLICANT: SHARMA, SHASHI B.
; TITLE OF INVENTION: GENETIC MANIPULATION OF CONDENSED TANNINS
; FILE REFERENCE: NBLE042:US
; CURRENT APPLICATION NUMBER: US/11/179,064B
; CURRENT FILING DATE: 2005-07-11
; PRIOR APPLICATION NUMBER: 60/587,020
; PRIOR FILING DATE: 2004-07-09
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-179-064B-76

Query Match 4.1%; Score 7; DB 7; Length 258;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 155 EFDFDRI 161
|||||||
Db 188 EFDFDRI 194

RESULT 6
US-11-056-355B-81940
; Sequence 81940, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 81940
; LENGTH: 258
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(258)
; OTHER INFORMATION: Ceres Seq. ID no. 12662413
US-11-056-355B-81940

Query Match 4.1%; Score 7; DB 7; Length 258;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 155 EFDFDRI 161

```
              |||||||
Db        188 EFDFDRI 194


RESULT 7
US-10-953-349-17570
; Sequence 17570, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17570
;   LENGTH: 264
;   TYPE: PRT
;   ORGANISM: Glycine max
US-10-953-349-17570

  Query Match             4.1%;  Score 7;  DB 6;  Length 264;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 QVQKSDE 10
              |||||||
Db         59 QVQKSDE 65


RESULT 8
US-11-056-355B-52964
; Sequence 52964, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 52964
;   LENGTH: 264
;   TYPE: prt
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(264)
;   OTHER INFORMATION: Ceres Seq. ID no. 14304596
US-11-056-355B-52964

  Query Match             4.1%;  Score 7;  DB 7;  Length 264;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 QVQKSDE 10
              |||||||
Db         59 QVQKSDE 65


RESULT 9
US-11-056-355B-81939
; Sequence 81939, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 81939
;   LENGTH: 279
;   TYPE: prt
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(279)
;   OTHER INFORMATION: Ceres Seq. ID no. 12662412
US-11-056-355B-81939

  Query Match             4.1%;  Score 7;  DB 7;  Length 279;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        155 EFDFDRI 161
              |||||||
Db        209 EFDFDRI 215


RESULT 10
US-10-953-349-17569
; Sequence 17569, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17569
;   LENGTH: 280
;   TYPE: PRT
;   ORGANISM: Glycine max
US-10-953-349-17569

  Query Match             4.1%;  Score 7;  DB 6;  Length 280;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 QVQKSDE 10
              |||||||
Db         75 QVQKSDE 81


RESULT 11
US-11-174-307B-4558
; Sequence 4558, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai
;  APPLICANT:  BROVER, Vyacheslav
;  TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
;  TITLE OF INVENTION:  USEFUL FOR MODIFYING PLANT CHARACTERISTICS
;  FILE REFERENCE: 2750-1601PUS2
;  CURRENT APPLICATION NUMBER: US/11/174,307B
;  CURRENT FILING DATE:  2005-06-30
;  PRIOR APPLICATION NUMBER: 60/583,671
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,781
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/583,651
;  PRIOR FILING DATE: 2004-06-30
```

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;  NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 4558
;   LENGTH: 280
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: PFam Name: WRKY; PFam Description: WRKY DNA -binding domain
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 40846374; NR Description: putative WRKY
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 30681651; NR Description: WRKY family
;   OTHER INFORMATION: transcription factor [Arabidopsis thaliana]
;   OTHER INFORMATION: >gi|24762209|gb|AAN64171.1| putative WRKY family transcription
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 21436293; NR Description: putative WRKY-type DNA
;   OTHER INFORMATION: binding protein [Arabidopsis thaliana] >gi|19423942|gb|AAL87292.1
;   OTHER INFORMATION: putative WRKY-type DNA binding protein [Arabidopsis thaliana]
;   OTHER INFORMATION: >gi|4559382|gb|AAD23042.1| putative WRKY-type DNA binding protein
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 46394402; NR Description: TPA: WRKY transcription
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: GI Number: 50843966; NR Description: transcription factor
;   OTHER INFORMATION: WRKY31 [Oryza sativa (indica cultivar-group)]
;   OTHER INFORMATION: >gi|50252562|dbj|BAD28735.1| WRKY family transcription factor-like
;   OTHER INFORMATION: [Oryza sativa (japonica cultivar-group)]
US-11-174-307B-4558

  Query Match             4.1%;  Score 7;  DB 7;  Length 280;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 QVQKSDE 10
              |||||||
Db         75 QVQKSDE 81


RESULT 12
US-11-056-355B-52963
; Sequence 52963, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 52963
;   LENGTH: 280
;   TYPE: prt
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(280)
;   OTHER INFORMATION: Ceres Seq. ID no. 14304595
US-11-056-355B-52963

  Query Match             4.1%;  Score 7;  DB 7;  Length 280;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 QVQKSDE 10
              |||||||
Db         75 QVQKSDE 81


RESULT 13
US-10-953-349-17568
; Sequence 17568, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  TITLE OF INVENTION:  ENCONDED THERBY
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17568
;   LENGTH: 292
;   TYPE: PRT
;   ORGANISM: Glycine max
US-10-953-349-17568

  Query Match             4.1%;  Score 7;  DB 6;  Length 292;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 QVQKSDE 10
              |||||||
Db         87 QVQKSDE 93


RESULT 14
US-11-056-355B-52962
; Sequence 52962, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
;  APPLICANT: Brover, Vyacheslav
;  APPLICANT:  Alexandrov, Nickolai
;  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
;  TITLE OF INVENTION:  Polypeptides Encoded Thereby
;  FILE REFERENCE: 2750-1590PUS2
;  CURRENT APPLICATION NUMBER: US/11/056,355B
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: 60/544,190
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 52962
;   LENGTH: 292
;   TYPE: prt
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: peptide
;   LOCATION: (1)..(292)
;   OTHER INFORMATION: Ceres Seq. ID no. 14304594
US-11-056-355B-52962

  Query Match             4.1%;  Score 7;  DB 7;  Length 292;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 QVQKSDE 10
              |||||||
Db         87 QVQKSDE 93


RESULT 15
US-10-953-349-16815
```

; Sequence 16815, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16815
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-16815

Query Match 4.1%; Score 7; DB 6; Length 357;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 QVQKSDE 10
              |||||||
Db        152 QVQKSDE 158
```

Search completed: December 5, 2006, 01:18:47
Job time : 46 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: December 5, 2006, 01:08:11 ; Search time 41 Seconds
(without alignments)
403.641 Million cell updates/sec

Title: US-10-507-132-4
Perfect score: 172
Sequence: 1 MGSQVQKSDEITFSDYLGLM.....WGEFDFDRIFEDGRETFGDK 172

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	169	98.3	172	2	JE0130	scytalone dehydrat
2	8	4.7	286	2	AE2988	amidohydrolase [im
3	8	4.7	290	2	C98295	hypothetical prote
4	7	4.1	98	2	C65058	Ferredoxin-like pr
5	7	4.1	152	2	AB2499	hypothetical prote
6	7	4.1	187	2	A69118	conserved hypothet
7	7	4.1	196	2	S70957	hypothetical prote
8	7	4.1	261	1	F64369	conserved hypothet
9	7	4.1	294	1	SYBEHS	thymidylate syntha
10	7	4.1	309	2	A82944	ribose/galactose A
11	7	4.1	385	2	T51127	GGPP synthase [imp
12	7	4.1	485	2	T41714	hypothetical serin
13	7	4.1	528	2	T34941	probable Na+/H+ an
14	7	4.1	573	2	AB2401	hypothetical prote
15	7	4.1	818	1	E64807	outer membrane ush
16	7	4.1	883	2	I58181	glutamate receptor
17	7	4.1	883	2	S47031	glutamate receptor
18	7	4.1	883	2	S13677	glutamate receptor
19	7	4.1	921	2	I49695	glutamate receptor
20	7	4.1	939	2	I49696	glutamate receptor
21	7	4.1	1036	2	T05687	beta-galactosidase
22	7	4.1	1046	2	T34566	hypothetical prote
23	7	4.1	1298	2	A64157	hypothetical prote
24	7	4.1	1323	2	S27224	N-methyl-D-asparta
25	7	4.1	1323	2	I78557	N-methyl-D-asparta
26	7	4.1	1356	1	C45219	N-methyl-D-asparta
27	7	4.1	1376	2	F83711	exopolygalacturona
28	6	3.5	52	2	G97873	hypothetical prote
29	6	3.5	71	2	F82606	hypothetical prote
30	6	3.5	73	2	T25763	hypothetical prote
31	6	3.5	77	2	D97718	acetate kinase (Ac
32	6	3.5	80	2	AC2394	hypothetical prote
33	6	3.5	83	2	H85762	probable transposa
34	6	3.5	91	1	S00060	phospholipid trans
35	6	3.5	99	2	D95223	hypothetical prote
36	6	3.5	99	2	F98087	hypothetical prote
37	6	3.5	105	2	B75035	hypothetical prote
38	6	3.5	105	2	F71128	hypothetical prote
39	6	3.5	108	2	T17826	hypothetical prote
40	6	3.5	114	2	S18109	ribosomal protein
41	6	3.5	117	2	T09155	lipid transfer pro
42	6	3.5	118	2	E27889	Ig heavy chain V r
43	6	3.5	119	2	B27889	Ig heavy chain V r
44	6	3.5	121	2	AI2244	dihydroneopterin a
45	6	3.5	125	2	C70162	ribosomal protein

ALIGNMENTS

RESULT 1
JE0130
scytalone dehydratase (EC 4.2.1.94) - Pyricularia oryzae
C;Species: Pyricularia oryzae
C;Date: 03-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 31-Dec-2004
C;Accession: JE0130
R;Motoyama, T.; Imanishi, K.; Yamaguchi, I.
Biosci. Biotechnol. Biochem. 62, 564-566, 1998
A;Title: cDNA cloning, expression, and mutagenesis of scytalone dehydratase needed for p
A;Reference number: JE0130; MUID:98233280; PMID:9571787
A;Accession: JE0130
A;Molecule type: mRNA
A;Residues: 1-172 <MOT>
A;Cross-references: UNIPARC:UPI0000179D1F; DDBJ:AB004701
C;Comment: The C-terminal protein of this enzyme is important in catalysis or/and structu
C;Superfamily: scytalone dehydratase
C;Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 98.3%; Score 169; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.2e-170;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60

Qy         61 MPAEEFVGMVSSKQVLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MPAEEFVGMVSSKQVLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE 120

Qy        121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETF 169
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETF 169
```

RESULT 2
AE2988
amidohydrolase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 31-Dec-2004
C;Accession: AE2988
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClella
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, B
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AE2988
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-286 <KUR>
A;Cross-references: UNIPROT:Q8UA64; UNIPARC:UPI0000164817; GB:AE008689; PIDN:AAL44323.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu3510
A;Map position: linear chromosome
C;Superfamily: nitrilase (carbon-nitrogen hydrolase)

Query Match 4.7%; Score 8; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 EDGRETFG 170
||||||||
Db 215 EDGRETFG 222

RESULT 3
C98295
hypothetical protein AGR_L_2636 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 31-Dec-2004
C;Accession: C98295
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: C98295
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-290 <KUR>
A;Cross-references: UNIPROT:Q8UA64; UNIPARC:UPI00000D2221; GB:AE007870; PIDN:AAK89885.1;
C;Genetics:
A;Gene: AGR_L_2636
A;Map position: linear chromosome
C;Superfamily: nitrilase (carbon-nitrogen hydrolase)

Query Match 4.7%; Score 8; DB 2; Length 290;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 EDGRETFG 170
||||||||
Db 219 EDGRETFG 226

RESULT 4
C65058
Ferredoxin-like protein ygcO - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 31-Dec-2004
C;Accession: C65058
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: C65058
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-98 <BLAT>
A;Cross-references: UNIPROT:Q46905; UNIPARC:UPI000013B043; GB:AE000360; GB:U00096; NID:g
A;Experimental source: strain K-12, substrain MG1655
C;Superfamily: ferredoxin-like protein, FixX type

Query Match 4.1%; Score 7; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 LRIDYRS 52
|||||||
Db 59 LRIDYRS 65

RESULT 5
AB2499
hypothetical protein all7170 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alp
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AB2499
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anab
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AB2499
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-152 <KUR>
A;Cross-references: UNIPROT:Q8YKW8; UNIPARC:UPI00000CEF05; GB:BA000020; PIDN:BAB78254.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all7170
A;Genome: plasmid

Query Match 4.1%; Score 7; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 EDEVIGY 103
|||||||
Db 58 EDEVIGY 64

RESULT 6
A69118
conserved hypothetical protein MTH1876 - Methanobacterium thermoautotrophicum (strain Del
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 12-Jul-2004
C;Accession: A69118
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; B
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: A69118
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-187 <MTH>
A;Cross-references: UNIPROT:O27904; UNIPARC:UPI00000665EF; GB:AE000940; GB:AE000666; NID:
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1876
A;Start codon: GTG
C;Superfamily: spore germination protein C2

Query Match 4.1%; Score 7; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 SEDEVIG 102
|||||||
Db 154 SEDEVIG 160

RESULT 7
S70957
hypothetical protein wbfE otnD [imported] - Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
C;Accession: S70957; T44317
R;Bik, E.M.; Bunschoten, A.E.; Willems, R.J.L.; Chang, A.C.Y.; Mooi, F.R.
Mol. Microbiol. 20, 799-811, 1996

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A;Title: Genetic organization and functional analysis of the otn DNA essential for cell-
A;Reference number: S70952; MUID:96386047; PMID:8793876
A;Accession: S70957
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-196 <BIK>
A;Cross-references: UNIPROT:Q56657; UNIPARC:UPI00000B1755; EMBL:X90547; NID:g1469276; PI
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
R;Yamasaki, S.; Shimizu, T.; Hoshino, K.; Ho, S.T.; Shimada, T.; Nair, G.B.; Takeda, Y.
Gene 237, 321-332, 1999
A;Title: The genes responsible for O-antigen synthesis of Vibrio cholerae O139 are close
A;Reference number: Z22749; MUID:99453293; PMID:10521656
A;Accession: T44317
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-196 <YAM>
A;Cross-references: UNIPARC:UPI00000B1755; EMBL:AB012957; PIDN:BAA33621.1
A;Experimental source: strain O22
C;Genetics:
A;Gene: otnD
A;Note: wbfE

  Query Match             4.1%;  Score 7;  DB 2;  Length 196;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 FSDYLGL 19
              |||||||
Db         88 FSDYLGL 94


RESULT 8
F64369
conserved hypothetical protein MJ0558 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: F64369
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: F64369
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-261 <BUL>
A;Cross-references: UNIPROT:Q57978; UNIPARC:UPI0000139A9F; GB:U67505; GB:L77117; NID:g28
C;Genetics:
A;Map position: REV493986-493201
C;Superfamily: HTH transcriptional regulator, archaeal type

  Query Match             4.1%;  Score 7;  DB 1;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        146 GLKPDIR 152
              |||||||
Db        205 GLKPDIR 211


RESULT 9
SYBEHS
thymidylate synthase (EC 2.1.1.45) - saimiriine herpesvirus 1
C;Species: saimiriine herpesvirus 1
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 05-Oct-2004
C;Accession: A26269
R;Honess, R.W.; Bodemer, W.; Cameron, K.R.; Niller, H.H.; Fleckenstein, B.; Randall, R.E
Proc. Natl. Acad. Sci. U.S.A. 83, 3604-3608, 1986
A;Title: The A+T-rich genome of Herpesvirus saimiri contains a highly conserved gene for
A;Reference number: A26269; MUID:86233282; PMID:3012520
A;Accession: A26269
A;Molecule type: DNA
A;Residues: 1-294 <HON>
A;Cross-references: UNIPARC:UPI00001378D3; GB:M13190; NID:g331074; PIDN:AAA46175.1; PID:g
C;Superfamily: thymidylate synthase; thymidylate synthase homology
C;Keywords: deoxyribonucleotide biosynthesis; methyltransferase
F;11-294/Domain: thymidylate synthase homology <TDS>
F;176/Active site: Cys #status predicted

  Query Match             4.1%;  Score 7;  DB 1;  Length 294;
  Best Local Similarity   100.0%;  Pred. No. 23;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         51 RSFLDKL 57
              |||||||
Db         96 RSFLDKL 102


RESULT 10
A82944
ribose/galactose ABC transporter UU013 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 03-Aug-2001
C;Accession: A82944
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mini
A;Reference number: A82870
A;Accession: A82944
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-309 <GLA>
A;Cross-references: UNIPARC:UPI00000C1B66; GB:AE002101; GB:AF222894; NID:g6898957; PIDN:A
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: rbsC-2; UU013
A;Genetic code: SGC3
C;Superfamily: probable ribose ABC transporter rbsC-2

  Query Match             4.1%;  Score 7;  DB 2;  Length 309;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 SDYLGLM 20
              |||||||
Db        132 SDYLGLM 138


RESULT 11
T51127
GGPP synthase [imported] - Brevibacterium linens
C;Species: Brevibacterium linens
C;Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 09-Jul-2004
C;Accession: T51127
R;Krubasik, P.; Sandmann, G.
Mol. Gen. Genet. 263, 423-432, 2000
A;Title: A carotenogenic gene cluster from Brevibacterium linens with novel lycopene cycl
A;Reference number: Z25303; MUID:20279196; PMID:10821176
A;Accession: T51127
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-385 <KRU>
A;Cross-references: UNIPROT:Q9KK76; UNIPARC:UPI00000B2FAB; EMBL:AF139916; PIDN:AAF65590.1
A;Experimental source: DSM 20426; ATCC9175
C;Genetics:
A;Gene: crtE

  Query Match             4.1%;  Score 7;  DB 2;  Length 385;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         36 DRLRKVI 42
              |||||||
Db        330 DRLRKVI 336
```

RESULT 12
T41714
hypothetical serine-rich protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T41714
R;Rieger, M.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1999
A;Reference number: Z22012
A;Accession: T41714
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-485 <RIE>
A;Cross-references: UNIPROT:Q9UT50; UNIPARC:UPI000006ADBC; EMBL:AL121770; PIDN:CAB57437.
A;Experimental source: strain 972h-; cosmid c821
C;Genetics:
A;Gene: SPDB:SPAC821.03c
A;Map position: 1

Query Match 4.1%; Score 7; DB 2; Length 485;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 PAEEFVG 68
|||||||
Db 346 PAEEFVG 352

RESULT 13
T34941
probable Na+/H+ antiporter - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T34941
R;Saunders, D.C.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21563
A;Accession: T34941
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-528 <SAU>
A;Cross-references: UNIPROT:Q9S2Y0; UNIPARC:UPI00000DB2C7; EMBL:AL109663; PIDN:CAB51980.
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC4A10.04c
C;Superfamily: hypothetical protein yvgP

Query Match 4.1%; Score 7; DB 2; Length 528;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 VLGDPTL 81
|||||||
Db 206 VLGDPTL 212

RESULT 14
AB2401
hypothetical protein all4762 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AB2401
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AB2401
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-573 <KUR>
A;Cross-references: UNIPROT:Q8YN11; UNIPARC:UPI00000CEC3F; GB:BA000019; PIDN:BAB76461.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all4762

Query Match 4.1%; Score 7; DB 2; Length 573;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 FSDYLGL 19
|||||||
Db 538 FSDYLGL 544

RESULT 15
E64807
outer membrane usher protein ybgQ precursor - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002
C;Accession: E64807
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: E64807
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-818 <BLAT>
A;Cross-references: UNIPARC:UPI000016804A; GB:AE000175; GB:U00096; NID:g1786934; PIDN:AAC
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: ybgQ
C;Function:
A;Description: biogenesis of fimbriae
C;Superfamily: outer membrane usher protein fimD
C;Keywords: membrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-818/Product: outer membrane usher protein ybgQ #status predicted <MAT>

Query Match 4.1%; Score 7; DB 1; Length 818;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 146 GLKPDIR 152
|||||||
Db 95 GLKPDIR 101

Search completed: December 5, 2006, 01:13:45
Job time : 43 secs

GenCore version 5.1.9

OM protein - protein search, using sw model

Run on: December 5, 2006, 01:04:36 ; Search time 301 Seconds
(without alignments)
528.580 Million cell updates/sec

Title: US-10-507-132-4
Perfect score: 172
Sequence: 1 MGSQVQKSDEITFSDYLGLM.....WGEFDFDRIFEDGRETFGDK 172

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	172	100.0	172	1	SCYD_MAGGR	P56221 magnaporthe
2	23	13.4	121	2	Q8NJI8_9PEZI	Q8nji8 ceratocysti
3	23	13.4	122	2	Q8NJI7_9PEZI	Q8nji7 ceratocysti
4	23	13.4	186	2	Q6XR11_9PEZI	Q6xr11 ceratocysti
5	17	9.9	216	2	Q9C426_OPHFL	Q9c426 ophiostoma
6	16	9.3	188	1	SCYD_GLOLA	Q00455 glomerella
7	13	7.6	121	2	Q8NJH9_9PEZI	Q8njh9 ophiostoma
8	13	7.6	121	2	Q8NJI0_OPHPI	Q8nji0 ophiostoma
9	13	7.6	121	2	Q8NJI5_OPHFL	Q8nji5 ophiostoma
10	13	7.6	122	2	Q8NIE1_9PEZI	Q8nie1 ophiostoma
11	13	7.6	122	2	Q8NJH8_9PEZI	Q8njh8 ophiostoma
12	13	7.6	122	2	Q8NJI1_OPHPI	Q8nji1 ophiostoma
13	13	7.6	122	2	Q8NJI2_OPHPI	Q8nji2 ophiostoma
14	13	7.6	122	2	Q8NJI3_9PEZI	Q8nji3 ophiostoma
15	13	7.6	122	2	Q8NJI4_9PEZI	Q8nji4 ophiostoma
16	13	7.6	122	2	Q8NJI6_9PEZI	Q8nji6 ophiostoma
17	13	7.6	174	2	Q7SBE1_NEUCR	Q7sbe1 neurospora
18	12	7.0	185	2	Q7Z8L5_9PLEO	Q7z8l5 bipolaris o
19	11	6.4	150	2	Q2WEI4_SORMA	Q2wei4 sordaria ma
20	11	6.4	168	1	SCYD_ASPFU	O14434 aspergillus
21	9	5.2	405	2	Q6CNL3_KLULA	Q6cnl3 kluyveromyc
22	8	4.7	281	2	Q37S66_SPHAR	Q37s66 novosphingo
23	8	4.7	285	2	Q2K3S6_RHIET	Q2k3s6 rhizobium e
24	8	4.7	285	2	Q92MJ9_RHIME	Q92mj9 rhizobium m
25	8	4.7	286	2	Q8UA64_AGRT5	Q8ua64 agrobacteri
26	8	4.7	290	2	Q7CSN1_AGRT5	Q7csn1 agrobacteri
27	8	4.7	405	2	Q6FAZ4_ACIAD	Q6faz4 acinetobact
28	8	4.7	600	2	Q2U221_ASPOR	Q2u221 aspergillus
29	8	4.7	898	2	Q6SFR3_9BACT	Q6sfr3 uncultured
30	7	4.1	86	2	Q2MA62_ECOLI	Q2ma62 escherichia
31	7	4.1	89	2	Q7N041_PHOLL	Q7n041 photorhabdu
32	7	4.1	98	1	YGCO_ECOLI	Q46905 escherichia
33	7	4.1	102	2	Q4ECJ8_9RICK	Q4ecj8 wolbachia e
34	7	4.1	114	2	Q4DHW6_TRYCR	Q4dhw6 trypanosoma
35	7	4.1	126	2	Q8Q0N6_METMA	Q8q0n6 methanosarc
36	7	4.1	141	2	Q4CT99_TRYCR	Q4ct99 trypanosoma
37	7	4.1	141	2	Q4DPH6_TRYCR	Q4dph6 trypanosoma
38	7	4.1	143	2	Q9AVM7_9ASTR	Q9avm7 chrysanthem
39	7	4.1	147	2	Q9DD26_CTEOR	Q9dd26 ctenophorus
40	7	4.1	152	2	Q8YKW8_ANASP	Q8ykw8 anabaena sp
41	7	4.1	177	2	Q9CWD1_MOUSE	Q9cwd1 mus musculu
42	7	4.1	187	2	O27904_METTH	O27904 methanobact
43	7	4.1	196	2	Q56657_VIBCH	Q56657 vibrio chol
44	7	4.1	198	2	Q8N8S1_HUMAN	Q8n8s1 homo sapien
45	7	4.1	210	2	Q4PG88_USTMA	Q4pg88 ustilago ma

ALIGNMENTS

RESULT 1
SCYD_MAGGR
ID SCYD_MAGGR STANDARD; PRT; 172 AA.
AC P56221;
DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT 15-JUL-1998, sequence version 1.
DT 07-FEB-2006, entry version 34.
DE Scytalone dehydratase (EC 4.2.1.94).
GN Name=Sdh1;
OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
OX NCBI_TaxID=148305;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=98233280; PubMed=9571787;
RA Motoyama T., Imanishi K., Yamaguchi I.;
RT "cDNA cloning, expression, and mutagenesis of scytalone dehydratase
RT needed for pathogenicity of the rice blast fungus, Pyricularia
RT oryzae.";
RL Biosci. Biotechnol. Biochem. 62:564-566(1998).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=95171111; PubMed=7866745;
RA Lundqvist T., Rice J., Hodge C.N., Basarab G.S., Pierce J.,
RA Lindqvist Y.;
RT "Crystal structure of scytalone dehydratase -- a disease determinant
RT of the rice pathogen, Magnaporthe grisea.";
RL Structure 2:937-944(1994).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX MEDLINE=98332516; PubMed=9665698; DOI=10.1021/bi980321b;
RA Nakasako M., Motoyama T., Kurahashi Y., Yamaguchi I.;
RT "Cryogenic X-ray crystal structure analysis for the complex of
RT scytalone dehydratase of a rice blast fungus and its tight-binding
RT inhibitor, carpropamid: the structural basis of tight-binding
RT inhibition.";
RL Biochemistry 37:9931-9939(1998).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).
RX MEDLINE=99119201; PubMed=9922139; DOI=10.1021/bi981848r;
RA Chen J.M., Xu S.L., Wawrzak Z., Basarab G.S., Jordan D.B.;
RT "Structure-based design of potent inhibitors of scytalone dehydratase:
RT displacement of a water molecule from the active site.";
RL Biochemistry 37:17735-17744(1998).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS).
RX MEDLINE=99310043; PubMed=10382670;
RX DOI=10.1002/(SICI)1097-0134(19990601)35:4<425::AID-PROT6>3.3.CO;2-T;
RA Wawrzak Z., Sandalova T., Steffens J.J., Basarab G.S., Lundqvist T.,
RA Lindqvist Y., Jordan D.B.;
RT "High-resolution structures of scytalone dehydratase-inhibitor
RT complexes crystallized at physiological pH.";
RL Proteins 35:425-439(1999).

```
CC   -!- FUNCTION: Catalyzes two steps in melanin biosynthesis. From
CC       scytalone they are two dehydration steps and one reduction step to
CC       yield melanin.
CC   -!- CATALYTIC ACTIVITY: Scytalone = 1,3,8-trihydroxynaphthalene +
CC       H(2)O.
CC   -!- PATHWAY: Fungal melanin biosynthesis; first step.
CC   -!- SUBUNIT: Homotrimer. Each subunit contains an active site, located
CC       in the central part of the hydrophobic core of the monomer, which
CC       functions independently.
CC   ---------------------------------------------------------------------
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CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB004741; BAA34046.1; -; mRNA.
DR   PDB; 1IDP; X-ray; A/B/C=1-172.
DR   PDB; 1STD; X-ray; @=1-172.
DR   PDB; 2STD; X-ray; @=1-172.
DR   PDB; 3STD; X-ray; A/B/C=10-172.
DR   PDB; 4STD; X-ray; A/B/C=10-172.
DR   PDB; 5STD; X-ray; A/B/C=10-172.
DR   PDB; 6STD; X-ray; A/B/C=10-172.
DR   PDB; 7STD; X-ray; A/B/C=10-172.
DR   LinkHub; P56221; -.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
KW   3D-structure; Lyase; Melanin biosynthesis.
FT   CHAIN         1    172       Scytalone dehydratase.
FT                                /FTId=PRO_0000097639.
FT   HELIX        13     32
FT   TURN         33     33
FT   HELIX        35     39
FT   TURN         40     41
FT   STRAND       42     49
FT   HELIX        51     54
FT   STRAND       55     55
FT   STRAND       57     62
FT   HELIX        63     71
FT   STRAND       72     72
FT   TURN         73     76
FT   TURN         79     80
FT   STRAND       81     83
FT   STRAND       86     96
FT   TURN         97     98
FT   STRAND       99    115
FT   TURN        116    117
FT   STRAND      121    138
FT   TURN        139    140
FT   STRAND      141    155
SQ   SEQUENCE   172 AA;  20250 MW;  2FA56296D5EE00DC CRC64;

  Query Match             100.0%;  Score 172;  DB 1;  Length 172;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-170;
  Matches  172;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGSQVQKSDEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEA 60

Qy         61 MPAEEFVGMVSSKQVLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MPAEEFVGMVSSKQVLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKE 120

Qy        121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFGDK 172


RESULT 2
Q8NJI8_9PEZI
ID   Q8NJI8_9PEZI   PRELIMINARY;   PRT;   121 AA.
AC   Q8NJI8;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Scytalone dehydratase (Fragment).
OS   Ceratocystis pinicola.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Hypocreomycetidae; Microascales; Microascales incertae sedis;
OC   Ceratocystis.
OX   NCBI_TaxID=72031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fleet C., Breuil C.;
RT   "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT   presence of DHN-melanin pathway in sapstain fungi.";
RL   Mycol. Res. 106:1331-1339(2002).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY098654; AAM34800.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
FT   NON_TER       1      1
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  14394 MW;  C183FA038FCF5820 CRC64;

  Query Match             13.4%;  Score 23;  DB 2;  Length 121;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-15;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 IAPTLRIDYRSFLDKLWEAMPAE 64
              |||||||||||||||||||||||
Db         18 IAPTLRIDYRSFLDKLWEAMPAE 40


RESULT 3
Q8NJI7_9PEZI
ID   Q8NJI7_9PEZI   PRELIMINARY;   PRT;   122 AA.
AC   Q8NJI7;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 11.
DE   Scytalone dehydratase (Fragment).
OS   Ceratocystis resinifera.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Hypocreomycetidae; Microascales; Microascales incertae sedis;
OC   Ceratocystis.
OX   NCBI_TaxID=95837;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fleet C., Breuil C.;
RT   "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT   presence of DHN-melanin pathway in sapstain fungi.";
RL   Mycol. Res. 106:1331-1339(2002).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY098655; AAM34801.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
DR   SMR; Q8NJI7; 1-122.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
FT   NON_TER       1      1
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  14376 MW;  D807589723063C91 CRC64;
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  Query Match            13.4%;  Score 23;  DB 2;  Length 122;
  Best Local Similarity  100.0%;  Pred. No. 3.2e-15;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 IAPTLRIDYRSFLDKLWEAMPAE 64
              |||||||||||||||||||||||
Db         18 IAPTLRIDYRSFLDKLWEAMPAE 40


RESULT 4
Q6XR11_9PEZI
ID   Q6XR11_9PEZI   PRELIMINARY;   PRT;   186 AA.
AC   Q6XR11;
DT   05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   05-JUL-2004, sequence version 1.
DT   07-FEB-2006, entry version 7.
DE   Syctalone dehydratase I.
GN   Name=SD1;
OS   Ceratocystis resinifera.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Hypocreomycetidae; Microascales; Microascales incertae sedis;
OC   Ceratocystis.
OX   NCBI_TaxID=95837;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Loppnau P.A.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -----------------------------------------------------------------------
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CC   -----------------------------------------------------------------------
DR   EMBL; AY214004; AAO60167.1; -; Genomic_DNA.
DR   SMR; Q6XR11; 21-182.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
SQ   SEQUENCE   186 AA;  21516 MW;  FD947DBB2534005F CRC64;

  Query Match            13.4%;  Score 23;  DB 2;  Length 186;
  Best Local Similarity  100.0%;  Pred. No. 4.5e-15;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 IAPTLRIDYRSFLDKLWEAMPAE 64
              |||||||||||||||||||||||
Db         52 IAPTLRIDYRSFLDKLWEAMPAE 74


RESULT 5
Q9C426_OPHFL
ID   Q9C426_OPHFL   PRELIMINARY;   PRT;   216 AA.
AC   Q9C426;
DT   01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2001, sequence version 1.
DT   07-FEB-2006, entry version 12.
DE   Scytalone dehydratase.
GN   Name=OSD1;
OS   Ophiostoma floccosum.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX   NCBI_TaxID=104300;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=387N;
RX   MEDLINE=21473268; PubMed=11589570; DOI=10.1007/s004380100534;
RA   Wang H.L., Kim S.H., Breuil C.;
RT   "A scytalone dehydratase gene from Ophiostoma floccosum restores the
RT   melanization and pathogenicity phenotypes of a melanin-deficient
RT   Colletotrichum lagenarium mutant.";
RL   Mol. Genet. Genomics 266:126-132(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=387N;
RA   Wang H., Breuil C.;
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
CC   -----------------------------------------------------------------------
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CC   -----------------------------------------------------------------------
DR   EMBL; AF316575; AAK11296.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
DR   SMR; Q9C426; 22-182.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
SQ   SEQUENCE   216 AA;  24167 MW;  D349BF7F4DDF3D4D CRC64;

  Query Match             9.9%;  Score 17;  DB 2;  Length 216;
  Best Local Similarity  100.0%;  Pred. No. 8.9e-09;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         24 YEWADSYDSKDWDRLRK 40
              |||||||||||||||||
Db         36 YEWADSYDSKDWDRLRK 52


RESULT 6
SCYD_GLOLA
ID   SCYD_GLOLA     STANDARD;      PRT;   188 AA.
AC   Q00455;
DT   15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1996, sequence version 1.
DT   07-FEB-2006, entry version 28.
DE   Scytalone dehydratase (EC 4.2.1.94).
GN   Name=SCD1;
OS   Glomerella lagenarium (Anthracnose fungus) (Colletotrichum
OS   lagenarium).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
OC   mitosporic Phyllachoraceae; Colletotrichum.
OX   NCBI_TaxID=5462;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC   STRAIN=104-T;
RX   MEDLINE=97111971; PubMed=8953707;
RA   Kubo Y., Takano Y., Endo N., Yasuda N., Tajima S., Furusawa I.;
RT   "Cloning and structural analysis of the melanin biosynthesis gene SCD1
RT   encoding scytalone dehydratase in Colletotrichum lagenarium.";
RL   Appl. Environ. Microbiol. 62:4340-4344(1996).
CC   -!- FUNCTION: Catalyzes two steps in melanin biosynthesis. From
CC       scytalone they are two dehydration steps and one reduction step to
CC       yield melanin.
CC   -!- CATALYTIC ACTIVITY: Scytalone = 1,3,8-trihydroxynaphthalene +
CC       H(2)O.
CC   -!- PATHWAY: Fungal melanin biosynthesis; first step.
CC   -!- SUBUNIT: Homotrimer. Each subunit contains an active site, located
CC       in the central part of the hydrophobic core of the monomer, which
CC       functions independently (By similarity).
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CC   -----------------------------------------------------------------------
DR   EMBL; D86079; BAA13009.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
DR   SMR; Q00455; 6-167.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
KW   Lyase; Melanin biosynthesis.
FT   CHAIN         1    188       Scytalone dehydratase.
FT                                /FTId=PRO_0000097638.
SQ   SEQUENCE   188 AA;  21687 MW;  A58F3EB940321EFA CRC64;
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  Query Match             9.3%;  Score 16;  DB 1;  Length 188;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         25 EWADSYDSKDWDRLRK 40
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Db         22 EWADSYDSKDWDRLRK 37


RESULT 7
Q8NJH9_9PEZI
ID   Q8NJH9_9PEZI   PRELIMINARY;   PRT;   121 AA.
AC   Q8NJH9;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Scytalone dehydratase (Fragment).
OS   Ophiostoma setosum.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX   NCBI_TaxID=107467;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fleet C., Breuil C.;
RT   "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT   presence of DHN-melanin pathway in sapstain fungi.";
RL   Mycol. Res. 106:1331-1339(2002).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY098665; AAM34811.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
DR   SMR; Q8NJH9; 1-121.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
FT   NON_TER       1      1
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  14117 MW;  E1974668F0DE17EC CRC64;

  Query Match             7.6%;  Score 13;  DB 2;  Length 121;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 IAPTLRIDYRSFL 54
              |||||||||||||
Db         18 IAPTLRIDYRSFL 30


RESULT 8
Q8NJI0_OPHPI
ID   Q8NJI0_OPHPI   PRELIMINARY;   PRT;   121 AA.
AC   Q8NJI0;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Scytalone dehydratase (Fragment).
OS   Ophiostoma piliferum.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX   NCBI_TaxID=38032;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fleet C., Breuil C.;
RT   "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT   presence of DHN-melanin pathway in sapstain fungi.";
RL   Mycol. Res. 106:1331-1339(2002).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY098664; AAM34810.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
DR   SMR; Q8NJI0; 1-121.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
FT   NON_TER       1      1
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  14150 MW;  1941990397735E1F CRC64;

  Query Match             7.6%;  Score 13;  DB 2;  Length 121;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 IAPTLRIDYRSFL 54
              |||||||||||||
Db         18 IAPTLRIDYRSFL 30


RESULT 9
Q8NJI5_OPHFL
ID   Q8NJI5_OPHFL   PRELIMINARY;   PRT;   121 AA.
AC   Q8NJI5;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Scytalone dehydratase (Fragment).
OS   Ophiostoma floccosum.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX   NCBI_TaxID=104300;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fleet C., Breuil C.;
RT   "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT   presence of DHN-melanin pathway in sapstain fungi.";
RL   Mycol. Res. 106:1331-1339(2002).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY098657; AAM34803.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
DR   SMR; Q8NJI5; 1-121.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
FT   NON_TER       1      1
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  14234 MW;  1940509D85F8A42A CRC64;

  Query Match             7.6%;  Score 13;  DB 2;  Length 121;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 IAPTLRIDYRSFL 54
              |||||||||||||
Db         18 IAPTLRIDYRSFL 30


RESULT 10
Q8NIE1_9PEZI
ID   Q8NIE1_9PEZI   PRELIMINARY;   PRT;   122 AA.
AC   Q8NIE1;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Scytalone dehydratase (Fragment).
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OS   Ophiostoma piceae.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX   NCBI_TaxID=61273;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fleet C., Breuil C.;
RT   "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT   presence of DHN-melanin pathway in sapstain fungi.";
RL   Mycol. Res. 106:1331-1339(2002).
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CC   ---------------------------------------------------------------------
DR   EMBL; AY098660; AAM34806.1; -; Genomic_DNA.
DR   EMBL; AY098661; AAM34807.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
DR   SMR; Q8NIE1; 1-122.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
FT   NON_TER       1      1
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  14246 MW;  A17A6DD02BD9CB0A CRC64;

  Query Match             7.6%;  Score 13;  DB 2;  Length 122;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 IAPTLRIDYRSFL 54
              |||||||||||||
Db         18 IAPTLRIDYRSFL 30


RESULT 11
Q8NJH8_9PEZI
ID   Q8NJH8_9PEZI   PRELIMINARY;   PRT;   122 AA.
AC   Q8NJH8;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Scytalone dehydratase (Fragment).
OS   Ophiostoma setosum.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX   NCBI_TaxID=107467;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fleet C., Breuil C.;
RT   "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT   presence of DHN-melanin pathway in sapstain fungi.";
RL   Mycol. Res. 106:1331-1339(2002).
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CC   ---------------------------------------------------------------------
DR   EMBL; AY098666; AAM34812.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
DR   SMR; Q8NJH8; 1-122.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
FT   NON_TER       1      1
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  14261 MW;  A72534D668F0DE0A CRC64;

  Query Match             7.6%;  Score 13;  DB 2;  Length 122;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 IAPTLRIDYRSFL 54
              |||||||||||||
Db         18 IAPTLRIDYRSFL 30


RESULT 12
Q8NJI1_OPHPI
ID   Q8NJI1_OPHPI   PRELIMINARY;   PRT;   122 AA.
AC   Q8NJI1;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Scytalone dehydratase (Fragment).
OS   Ophiostoma piliferum.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX   NCBI_TaxID=38032;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fleet C., Breuil C.;
RT   "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT   presence of DHN-melanin pathway in sapstain fungi.";
RL   Mycol. Res. 106:1331-1339(2002).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY098663; AAM34809.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
DR   SMR; Q8NJI1; 1-122.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
FT   NON_TER       1      1
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  14226 MW;  7A995CA5F045735E CRC64;

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Qy         42 IAPTLRIDYRSFL 54
              |||||||||||||
Db         18 IAPTLRIDYRSFL 30


RESULT 13
Q8NJI2_OPHPI
ID   Q8NJI2_OPHPI   PRELIMINARY;   PRT;   122 AA.
AC   Q8NJI2;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Scytalone dehydratase (Fragment).
OS   Ophiostoma piliferum.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX   NCBI_TaxID=38032;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fleet C., Breuil C.;
RT   "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT   presence of DHN-melanin pathway in sapstain fungi.";
RL   Mycol. Res. 106:1331-1339(2002).
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CC   ---------------------------------------------------------------------
DR   EMBL; AY098662; AAM34808.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
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DR   SMR; Q8NJI2; 1-122.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
FT   NON_TER       1      1
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  14221 MW;  7A99419E73E0735E CRC64;

  Query Match             7.6%;  Score 13;  DB 2;  Length 122;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 IAPTLRIDYRSFL 54
              |||||||||||||
Db         18 IAPTLRIDYRSFL 30


RESULT 14
Q8NJI3_9PEZI
ID   Q8NJI3_9PEZI   PRELIMINARY;   PRT;   122 AA.
AC   Q8NJI3;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Scytalone dehydratase (Fragment).
OS   Ophiostoma minus.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX   NCBI_TaxID=150568;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fleet C., Breuil C.;
RT   "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT   presence of DHN-melanin pathway in sapstain fungi.";
RL   Mycol. Res. 106:1331-1339(2002).
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CC   ---------------------------------------------------------------------
DR   EMBL; AY098659; AAM34805.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
DR   SMR; Q8NJI3; 1-122.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
FT   NON_TER       1      1
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  14117 MW;  6FE184D0CDE657FC CRC64;

  Query Match             7.6%;  Score 13;  DB 2;  Length 122;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 IAPTLRIDYRSFL 54
              |||||||||||||
Db         18 IAPTLRIDYRSFL 30


RESULT 15
Q8NJI4_9PEZI
ID   Q8NJI4_9PEZI   PRELIMINARY;   PRT;   122 AA.
AC   Q8NJI4;
DT   01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2002, sequence version 1.
DT   07-FEB-2006, entry version 10.
DE   Scytalone dehydratase (Fragment).
OS   Ophiostoma minus.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
OX   NCBI_TaxID=150568;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fleet C., Breuil C.;
RT   "Inhibitors and genetic analysis of scytalone dehydratase confirm the
RT   presence of DHN-melanin pathway in sapstain fungi.";
RL   Mycol. Res. 106:1331-1339(2002).
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CC   ---------------------------------------------------------------------
DR   EMBL; AY098658; AAM34804.1; -; Genomic_DNA.
DR   HSSP; P56221; 1IDP.
DR   SMR; Q8NJI4; 1-122.
DR   GO; GO:0016836; F:hydro-lyase activity; IEA.
DR   GO; GO:0006582; P:melanin metabolism; IEA.
DR   InterPro; IPR004235; Scytalone_DH.
DR   Pfam; PF02982; Scytalone_dh; 1.
DR   ProDom; PD022193; Scytalone_DH; 1.
FT   NON_TER       1      1
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  14233 MW;  819384D0C70F2DFE CRC64;

  Query Match             7.6%;  Score 13;  DB 2;  Length 122;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         42 IAPTLRIDYRSFL 54
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Db         18 IAPTLRIDYRSFL 30


Search completed: December  5, 2006, 01:12:59
Job time : 304 secs
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GenCore version 5.1.9

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2006, 16:44:35 ; Search time 5103 Seconds
(without alignments)
3233.085 Million cell updates/sec

Title: US-10-507-132-4
Perfect score: 172
Sequence: 1 MGSQVQKSDEITFSDYLGLM.....WGEFDFDRIFEDGRETFGDK 172

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 6366136 seqs, 31973710525 residues

Word size: 1

Total number of hits satisfying chosen parameters: 12722146

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10507132/runat_04122006_143526_9604/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=olip2n_rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03h
-USER=US10507132_@CGN_1_1_5548_@runat_04122006_143526_9604 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database : GenEmbl:*
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2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	172	100.0	807	4	AB004741	AB004741 Magnaport
	2	17	9.9	432	4	AY098654	AY098654 Ceratocys
	3	17	9.9	433	4	AY098655	AY098655 Ceratocys
	4	17	9.9	1215	4	AY214004	AY214004 Ceratocys
	5	17	9.9	1477	4	AF316575	AF316575 Ophiostom
	6	16	9.3	1151	4	COGSCD1	D86079 Colletotric
	7	13	7.6	421	4	AY098661	AY098661 Ophiostom
	8	13	7.6	423	4	AY098660	AY098660 Ophiostom
	9	13	7.6	423	4	AY098666	AY098666 Ophiostom
	10	13	7.6	428	4	AY098659	AY098659 Ophiostom
	11	13	7.6	433	4	AY098658	AY098658 Ophiostom
	12	12	7.0	422	4	AY098665	AY098665 Ophiostom
	13	12	7.0	770	4	AB100172	AB100172 Bipolaris
	14	11	6.4	414	4	AY098663	AY098663 Ophiostom
	15	11	6.4	414	4	AY098664	AY098664 Ophiostom
	16	11	6.4	415	4	AY098662	AY098662 Ophiostom
	17	11	6.4	424	4	AY098657	AY098657 Ophiostom
	18	11	6.4	427	4	AY098656	AY098656 Ophiostom
	19	11	6.4	573	4	SMA575152	AJ575152 Sordaria
	20	11	6.4	1447	4	AFU95042	U95042 Aspergillus
	21	9	5.2	110000	4	CR382125_10	Continuation (11 o
	22	9	5.2	203240	12	AC136859	AC136859 Rattus no
	23	9	5.2	226999	12	AC119491	AC119491 Rattus no
	24	8	4.7	298	7	AU047502	AU047502 Rattus no
	25	8	4.7	375	2	AX907566	AX907566 Sequence
	26	8	4.7	375	2	BD043099	BD043099 Sequence
	27	8	4.7	375	2	AR743360	AR743360 Sequence
	28	8	4.7	405	2	CQ460252	CQ460252 Sequence
	29	8	4.7	491	7	BV677144	BV677144 ST8BE039
	30	8	4.7	586	7	BV446403	BV446403 MARC 3387
	31	8	4.7	588	7	BV403559	BV403559 S229P6190
	32	8	4.7	606	7	BV320788	BV320788 S236P6458
	33	8	4.7	1047	11	CR406004	CR406004 Gallus ga
	34	8	4.7	1690	2	CQ583449	CQ583449 Sequence
	35	8	4.7	1995	5	BC107795	BC107795 Homo sapi
	36	8	4.7	2002	2	AX714038	AX714038 Sequence
	37	8	4.7	2002	5	AK056080	AK056080 Homo sapi
	38	8	4.7	2095	5	BC073888	BC073888 Homo sapi
	39	8	4.7	3270	5	HSM804017	AL832706 Homo sapi
	40	8	4.7	3278	5	BC050354	BC050354 Homo sapi
c	41	8	4.7	4182	2	CQ583448	CQ583448 Sequence
	42	8	4.7	10765	15	AE008331	AE008331 Agrobacte
c	43	8	4.7	11689	15	AE009281	AE009281 Agrobacte
	44	8	4.7	12647	15	AE012088	AE012088 Xanthomon
	45	8	4.7	29188	5	HS77O19	AL035609 Human DNA

ALIGNMENTS

RESULT 1
AB004741
LOCUS AB004741 807 bp mRNA linear PLN 13-NOV-1998
DEFINITION Magnaporthe grisea mRNA for scytalone dehydratase, complete cds.
ACCESSION AB004741
VERSION AB004741.1 GI:3798733
KEYWORDS scytalone dehydratase; sdh1.
SOURCE Magnaporthe grisea
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE 1 (sites)
AUTHORS Motoyama,T., Imanishi,K. and Yamaguchi,I.
TITLE cDNA cloning, expression, and mutagenesis of scytalone dehydratase needed for pathogenicity of the rice blast fungus, Pyricularia oryzae
JOURNAL Biosci. Biotechnol. Biochem. 62 (3), 564-566 (1998)
PUBMED 9571787
REFERENCE 2 (bases 1 to 807)
AUTHORS Motoyama,T.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-1997) Takayuki Motoyama, The Institute of Physical and Chemical Research (RIKEN), Miclobial Toxicology Lab.; 2-1 Hirosawa, Wako-shi, Saitama 351-0198, Japan
(E-mail:tmotoyam@postman.riken.go.jp, Tel:+81-48-467-9518)
COMMENT Sequence updated (27-Oct-1998).
FEATURES Location/Qualifiers

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     source          1. .807
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /db_xref="taxon:148305"
                     /note="sequence obtained from anamorph Pyricularia oryzae
                     whose telemorphic form is unknown"
     gene            1. .807
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     CDS             81. .599
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                     YHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDR
                     IFEDGRETFGDK"
ORIGIN

Alignment Scores:
Pred. No.:              2.03e-178       Length:         807
Score:                  172.00          Matches:        172
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            100.0%          Indels:         0
DB:                     4               Gaps:           0

US-10-507-132-4 (1-172) x AB004741 (1-807)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
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Db         81 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 140

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 200

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 260

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 320

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 380

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 440

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
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Db        441 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 500

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 560

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
              ||||||||||||||||||||||||||||||||||
Db        561 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 596

RESULT 2
AY098654
LOCUS       AY098654                 432 bp    DNA     linear   PLN 16-JAN-2003
DEFINITION  Ceratocystis pinicola scytalone dehydratase (SD) gene, partial cds.
ACCESSION   AY098654
VERSION     AY098654.1  GI:21238817
KEYWORDS    .
SOURCE      Ceratocystis pinicola
  ORGANISM  Ceratocystis pinicola
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Microascales; Microascales incertae sedis;
            Ceratocystis.
REFERENCE   1  (bases 1 to 432)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Inhibitors and genetic analysis of scytalone dehydratase confirm
            the presence of DHN-melanin pathway in sapstain fungi
  JOURNAL   Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE   2  (bases 1 to 432)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2002) Wood Science, University of British
            Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES             Location/Qualifiers
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                     /organism="Ceratocystis pinicola"
                     /mol_type="genomic DNA"
                     /isolate="0901"
                     /db_xref="taxon:72031"
                     /country="United Kingdom"
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     mRNA            join(<1. .69,138. .>432)
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                     /product="scytalone dehydratase"
     CDS             join(<1. .69,138. .>432)
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                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAM34800.1"
                     /db_xref="GI:21238818"
                     /translation="EWADWYDSKDWDRLRRTIAPTLRIDYRSFLDKLWEAMPAEDFIK
                     MISDPNVLGDPLLKTQHFVGASRWERVSDDEVVGWHQLRVPHQRYTDATKTTVKVKGH
                     AHSANKHWYKKVDGVWKFA"
ORIGIN

Alignment Scores:
Pred. No.:              7.48e-09        Length:         432
Score:                  17.00           Matches:        17
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            9.9%            Indels:         0
DB:                     4               Gaps:           0

US-10-507-132-4 (1-172) x AY098654 (1-432)

Qy         48 IleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetProAlaGlu 64
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 ATCGACTATCGCTCGTTCCTGGATAAGCTGTGGGAAGCCATGCCTGCCGAG 188

RESULT 3
AY098655
LOCUS       AY098655                 433 bp    DNA     linear   PLN 16-JAN-2003
DEFINITION  Ceratocystis resinifera scytalone dehydratase (SD) gene, partial
            cds.
ACCESSION   AY098655
VERSION     AY098655.1  GI:21238819
KEYWORDS    .
SOURCE      Ceratocystis resinifera
  ORGANISM  Ceratocystis resinifera
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Microascales; Microascales incertae sedis;
            Ceratocystis.
REFERENCE   1  (bases 1 to 433)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Inhibitors and genetic analysis of scytalone dehydratase confirm
            the presence of DHN-melanin pathway in sapstain fungi
  JOURNAL   Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE   2  (bases 1 to 433)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Direct Submission
```

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  JOURNAL   Submitted (22-APR-2002) Wood Science, University of British
            Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .433
                     /organism="Ceratocystis resinifera"
                     /mol_type="genomic DNA"
                     /isolate="125-214"
                     /db_xref="taxon:95837"
                     /country="Canada"
     gene            <1. .>433
                     /gene="SD"
     mRNA            join(<1. .69,138. .>433)
                     /gene="SD"
                     /product="scytalone dehydratase"
     CDS             join(<1. .69,138. .>433)
                     /gene="SD"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAM34801.1"
                     /db_xref="GI:21238820"
                     /translation="EWADRYDSKDWDRLXRTIAPTLRIDYRSFLDKLWEAMPAEDFIK
                     MISDPNVLGDPLLKTQHFVGASRWERVSDDEVVGWHQLRVPHQRYTDATKTTVKVKGH
                     AHSANKHWYKKVDGVWKFAG"
ORIGIN

Alignment Scores:
Pred. No.:                7.49e-09      Length:         433
Score:                    17.00         Matches:        17
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              9.9%          Indels:         0
DB:                       4             Gaps:           0

US-10-507-132-4 (1-172) x AY098655 (1-433)

Qy          48 IleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetProAlaGlu 64
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         138 ATCGACTACCGCTCGTTCCTGGATAAGCTATGGGAAGCAATGCCTGCCGAG 188

RESULT 4
AY214004
LOCUS       AY214004               1215 bp    DNA     linear   PLN 10-MAR-2004
DEFINITION  Ceratocystis resinifera syctalone dehydratase I (SD1) gene,
            complete cds.
ACCESSION   AY214004
VERSION     AY214004.1  GI:37787189
KEYWORDS    .
SOURCE      Ceratocystis resinifera
  ORGANISM  Ceratocystis resinifera
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Microascales; Microascales incertae sedis;
            Ceratocystis.
REFERENCE   1  (bases 1 to 1215)
  AUTHORS   Loppnau,P.A.
  TITLE     Canadian Populations and Melanin Biosynthesis Genes of Ceratocystis
            resinifera
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1215)
  AUTHORS   Loppnau,P.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JAN-2003) Wood Science, University of British
            Columbia, 4041-2424 Main Mall, Vancouver, BC V6T 1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .1215
                     /organism="Ceratocystis resinifera"
                     /mol_type="genomic DNA"
                     /isolate="EL3-21"
                     /specific_host="Pinus contorta"
                     /db_xref="taxon:95837"
                     /country="Canada: Alberta, Edson"
     gene            <233. .>934
                     /gene="SD1"
     mRNA            join(<233. .305,379. .476,545. .>934)
                     /gene="SD1"
                     /product="syctalone dehydratase I"
     CDS             join(233. .305,379. .476,545. .934)
                     /gene="SD1"
                     /codon_start=1
                     /product="syctalone dehydratase I"
                     /protein_id="AAO60167.1"
                     /db_xref="GI:37787190"
                     /translation="MVAGSSDSTQVTASTVNPKTISFEDYCGLNTALYEWADSYDSKD
                     WDRLRRTIAPTLRIDYRSFLDKLWEAMPAEDFIKMISDPNVLGDPLLKTQHFVGASRW
                     ERVSDDEVVGWHQLRVPHQRYTDATKTTVKVKGHAHSANKHWYKKVDGVWKFAGLYPE
                     IRWSEYDFDKVFASGREEFGDEDIDV"
     exon            233. .305
                     /gene="SD1"
                     /number=1
     exon            379. .476
                     /gene="SD1"
                     /number=2
     exon            545. .934
                     /gene="SD1"
                     /number=3
ORIGIN

Alignment Scores:
Pred. No.:                1.55e-08      Length:         1215
Score:                    17.00         Matches:        17
Percent Similarity:       100.0%        Conservative:   0
Best Local Similarity:    100.0%        Mismatches:     0
Query Match:              9.9%          Indels:         0
DB:                       4             Gaps:           0

US-10-507-132-4 (1-172) x AY214004 (1-1215)

Qy          48 IleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetProAlaGlu 64
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         545 ATCGACTACCGCTCGTTCCTGGATAAGCTATGGGAAGCAATGCCTGCCGAG 595

RESULT 5
AF316575
LOCUS       AF316575               1477 bp    DNA     linear   PLN 22-MAY-2002
DEFINITION  Ophiostoma floccosum strain 387N scytalone dehydratase (OSD1) gene,
            complete cds.
ACCESSION   AF316575
VERSION     AF316575.1  GI:12964737
KEYWORDS    .
SOURCE      Ophiostoma floccosum
  ORGANISM  Ophiostoma floccosum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE   1  (bases 1 to 1477)
  AUTHORS   Wang,H.L., Kim,S.H. and Breuil,C.
  TITLE     A scytalone dehydratase gene from Ophiostoma floccosum restores the
            melanization and pathogenicity phenotypes of a melanin-deficient
            Colletotrichum lagenarium mutant
  JOURNAL   Mol. Genet. Genomics 266 (1), 126-132 (2001)
   PUBMED   11589570
REFERENCE   2  (bases 1 to 1477)
  AUTHORS   Wang,H. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-OCT-2000) Wood Science, University of British
            Columbia, 2424 Main Mall, Vancouver, BC V6T 1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .1477
                     /organism="Ophiostoma floccosum"
                     /mol_type="genomic DNA"
                     /strain="387N"
                     /db_xref="taxon:104300"
     gene            <316. .>1105
                     /gene="OSD1"
     mRNA            join(<316. .394,471. .571,635. .>1105)
                     /gene="OSD1"
                     /product="scytalone dehydratase"
     CDS             join(316. .394,471. .571,635. .1105)
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                     /gene="OSD1"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAK11296.1"
                     /db_xref="GI:12964738"
                     /translation="MGLNISSLTSTTSSAPKTTGSDISFEDYMGLCSAAYEWADSYDS
                     KDWDRLRKCIAPTLRIDYRSFLNKLWEAMPAEEFIGMISDPSVLGNPLLRTQHFFGAS
                     RWERISDTEVVGYHQLRVPHQVYTDTTLTQVAVKGHAHSANTHWYRKVDGVWKFAGLD
                     PKIRWFEYDFDKVFASGRDQFGTEEKAAATAGPELLAKDKVQSAIASAQRAVAVSA"
ORIGIN

Alignment Scores:
Pred. No.:                1.78e-08        Length:         1477
Score:                    17.00           Matches:        17
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              9.9%            Indels:         0
DB:                       4               Gaps:           0

US-10-507-132-4 (1-172) x AF316575 (1-1477)

Qy          24 TyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         497 TACGAGTGGGCCGACAGCTATGATTCCAAGGACTGGGACCGTCTGCGCAAG 547

RESULT 6
COGSCD1
LOCUS       COGSCD1                 1151 bp    DNA     linear   PLN 25-DEC-2002
DEFINITION  Colletotrichum lagenarium DNA for scytalone dehydratase, complete
            cds.
ACCESSION   D86079
VERSION     D86079.1  GI:1395159
KEYWORDS    melanin biosynthesis; scytalone dehydratase.
SOURCE      Colletotrichum lagenarium
  ORGANISM  Colletotrichum lagenarium
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
            mitosporic Phyllachoraceae; Colletotrichum.
REFERENCE   1
  AUTHORS   Kubo,Y., Takano,Y., Endo,N., Yasuda,N., Tajima,S. and Furusawa,I.
  TITLE     Cloning and structural analysis of the melanin biosynthesis gene
            SCD1 encoding scytalone dehydratase in Colletotrichum lagenarium
  JOURNAL   Appl. Environ. Microbiol. 62 (12), 4340-4344 (1996)
   PUBMED   8953707
REFERENCE   2  (bases 1 to 1151)
  AUTHORS   Kubo,Y., Takano,Y., Noriko,E., Yasuda,N., Tajima,S. and Furusawa,I.
  TITLE     Cloning and structural analysis of the melanin biosynthesis gene
            encoding scytalone dehydratase of Colletotrichum lagenarium
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1151)
  AUTHORS   Kubo,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-JUN-1996) Yasuyuki Kubo, Laboratory of Plant
            Pathology, Faculty of Agriculture, Kyoto Prefectural University;
            Shimogamo, Kyoto, Kyoto 606, Japan (E-mail:y_kubo@kpu.ac.jp,
            Tel:075-702-0957, Fax:075-702-0957)
FEATURES             Location/Qualifiers
     source          1. .1151
                     /organism="Colletotrichum lagenarium"
                     /mol_type="genomic DNA"
                     /isolate="104-T"
                     /db_xref="taxon:5462"
     TATA_signal     117. .121
     gene            join(233. .266,324. .421,489. .923)
                     /gene="SCD1"
     CDS             join(233. .266,324. .421,489. .923)
                     /gene="SCD1"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="BAA13009.1"
                     /db_xref="GI:1395160"
                     /translation="MASPAGNITFEDYLGLNAALFEWADSYDSKDWDRLRKCIAPELR
                     IDYRSFLDKIWEAMPAEEFIAMISDKSVLGNPLLKTQHFIGGSRWEKVSDTEVIGHHQ
                     LRVPHQKYTDASRTEVAVKGHAHSYNMHWYRKVNGVWKFAGLNPEIRWSEYDFDAVFA
                     DGRDSYGTEDQKTDVKVVEKEIKFAAAH"
     exon            <233. .266
                     /gene="SCD1"
                     /number=1
     intron          267. .323
                     /gene="SCD1"
                     /number=1
     exon            324. .421
                     /gene="SCD1"
                     /number=2
     intron          422. .488
                     /gene="SCD1"
                     /number=2
     exon            489. .923
                     /gene="SCD1"
                     /number=3
     polyA_signal    1054. .1057
     polyA_site      1073
ORIGIN

Alignment Scores:
Pred. No.:                1.86e-07        Length:         1151
Score:                    16.00           Matches:        16
Percent Similarity:       100.0%          Conservative:   0
Best Local Similarity:    100.0%          Mismatches:     0
Query Match:              9.3%            Indels:         0
DB:                       4               Gaps:           0

US-10-507-132-4 (1-172) x COGSCD1 (1-1151)

Qy          25 GluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         353 GAGTGGGCCGACTCCTACGACTCCAAGGACTGGGACCGTCTCCGCAAG 400

RESULT 7
AY098661
LOCUS       AY098661                421 bp    DNA     linear   PLN 16-JAN-2003
DEFINITION  Ophiostoma piceae isolate W5 scytalone dehydratase (SD) gene,
            partial cds.
ACCESSION   AY098661
VERSION     AY098661.1  GI:21238831
KEYWORDS    .
SOURCE      Ophiostoma piceae
  ORGANISM  Ophiostoma piceae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE   1  (bases 1 to 421)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Inhibitors and genetic analysis of scytalone dehydratase confirm
            the presence of DHN-melanin pathway in sapstain fungi
  JOURNAL   Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE   2  (bases 1 to 421)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2002) Wood Science, University of British
            Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .421
                     /organism="Ophiostoma piceae"
                     /mol_type="genomic DNA"
                     /isolate="W5"
                     /db_xref="taxon:61273"
                     /country="Austria"
     gene            <1. .>421
                     /gene="SD"
     mRNA            join(<1. .69,126. .>421)
                     /gene="SD"
                     /product="scytalone dehydratase"
     CDS             join(<1. .69,126. .>421)
                     /gene="SD"
                     /codon_start=1
                     /product="scytalone dehydratase"
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                     /protein_id="AAM34807.1"
                     /db_xref="GI:21238832"
                     /translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIG
                     MISDPNVLGNPLLRTQHFFGASRWERVSDTEVIGYHQLRVPHQVYTDASLSTVAVKGH
                     AHSANQHWYRKVDGVWKFAG"
ORIGIN

Alignment Scores:
Pred. No.:              0.000177        Length:         421
Score:                  13.00           Matches:        13
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            7.6%            Indels:         0
DB:                     4               Gaps:           0

US-10-507-132-4 (1-172) x AY098661 (1-421)

Qy          99 GluValIleGlyTyrHisGlnLeuArgValProHisGln 111
               |||||||||||||||||||||||||||||||||||||||
Db         279 GAGGTCATTGGCTACCACCAGCTGCGCGTCCCCCACCAG 317

RESULT 8
AY098660
LOCUS       AY098660                423 bp    DNA     linear   PLN 16-JAN-2003
DEFINITION  Ophiostoma piceae isolate 187-1 scytalone dehydratase (SD) gene,
            partial cds.
ACCESSION   AY098660
VERSION     AY098660.1  GI:21238829
KEYWORDS    .
SOURCE      Ophiostoma piceae
  ORGANISM  Ophiostoma piceae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE   1  (bases 1 to 423)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Inhibitors and genetic analysis of scytalone dehydratase confirm
            the presence of DHN-melanin pathway in sapstain fungi
  JOURNAL   Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE   2  (bases 1 to 423)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2002) Wood Science, University of British
            Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .423
                     /organism="Ophiostoma piceae"
                     /mol_type="genomic DNA"
                     /isolate="187-1"
                     /db_xref="taxon:61273"
                     /country="Canada"
     gene            <1. .>423
                     /gene="SD"
     mRNA            join(<1. .69,128. .>423)
                     /gene="SD"
                     /product="scytalone dehydratase"
     CDS             join(<1. .69,128. .>423)
                     /gene="SD"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAM34806.1"
                     /db_xref="GI:21238830"
                     /translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIG
                     MISDPNVLGNPLLRTQHFFGASRWERVSDTEVIGYHQLRVPHQVYTDASLSTVAVKGH
                     AHSANQHWYRKVDGVWKFAG"
ORIGIN

Alignment Scores:
Pred. No.:              0.000177        Length:         423
Score:                  13.00           Matches:        13
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            7.6%            Indels:         0
DB:                     4               Gaps:           0

US-10-507-132-4 (1-172) x AY098660 (1-423)

Qy          99 GluValIleGlyTyrHisGlnLeuArgValProHisGln 111
               |||||||||||||||||||||||||||||||||||||||
Db         281 GAGGTTATTGGCTACCACCAGCTGCGCGTCCCCCACCAG 319

RESULT 9
AY098666
LOCUS       AY098666                423 bp    DNA     linear   PLN 16-JAN-2003
DEFINITION  Ophiostoma setosum isolate NZFS3734 scytalone dehydratase (SD)
            gene, partial cds.
ACCESSION   AY098666
VERSION     AY098666.1  GI:21238841
KEYWORDS    .
SOURCE      Ophiostoma setosum
  ORGANISM  Ophiostoma setosum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE   1  (bases 1 to 423)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Inhibitors and genetic analysis of scytalone dehydratase confirm
            the presence of DHN-melanin pathway in sapstain fungi
  JOURNAL   Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE   2  (bases 1 to 423)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2002) Wood Science, University of British
            Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .423
                     /organism="Ophiostoma setosum"
                     /mol_type="genomic DNA"
                     /isolate="NZFS3734"
                     /db_xref="taxon:107467"
                     /country="New Zealand"
     gene            <1. .>423
                     /gene="SD"
     mRNA            join(<1. .69,128. .>423)
                     /gene="SD"
                     /product="scytalone dehydratase"
     CDS             join(<1. .69,128. .>423)
                     /gene="SD"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAM34812.1"
                     /db_xref="GI:21238842"
                     /translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIV
                     MISDPSVLGNPLLRTQHFFGASRWERVSDTEVIGYHQLRVPHQVYTDASLSTVAVKGH
                     AHSANQHWYRKVDGVWKFAG"
ORIGIN

Alignment Scores:
Pred. No.:              0.000177        Length:         423
Score:                  13.00           Matches:        13
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            7.6%            Indels:         0
DB:                     4               Gaps:           0

US-10-507-132-4 (1-172) x AY098666 (1-423)

Qy          99 GluValIleGlyTyrHisGlnLeuArgValProHisGln 111
               |||||||||||||||||||||||||||||||||||||||
Db         281 GAAGTCATTGGTTACCACCAGCTGCGCGTCCCCCACCAG 319

RESULT 10
AY098659
LOCUS       AY098659                428 bp    DNA     linear   PLN 16-JAN-2003
DEFINITION  Ophiostoma minus isolate OM3 scytalone dehydratase (SD) gene,
            partial cds.
ACCESSION   AY098659
VERSION     AY098659.1  GI:21238827
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```
KEYWORDS    .
SOURCE      Ophiostoma minus
  ORGANISM  Ophiostoma minus
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE   1  (bases 1 to 428)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Inhibitors and genetic analysis of scytalone dehydratase confirm
            the presence of DHN-melanin pathway in sapstain fungi
  JOURNAL   Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE   2  (bases 1 to 428)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2002) Wood Science, University of British
            Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .428
                     /organism="Ophiostoma minus"
                     /mol_type="genomic DNA"
                     /isolate="OM3"
                     /db_xref="taxon:150568"
                     /country="United Kingdom"
     gene            <1. .>428
                     /gene="SD"
     mRNA            join(<1. .69,133. .>428)
                     /gene="SD"
                     /product="scytalone dehydratase"
     CDS             join(<1. .69,133. .>428)
                     /gene="SD"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAM34805.1"
                     /db_xref="GI:21238828"
                     /translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIS
                     MISDPSVLGNPLLRTQHSFGASRWGRVSDTEVIGYHQLRVPHQVYTDASLSTVAVKGH
                     AHSANQHWYRKVDGVWKFAG"
ORIGIN

Alignment Scores:
Pred. No.:              0.000179        Length:         428
Score:                  13.00           Matches:        13
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            7.6%            Indels:         0
DB:                     4               Gaps:           0

US-10-507-132-4 (1-172) x AY098659 (1-428)

Qy          99 GluValIleGlyTyrHisGlnLeuArgValProHisGln 111
               |||||||||||||||||||||||||||||||||||||||
Db         286 GAGGTCATTGGCTACCACCAGCTGCGCGTCCCCCACCAG 324

RESULT 11
AY098658
LOCUS       AY098658                433 bp    DNA     linear   PLN 16-JAN-2003
DEFINITION  Ophiostoma minus isolate 58-4 scytalone dehydratase (SD) gene,
            partial cds.
ACCESSION   AY098658
VERSION     AY098658.1  GI:21238825
KEYWORDS    .
SOURCE      Ophiostoma minus
  ORGANISM  Ophiostoma minus
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE   1  (bases 1 to 433)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Inhibitors and genetic analysis of scytalone dehydratase confirm
            the presence of DHN-melanin pathway in sapstain fungi
  JOURNAL   Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE   2  (bases 1 to 433)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2002) Wood Science, University of British
            Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .433
                     /organism="Ophiostoma minus"
                     /mol_type="genomic DNA"
                     /isolate="58-4"
                     /db_xref="taxon:150568"
                     /country="Canada"
     gene            <1. .>433
                     /gene="SD"
     mRNA            join(<1. .69,138. .>433)
                     /gene="SD"
                     /product="scytalone dehydratase"
     CDS             join(<1. .69,138. .>433)
                     /gene="SD"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAM34804.1"
                     /db_xref="GI:21238826"
                     /translation="EWADRYDSKDWVRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIS
                     MISDPSVLGNPLLRTQHFFGASRWERVSDTEVIGYHQLRVPHQVYTDASLSTVAVKGH
                     AHSANQHWYRKVDGVWKFAG"
ORIGIN

Alignment Scores:
Pred. No.:              0.00018         Length:         433
Score:                  13.00           Matches:        13
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            7.6%            Indels:         0
DB:                     4               Gaps:           0

US-10-507-132-4 (1-172) x AY098658 (1-433)

Qy          99 GluValIleGlyTyrHisGlnLeuArgValProHisGln 111
               |||||||||||||||||||||||||||||||||||||||
Db         291 GAGGTCATTGGCTACCACCAGCTGCGCGTCCCCCACCAG 329

RESULT 12
AY098665
LOCUS       AY098665                422 bp    DNA     linear   PLN 16-JAN-2003
DEFINITION  Ophiostoma setosum isolate 160-38 scytalone dehydratase (SD) gene,
            partial cds.
ACCESSION   AY098665
VERSION     AY098665.1  GI:21238839
KEYWORDS    .
SOURCE      Ophiostoma setosum
  ORGANISM  Ophiostoma setosum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE   1  (bases 1 to 422)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Inhibitors and genetic analysis of scytalone dehydratase confirm
            the presence of DHN-melanin pathway in sapstain fungi
  JOURNAL   Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE   2  (bases 1 to 422)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2002) Wood Science, University of British
            Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .422
                     /organism="Ophiostoma setosum"
                     /mol_type="genomic DNA"
                     /isolate="160-38"
                     /db_xref="taxon:107467"
                     /country="Canada"
     gene            <1. .>422
                     /gene="SD"
     mRNA            join(<1. .69,128. .>422)
                     /gene="SD"
                     /product="scytalone dehydratase"
     CDS             join(<1. .69,128. .>422)
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                     /gene="SD"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAM34811.1"
                     /db_xref="GI:21238840"
                     /translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIV
                     MISDPSVLGNPLLRTQHFFGASRWERVSDTVVIGYHQLRVPHQVYTGASLSTVAVKGH
                     AHSADQHWYRKVDGVWKFA"
ORIGIN

Alignment Scores:
Pred. No.:              0.0022          Length:         422
Score:                  12.00           Matches:        12
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            7.0%            Indels:         0
DB:                     4               Gaps:           0

US-10-507-132-4 (1-172) x AY098665 (1-422)

Qy         100 ValIleGlyTyrHisGlnLeuArgValProHisGln 111
               ||||||||||||||||||||||||||||||||||||
Db         284 GTCATTGGTTACCACCAGCTGCGCGTCCCCCACCAG 319

RESULT 13
AB100172
LOCUS       AB100172                770 bp    DNA     linear   PLN 01-APR-2004
DEFINITION  Bipolaris oryzae BSCD1gene for scytalone dehydratase, complete cds.
ACCESSION   AB100172
VERSION     AB100172.1  GI:32879676
KEYWORDS    .
SOURCE      Bipolaris oryzae
  ORGANISM  Bipolaris oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
            Pleosporales; Pleosporaceae; mitosporic Cochliobolus; Bipolaris.
REFERENCE   1
  AUTHORS   Kihara,J., Moriwaki,A., Ueno,M., Tokunaga,T., Arase,S. and Honda,Y.
  TITLE     Cloning, functional analysis and expression of a scytalone
            dehydratase gene (SCD1) involved in melanin biosynthesis of the
            phytopathogenic fungus Bipolaris oryzae
  JOURNAL   Curr. Genet. 45 (4), 197-204 (2004)
   PUBMED   14716498
REFERENCE   2  (bases 1 to 770)
  AUTHORS   Kihara,J. and Moriwaki,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JAN-2003) Junichi Kihara, Shimane University, Faculty
            of Life and Environmental Science; Nishikawatsu 1060, Matsue,
            Shimane 690-8504, Japan (E-mail:j-kihara@life.shimane-u.ac.jp,
            Tel:81-852-32-6520, Fax:81-852-32-6597)
FEATURES             Location/Qualifiers
     source          1. .770
                     /organism="Bipolaris oryzae"
                     /mol_type="genomic DNA"
                     /strain="D9/F6-69"
                     /db_xref="taxon:33195"
     gene            join(34. .70,125. .645)
                     /gene="BSCD1"
     CDS             join(34. .70,125. .645)
                     /gene="BSCD1"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="BAC79365.1"
                     /db_xref="GI:32879677"
                     /translation="MFEKKELQPTFEEVMGCQSACYEWADSYDSKDWERLRKCVAPTL
                     KIDYRSFLDKIWEAMPADEFVAMASDPAVLGNPLLKTQHFIGGTRWEKTAEDEITGYH
                     QLRVPHQRYTDESRATVAVKGHAHSFNTHWYKKIDGEWKFAGLNPDIRWYEYDFDKVF
                     AEGREQLGEAKAAAGIPETAPGQAV"
ORIGIN

Alignment Scores:
Pred. No.:              0.00337         Length:         770
Score:                  12.00           Matches:        12
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            7.0%            Indels:         0
DB:                     4               Gaps:           0

US-10-507-132-4 (1-172) x AB100172 (1-770)

Qy          24 TyrGluTrpAlaAspSerTyrAspSerLysAspTrp 35
               ||||||||||||||||||||||||||||||||||||
Db         151 TACGAATGGGCAGACAGCTACGACAGCAAGGACTGG 186

RESULT 14
AY098663
LOCUS       AY098663                414 bp    DNA     linear   PLN 16-JAN-2003
DEFINITION  Ophiostoma piliferum isolate 198-2GF scytalone dehydratase (SD)
            gene, partial cds.
ACCESSION   AY098663
VERSION     AY098663.1  GI:21238835
KEYWORDS    .
SOURCE      Ophiostoma piliferum
  ORGANISM  Ophiostoma piliferum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE   1  (bases 1 to 414)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Inhibitors and genetic analysis of scytalone dehydratase confirm
            the presence of DHN-melanin pathway in sapstain fungi
  JOURNAL   Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE   2  (bases 1 to 414)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2002) Wood Science, University of British
            Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .414
                     /organism="Ophiostoma piliferum"
                     /mol_type="genomic DNA"
                     /isolate="198-2GF"
                     /db_xref="taxon:38032"
                     /country="United Kingdom"
     gene            <1. .>414
                     /gene="SD"
     mRNA            join(<1. .69,119. .>414)
                     /gene="SD"
                     /product="scytalone dehydratase"
     CDS             join(<1. .69,119. .>414)
                     /gene="SD"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAM34809.1"
                     /db_xref="GI:21238836"
                     /translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIG
                     MISDPSVLGNPLLRTQHFFGASRWERISDTEVVGHRQLRVPHQVYTDATLSQVAVKGH
                     AHSANTHWYRKVDGVWKFAG"
ORIGIN

Alignment Scores:
Pred. No.:              0.0271          Length:         414
Score:                  11.00           Matches:        11
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            6.4%            Indels:         0
DB:                     4               Gaps:           0

US-10-507-132-4 (1-172) x AY098663 (1-414)

Qy          30 TyrAspSerLysAspTrpAspArgLeuArgLys 40
               ||||||||||||||||||||||||||||||||
Db          16 TACGACTCCAAGGACTGGGACCGTCTGCGCAAG 48

RESULT 15
AY098664
LOCUS       AY098664                414 bp    DNA     linear   PLN 16-JAN-2003
DEFINITION  Ophiostoma piliferum isolate 201-1A scytalone dehydratase (SD)
```

```
            gene, partial cds.
ACCESSION   AY098664
VERSION     AY098664.1  GI:21238837
KEYWORDS    .
SOURCE      Ophiostoma piliferum
  ORGANISM  Ophiostoma piliferum
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetidae; Ophiostomatales; Ophiostomataceae; Ophiostoma.
REFERENCE   1  (bases 1 to 414)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Inhibitors and genetic analysis of scytalone dehydratase confirm
            the presence of DHN-melanin pathway in sapstain fungi
  JOURNAL   Mycol. Res. 106 (11), 1331-1339 (2002)
REFERENCE   2  (bases 1 to 414)
  AUTHORS   Fleet,C. and Breuil,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-2002) Wood Science, University of British
            Columbia, 4th Floor, 2424 Main Mall, Vancouver, BC V6T1Z4, Canada
FEATURES             Location/Qualifiers
     source          1. .414
                     /organism="Ophiostoma piliferum"
                     /mol_type="genomic DNA"
                     /isolate="201-1A"
                     /db_xref="taxon:38032"
                     /country="Austria"
     gene            <1. .>414
                     /gene="SD"
     mRNA            join(<1. .69,120. .>414)
                     /gene="SD"
                     /product="scytalone dehydratase"
     CDS             join(<1. .69,120. .>414)
                     /gene="SD"
                     /codon_start=1
                     /product="scytalone dehydratase"
                     /protein_id="AAM34810.1"
                     /db_xref="GI:21238838"
                     /translation="EWADRYDSKDWDRLRKCIAPTLRIDYRSFLNKLWEAMPADEFIG
                     MISDPSVLGNPLLRTQHFFGASRWERISDTEVVGHHQLRVPHQVYTDATLSQVAVKGH
                     AHSANTHWYRKVDGVWKFA"
ORIGIN

Alignment Scores:
Pred. No.:              0.0271          Length:         414
Score:                  11.00           Matches:        11
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            6.4%            Indels:         0
DB:                     4               Gaps:           0

US-10-507-132-4 (1-172) x AY098664 (1-414)

Qy         30 TyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||
Db         16 TACGACTCCAAGGACTGGGACCGTCTGCGCAAG 48


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Job time : 5108 secs
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GenCore version 5.1.9

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2006, 16:36:09 ; Search time 583 Seconds
(without alignments)
3085.489 Million cell updates/sec

Title: US-10-507-132-4
Perfect score: 172
Sequence: 1 MGSQVQKSDEITFSDYLGLM.....WGEFDFDRIFEDGRETFGDK 172

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 5244920 seqs, 3486124231 residues

Word size: 1

Total number of hits satisfying chosen parameters: 10484873

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
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-DB=N_Geneseq -QFMT=fastap -SUFFIX=olip2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05h
-USER=US10507132_@CGN_1_1_761_@runat_04122006_143523_9593 -NCPU=6 -ICPU=3
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database : N_Geneseq_8:*
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5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
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9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	172	100.0	516	10	ADC16592	Adc16592 Scytalone
2	172	100.0	600	10	ADC16602	Adc16602 Scytalone
3	172	100.0	610	10	ADC16603	Adc16603 Scytalone
4	97	56.4	516	10	ADC16590	Adc16590 Scytalone
5	8	4.7	375	3	AAC19354	Aac19354 Human sec
6	8	4.7	405	6	ABL80052	Abl80052 Human ova
7	8	4.7	512	9	ACH45193	Ach45193 Human foe
8	8	4.7	1521	4	AAH33155	Aah33155 Human col
9	8	4.7	1690	4	ABL09311	Abl09311 Drosophil
10	8	4.7	2002	10	ADA53154	Ada53154 Human cod
c 11	8	4.7	4182	4	ABL09310	Abl09310 Drosophil
12	8	4.7	12822	4	ABK42692	Abk42692 Genomic s
13	8	4.7	12822	9	ADB60848	Adb60848 Connectiv
14	7	4.1	21	10	ADC16597	Adc16597 SCDH rela
c 15	7	4.1	23	10	ADC16598	Adc16598 SCDH rela
16	7	4.1	27	10	ADC16601	Adc16601 SCDH rela
c 17	7	4.1	41	6	ABZ49282	Abz49282 Human alc
18	7	4.1	89	2	AAT26268	Aat26268 Human gen
19	7	4.1	100	8	ACD80651	Acd80651 E. coli K
c 20	7	4.1	166	2	AAV13085	Aav13085 Xylanase
c 21	7	4.1	181	2	AAV13087	Aav13087 Xylanase
22	7	4.1	270	10	ACF71276	Acf71276 Photorhab
23	7	4.1	279	6	ABQ67328	Abq67328 Listeria
c 24	7	4.1	294	13	ADU25639	Adu25639 cDNA enco
25	7	4.1	297	4	AAH84614	Aah84614 E. coli g
26	7	4.1	303	3	AAC12719	Aac12719 Human sec
c 27	7	4.1	308	6	ABN24458	Abn24458 Human ORF
c 28	7	4.1	313	6	ABN75514	Abn75514 Human ORF
29	7	4.1	326	8	ABX48280	Abx48280 Bovine ES
30	7	4.1	371	6	ABN24338	Abn24338 Human ORF
31	7	4.1	384	3	AAA43215	Aaa43215 Xenopus s
c 32	7	4.1	393	3	AAC74929	Aac74929 Human ORF
c 33	7	4.1	393	6	ABN77234	Abn77234 Human ORF
c 34	7	4.1	393	9	ACH29653	Ach29653 Human tes
c 35	7	4.1	393	12	ADP93576	Adp93576 Cotton ex
36	7	4.1	397	6	ABN17793	Abn17793 Human ORF
37	7	4.1	399	11	ACH95962	Ach95962 Klebsiell
c 38	7	4.1	406	5	AAF66611	Aaf66611 Novel hum
39	7	4.1	411	10	ABX61362	Abx61362 Arabidops
40	7	4.1	440	4	AAK73808	Aak73808 Human imm
c 41	7	4.1	441	13	ADQ50306	Adq50306 Novel can
c 42	7	4.1	445	4	AAK59789	Aak59789 Human imm
43	7	4.1	449	4	AAI83543	Aai83543 Human pol
44	7	4.1	449	9	ACH38954	Ach38954 Human foe
c 45	7	4.1	449	14	AED94874	Aed94874 Germ cell

ALIGNMENTS

RESULT 1
ADC16592
ID ADC16592 standard; DNA; 516 BP.
XX
AC ADC16592;
XX
DT 18-DEC-2003 (first entry)
XX
DE Scytalone dehydrogenase gene #SEQ ID 3.
XX
KW Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor;
KW gene; ds.
XX
OS Magnaporthe grisea.
XX
FH Key Location/Qualifiers
FT CDS 1. .516
FT /*tag= a
FT /product= "scytalone dehydrogenase"
FT /partial
FT /note= "no stop codon"
XX
PN WO2003076628-A1.
XX
PD 18-SEP-2003.
XX
PF 24-FEB-2003; 2003WO-JP001980.

XX
PR 12-MAR-2002; 2002JP-00066955.
XX
PA (TSUB) KUMIAI CHEM IND CO LTD.
XX
PI Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;
XX
DR WPI; 2003-748394/70.
DR P-PSDB; ADC16593.
XX
PT Gene encoding for scytalone dehydrogenase (SCDH), useful for screening
PT for SCDH inhibitors and evaluating sensitivity to them.
XX
PS Example 2; SEQ ID NO 3; 50pp; Japanese.
XX
CC The invention relates to a gene encoding scytalone dehydrogenase (SCDH),
CC that functions in the presence of an inhibitor, comprising an optionally
CC mutated, defined amino acid sequence given in the specification. Also
CC disclosed is a method for evaluating rice blast fungus (Pyricularia
CC oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase
CC inhibitors. The gene is useful for screening for new SCDH inhibitors and
CC evaluating sensitivity to them. The current sequence represents the
CC Scytalone dehydrogenase gene sequence.
XX
SQ Sequence 516 BP; 118 A; 151 C; 156 G; 91 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	9.85e-180	Length:	516
Score:	172.00	Matches:	172
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	10	Gaps:	0

US-10-507-132-4 (1-172) x ADC16592 (1-516)

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Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 240

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
              ||||||||||||||||||||||||||||||||||
Db        481 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516
```

RESULT 2

ADC16602
ID ADC16602 standard; DNA; 600 BP.
XX
AC ADC16602;
XX
DT 18-DEC-2003 (first entry)
XX
DE Scytalone dehydrogenase DNA #1.
XX
KW Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor;
KW gene; ds.
XX
OS Magnaporthe grisea.
XX
PN WO2003076628-A1.
XX
PD 18-SEP-2003.
XX
PF 24-FEB-2003; 2003WO-JP001980.
XX
PR 12-MAR-2002; 2002JP-00066955.
XX
PA (TSUB) KUMIAI CHEM IND CO LTD.
XX
PI Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;
XX
DR WPI; 2003-748394/70.
XX
PT Gene encoding for scytalone dehydrogenase (SCDH), useful for screening
PT for SCDH inhibitors and evaluating sensitivity to them.
XX
PS Example 2; Fig 3; 50pp; Japanese.
XX
CC The invention relates to a gene encoding scytalone dehydrogenase (SCDH),
CC that functions in the presence of an inhibitor, comprising an optionally
CC mutated, defined amino acid sequence given in the specification. Also
CC disclosed is a method for evaluating rice blast fungus (Pyricularia
CC oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase
CC inhibitors. The gene is useful for screening for new SCDH inhibitors and
CC evaluating sensitivity to them. The current sequence represents the
CC Scytalone dehydrogenase DNA sequence. Note: gene sequence from this is
CC given in ADC16590.
XX
SQ Sequence 600 BP; 146 A; 176 C; 168 G; 110 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.14e-179	Length:	600
Score:	172.00	Matches:	172
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	10	Gaps:	0

US-10-507-132-4 (1-172) x ADC16602 (1-600)

```
Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 140

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 200

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 260

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 320

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        321 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 380

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 440

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 500

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 560

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
              ||||||||||||||||||||||||||||||||||
Db        561 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 596
```

RESULT 3
ADC16603
ID ADC16603 standard; DNA; 610 BP.
XX
AC ADC16603;
XX
DT 18-DEC-2003 (first entry)
XX
DE Scytalone dehydrogenase DNA #2.
XX
KW Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor;
KW gene; ds.
XX
OS Magnaporthe grisea.
XX
PN WO2003076628-A1.
XX
PD 18-SEP-2003.
XX
PF 24-FEB-2003; 2003WO-JP001980.
XX
PR 12-MAR-2002; 2002JP-00066955.
XX
PA (TSUB) KUMIAI CHEM IND CO LTD.
XX
PI Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;
XX
DR WPI; 2003-748394/70.
XX
PT Gene encoding for scytalone dehydrogenase (SCDH), useful for screening
PT for SCDH inhibitors and evaluating sensitivity to them.
XX
PS Example 2; Fig 4; 50pp; Japanese.
XX
CC The invention relates to a gene encoding scytalone dehydrogenase (SCDH),
CC that functions in the presence of an inhibitor, comprising an optionally
CC mutated, defined amino acid sequence given in the specification. Also
CC disclosed is a method for evaluating rice blast fungus (Pyricularia
CC oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase
CC inhibitors. The gene is useful for screening for new SCDH inhibitors and
CC evaluating sensitivity to them. The current sequence represents the
CC Scytalone dehydrogenase DNA sequence. Note: gene sequence from this is
CC given in ADC16592.
XX
SQ Sequence 610 BP; 148 A; 179 C; 170 G; 113 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.16e-179	Length:	610
Score:	172.00	Matches:	172
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	10	Gaps:	0

US-10-507-132-4 (1-172) x ADC16603 (1-610)

```
Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 140

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 200

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 260

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 320

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 380

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 440

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 500

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 560

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
              ||||||||||||||||||||||||||||||||||
Db        561 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 596
```

RESULT 4
ADC16590
ID ADC16590 standard; DNA; 516 BP.
XX
AC ADC16590;
XX
DT 18-DEC-2003 (first entry)
XX
DE Scytalone dehydrogenase gene #SEQ ID 1.
XX
KW Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor;
KW gene; ds.
XX
OS Magnaporthe grisea.
XX
FH Key Location/Qualifiers
FT CDS 1. .516
FT /*tag= a
FT /product= "scytalone dehydrogenase"
FT /partial
FT /note= "no stop codon"
XX
PN WO2003076628-A1.
XX
PD 18-SEP-2003.
XX
PF 24-FEB-2003; 2003WO-JP001980.
XX
PR 12-MAR-2002; 2002JP-00066955.
XX
PA (TSUB) KUMIAI CHEM IND CO LTD.
XX
PI Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;
XX
DR WPI; 2003-748394/70.
DR P-PSDB; ADC16591.

XX
PT Gene encoding for scytalone dehydrogenase (SCDH), useful for screening
PT for SCDH inhibitors and evaluating sensitivity to them.
XX
PS Example 2; SEQ ID NO 1; 50pp; Japanese.
XX
CC The invention relates to a gene encoding scytalone dehydrogenase (SCDH),
CC that functions in the presence of an inhibitor, comprising an optionally
CC mutated, defined amino acid sequence given in the specification. Also
CC disclosed is a method for evaluating rice blast fungus (Pyricularia
CC oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase
CC inhibitors. The gene is useful for screening for new SCDH inhibitors and
CC evaluating sensitivity to them. The current sequence represents the
CC Scytalone dehydrogenase gene sequence.
XX
SQ Sequence 516 BP; 119 A; 151 C; 155 G; 91 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.21e-97	Length:	516
Score:	97.00	Matches:	97
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	56.4%	Indels:	0
DB:	10	Gaps:	0

US-10-507-132-4 (1-172) x ADC16590 (1-516)

```
Qy          76 LeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysVal 95
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         226 CTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTG 285

Qy          96 SerGluAspGluValIleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAsp 115
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         286 TCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGAC 345

Qy         116 ThrThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyr 135
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         346 ACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTAC 405

Qy         136 LysLysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGlu 155
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         406 AAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAG 465

Qy         156 PheAspPheAspArgIlePheGluAspGlyArgGluThrPheGlyAspLys 172
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         466 TTCGACTTTGACAGGATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516
```

RESULT 5
AAC19354
ID AAC19354 standard; cDNA; 375 BP.
XX
AC AAC19354;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 23429.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-00200610.
XX
PR 26-FEB-1999; 99US-0122487P.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 1; SEQ ID NO 23429; 71pp + Sequence Listing; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors
XX
SQ Sequence 375 BP; 106 A; 96 C; 67 G; 104 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.:	35.2	Length:	375
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	3	Gaps:	0

US-10-507-132-4 (1-172) x AAC19354 (1-375)

```
Qy          70 ValSerSerLysGlnValLeuGly 77
               |||||||||||||||||||||||
Db         347 GTGAGCTCCAAACAAGTTTTAGGA 370
```

RESULT 6
ABL80052
ID ABL80052 standard; cDNA; 405 BP.
XX
AC ABL80052;
XX
DT 17-MAY-2002 (first entry)
XX
DE Human ovarian cancer related cDNA clone SEQ ID NO:3030.
XX
KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200192581-A2.
XX
PD 06-DEC-2001.
XX
PF 29-MAY-2001; 2001WO-US017756.
XX
PR 26-MAY-2000; 2000US-0207484P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Algate PA, Harlocker SL, Jones R;
XX
DR WPI; 2002-122075/16.
XX
PT Composition for therapy and diagnosis of ovarian cancer comprising
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
PT polypeptide, antibody specific to polypeptide or T cell expressing
PT polypeptide.
XX

PS Claim 1; SEQ ID NO 3030; 489pp; English.
XX
CC The present invention describes a composition (I) comprising: carriers
CC and immunostimulants; and a polypeptide (II) of a ovarian tumour
CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1)
CC from the 10912 nucleotide sequences as given in ABL77023 to ABL87934,
CC (III) encoding (II) having a sequence (S2), a T cell population of (II),
CC or antigen presenting cells that express (II). (I) has cytostatic
CC activity. An oligonucleotide (IV) that hybridises to (S1) can be used for
CC detecting ovarian cancer in a patient's biological sample preferably
CC serum or ovarian tissue. The method comprises contacting a biological
CC sample from a patient with (IV), detecting the amount of polynucleotide
CC hybridising to (IV) and comparing the amount to a predetermined cutoff
CC value and thereby detecting ovarian cancer in the patient, where the
CC amount of polynucleotide hybridising to (IV) is detected preferably by
CC polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is
CC useful for stimulating and/or expanding T cells specific for an ovarian
CC tumour protein comprising contacting T cells with (III) or (II). (III) is
CC useful in design and preparation of ribozyme molecules for inhibiting
CC expression of the tumour polypeptides and proteins in tumour cells; and
CC to isolate a full length gene from a suitable library e.g., a tumour cDNA
CC library using well known techniques
XX
SQ Sequence 405 BP; 127 A; 86 C; 77 G; 115 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	37.9	Length:	405
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	6	Gaps:	0

US-10-507-132-4 (1-172) x ABL80052 (1-405)

```
Qy         70 ValSerSerLysGlnValLeuGly 77
              |||||||||||||||||||||||
Db        111 GTGAGCTCCAAACAAGTTTTAGGA 134
```

RESULT 7
ACH45193
ID ACH45193 standard; cDNA; 512 BP.
XX
AC ACH45193;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human foetal brain cDNA #5918.
XX
KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX
OS Homo sapiens.
XX
PN US2003073623-A1.
XX
PD 17-APR-2003.
XX
PF 30-JUL-2001; 2001US-00918995.
XX
PR 30-JUL-2001; 2001US-00918995.
XX
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
DR WPI; 2003-615964/58.
XX
PT New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
PS Claim 1; SEQ ID NO 32405; 44pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversities, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
SQ Sequence 512 BP; 145 A; 119 C; 103 G; 133 T; 0 U; 12 Other;

Alignment Scores:

Pred. No.:	47.4	Length:	512
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	9	Gaps:	0

US-10-507-132-4 (1-172) x ACH45193 (1-512)

```
Qy         70 ValSerSerLysGlnValLeuGly 77
              |||||||||||||||||||||||
Db        440 GTGAGCTCCAAACAAGTTTTAGGA 463
```

RESULT 8
AAH33155
ID AAH33155 standard; cDNA; 1521 BP.
XX
AC AAH33155;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:211.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; ss.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US026524.
XX
PR 29-SEP-1999; 99US-0157137P.
PR 03-NOV-1999; 99US-0163280P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI; 2001-235357/24.
DR P-PSDB; AAG73724.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers.

```
XX
PS   Claim 1; Page 2354; 9803pp; English.
XX
CC   AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC   cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC   proteins are collectively known as colon cancer antigens. The colon
CC   cancer antigens have cytostatic activity and can be used in gene therapy
CC   and vaccine production. N and P may be used in the prevention, diagnosis
CC   and treatment of diseases associated with inappropriate P expression. For
CC   example, N and P may be used to treat disorders associated with decreased
CC   expression by rectifying mutations or deletions in a patient's genome
CC   that affect the activity of P by expressing inactive proteins or to
CC   supplement the patients own production of P. Additionally, N may be used
CC   to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC   into a host cell and culturing the cell to express the proteins. N and P
CC   can be used in the prevention, diagnosis and treatment of colorectal
CC   carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
CC   sequences used in the exemplification of the present invention. N.B.
CC   Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC   time of publication, meaning no sequences are present for SEQ ID NO:1027
CC   to 1052, 7921 and 7922
XX
SQ   Sequence 1521 BP; 411 A; 355 C; 380 G; 371 T; 0 U; 4 Other;

Alignment Scores:
Pred. No.:              135             Length:         1521
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     4               Gaps:           0

US-10-507-132-4 (1-172) x AAH33155 (1-1521)

Qy          70 ValSerSerLysGlnValLeuGly 77
               |||||||||||||||||||||||
Db         310 GTGAGCTCCAAACAAGTTTTAGGA 333

RESULT 9
ABL09311
ID   ABL09311 standard; cDNA; 1690 BP.
XX
AC   ABL09311;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 22415.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ss.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US009231.
XX
PR   23-MAR-2000; 2000US-0191637P.
PR   11-JUL-2000; 2000US-00614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   P-PSDB; ABB65208.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signaling and cell-cell
PT   interactions.
XX
PS   Claim 1; SEQ ID NO 22415; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC   ABB72072). The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1690 BP; 611 A; 335 C; 351 G; 393 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              149             Length:         1690
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     4               Gaps:           0

US-10-507-132-4 (1-172) x ABL09311 (1-1690)

Qy          40 LysValIleAlaProThrLeuArg 47
               |||||||||||||||||||||||
Db        1040 AAAGTTATAGCTCCGACTCTGAGA 1063

RESULT 10
ADA53154
ID   ADA53154 standard; cDNA; 2002 BP.
XX
AC   ADA53154;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human coding sequence, SEQ ID 722.
XX
KW   Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW   Gene Therapy; human; secretory protein; membrane proteins; cancer;
KW   inflammatory disease; osteoporosis; neurological disease; gene; ss.
XX
OS   Homo sapiens.
XX
PN   EP1293569-A2.
XX
PD   19-MAR-2003.
XX
PF   21-MAR-2002; 2002EP-00006586.
XX
PR   14-SEP-2001; 2001JP-00328381.
PR   24-JAN-2002; 2002US-0350435P.
XX
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI   Isogai T,  Sugiyama T,  Otsuki T,  Wakamatsu A,  Sato H,  Ishii S;
PI   Yamamoto J,  Isono Y,  Hio Y,  Otsuka K,  Nagai K,  Irie R,  Tamechika I;
PI   Seki N,  Yoshikawa T,  Otsuka M,  Nagahari K,  Masuho Y;
XX
DR   WPI; 2003-395539/38.
DR   P-PSDB; ADA54793.
XX
PT   New polynucleotides encoding full-length polypeptides, e.g. secretory
PT   and/or membrane proteins, useful for developing medicines for diseases in
PT   which the gene is involved, or as target molecules for gene therapy.
XX
PS   Claim 1; SEQ ID NO 722; 205pp; English.
XX
CC   The present invention relates to novel human secretory or membrane
CC   proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC   ADA54071). The coding sequences are useful in the gene therapy of
```

```
CC   diseases caused by abnormalities of the proteins, e.g. cancer,
CC   inflammatory diseases, osteoporosis or neurological disease.
XX
SQ   Sequence 2002 BP; 526 A; 466 C; 514 G; 496 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              175             Length:         2002
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     10              Gaps:           0

US-10-507-132-4 (1-172) x ADA53154 (1-2002)

Qy         70 ValSerSerLysGlnValLeuGly 77
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Db        802 GTGAGCTCCAAACAAGTTTTAGGA 825

RESULT 11
ABL09310/c
ID   ABL09310 standard; cDNA; 4182 BP.
XX
AC   ABL09310;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 22412.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ss.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US009231.
XX
PR   23-MAR-2000; 2000US-0191637P.
PR   11-JUL-2000; 2000US-00614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   P-PSDB; ABB65207.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signaling and cell-cell
PT   interactions.
XX
PS   Claim 1; SEQ ID NO 22412; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC   ABB72072). The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 4182 BP; 1284 A; 747 C; 676 G; 1475 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              356             Length:         4182
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     4               Gaps:           0

US-10-507-132-4 (1-172) x ABL09310 (1-4182)

Qy         40 LysValIleAlaProThrLeuArg 47
              |||||||||||||||||||||||
Db       1714 AAAGTTATAGCTCCGACTCTGAGA 1691

RESULT 12
ABK42692
ID   ABK42692 standard; DNA; 12822 BP.
XX
AC   ABK42692;
XX
DT   21-MAY-2002  (first entry)
XX
DE   Genomic sequence #591 encoding novel human connective tissue polypeptide.
XX
KW   Human; connective tissue related disorder; cancer; gene therapy;
KW   cytostatic; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200155343-A1.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001322.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
PR   24-FEB-2000; 2000US-0184664P.
PR   02-MAR-2000; 2000US-0186350P.
PR   16-MAR-2000; 2000US-0189874P.
PR   17-MAR-2000; 2000US-0190076P.
PR   18-APR-2000; 2000US-0198123P.
PR   19-MAY-2000; 2000US-0205515P.
PR   07-JUN-2000; 2000US-0209467P.
PR   28-JUN-2000; 2000US-0214886P.
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PR   01-SEP-2000; 2000US-0229343P.
PR   01-SEP-2000; 2000US-0229344P.
PR   01-SEP-2000; 2000US-0229345P.
PR   05-SEP-2000; 2000US-0229509P.
PR   05-SEP-2000; 2000US-0229513P.
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PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
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PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
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PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
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PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
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PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
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PR 08-NOV-2000; 2000US-0246476P.
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PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
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PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-565190/63.
XX
PT Nucleic acid encoding novel connective tissue associated polypeptides,
PT used in diagnosing, preventing, treating or ameliorating a disorder such
PT as cancer or rheumatoid arthritis.
XX
PS Disclosure; SEQ ID NO 1579; 673pp; English.
XX
CC The present invention relates to the isolation of novel human connective
CC tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide
CC (cDNA and genomic) sequences encoding them. The sequences of the
CC invention are useful in the diagnosis, treatment, prevention and/or
CC prognosis of diseases associated with connective tissue(s), including
CC cancer. The polynucleotide sequences of the invention are also useful in
CC gene therapy. ABK42102-ABK43116 represent genomic sequences encoding the
CC novel human connective tissue related polypeptides. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12822 BP; 3353 A; 2570 C; 2626 G; 4273 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.04e+03	Length:	12822
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	4	Gaps:	0

US-10-507-132-4 (1-172) x ABK42692 (1-12822)

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Qy         70 ValSerSerLysGlnValLeuGly 77
              |||||||||||||||||||||||
Db      11559 GTGAGCTCCAAACAAGTTTTAGGA 11582
```

RESULT 13
ADB60848
ID ADB60848 standard; DNA; 12822 BP.
XX
AC ADB60848;
XX
DT 04-DEC-2003 (first entry)
XX
DE Connective tissue related genomic DNA #591.
XX
KW cytostatic; neuroprotective; nootropic; antiparkinsonian; cardiovascular;

KW antiarteriosclerotic; immunosuppressive; antirheumatic; antiarthritic;
KW antiinflammatory; antiallergic; antiasthmatic; dermatological;
KW nephrotopic; virucide; fungicide; antibacterial; antiparasitic;
KW gene therapy; ds; connective tissues disorder; rheumatoid arthritis;
KW systemic lupus erythematosus; scleroderma; Sjogren's syndrome; cancer;
KW cancer metastasis; neoplasia; leukaemia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; cardiovascular disease;
KW atherosclerosis; myocarditis; cardiopulmonary bypass complication;
KW autoimmune disease; multiple sclerosis; allergic reaction; asthma;
KW rhinitis; eczema; inflammatory condition; Crohn's disease; nephritis;
KW gastrointestinal disorder; inflammatory bowel disease;
KW organ transplant rejection; immune system disorder; Bruton's disease;
KW X-linked lymphoproliferative syndrome;
KW B-cell lymphoproliferative disorder; HIV; AIDS; infection;
KW chromosome identification; chromosome mapping;
KW connective tissue related polynucleotide; gene; ds.
XX
OS Homo sapiens.
XX
PN US2003054375-A1.
XX
PD 20-MAR-2003.
XX
PF 07-MAR-2002; 2002US-00092154.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
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PR 08-SEP-2000; 2000US-0232081P.
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PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
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PR 06-DEC-2000; 2000US-0251479P.
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PR 08-DEC-2000; 2000US-0251989P.
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PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764847.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Barash SC;
XX
DR WPI; 2003-634869/60.
DR P-PSDB; ADB59591.
XX
PT New connective tissue-related polypeptides and polynucleotides, useful
PT for treating, preventing and/or prognosing e.g. disorders of connective
PT tissue, (e.g. rheumatoid arthritis), cancers, cancer metastases and/or
PT neoplasias.
XX
PS Disclosure; SEQ ID NO 1579; 248pp; English.
XX
CC The invention describes an isolated nucleic acid molecule (I), which
CC comprises a sequence that is at least 95 % identical to a connective
CC tissue-related polynucleotide encoding connective tissue antigens (CTA).
CC The polypeptide or polynucleotide is useful for preventing, treating, or
CC ameliorating medical conditions in a mammal. The connective tissue
CC polypeptides, polynucleotides and antibodies are particularly useful for
CC treating, preventing and/or prognosing disorders of connective tissues
CC (e.g. rheumatoid arthritis, discoid and systemic lupus erythematosus,
CC scleroderma, or Sjogren's syndrome), cancers, cancer metastases and/or
CC neoplasias (e.g. leukaemia), neurodegenerative disorders (e.g.
CC Alzheimer's disease, or Parkinson's disease), cardiovascular diseases
CC (e.g. atherosclerosis, myocarditis or cardiopulmonary bypass
CC complications), autoimmune diseases (e.g. systemic lupus erythematosus,
CC rheumatoid arthritis, or multiple sclerosis), allergic reactions (e.g.

Alignment Scores:

Pred. No.:	1.04e+03	Length:	12822
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	9	Gaps:	0

US-10-507-132-4 (1-172) x ADB60848 (1-12822)

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Qy         70 ValSerSerLysGlnValLeuGly 77
              |||||||||||||||||||||||
Db      11559 GTGAGCTCCAAACAAGTTTTAGGA 11582
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RESULT 14
ADC16597
ID ADC16597 standard; DNA; 21 BP.
XX
AC ADC16597;
XX
DT 18-DEC-2003 (first entry)
XX
DE SCDH related primer #SEQ ID 8.
XX
KW Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor; PCR;
KW primer; ss.
XX
OS Magnaporthe grisea.
XX
PN WO2003076628-A1.
XX
PD 18-SEP-2003.
XX
PF 24-FEB-2003; 2003WO-JP001980.
XX
PR 12-MAR-2002; 2002JP-00066955.
XX
PA (TSUB) KUMIAI CHEM IND CO LTD.
XX
PI Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;
XX
DR WPI; 2003-748394/70.
XX
PT Gene encoding for scytalone dehydrogenase (SCDH), useful for screening
PT for SCDH inhibitors and evaluating sensitivity to them.
XX
PS Example 3; SEQ ID NO 8; 50pp; Japanese.
XX
CC The invention relates to a gene encoding scytalone dehydrogenase (SCDH),
CC that functions in the presence of an inhibitor, comprising an optionally
CC mutated, defined amino acid sequence given in the specification. Also
CC disclosed is a method for evaluating rice blast fungus (Pyricularia
CC oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase
CC inhibitors. The gene is useful for screening for new SCDH inhibitors and
CC evaluating sensitivity to them. The current sequence represents a primer
CC for amplifying the Scytalone dehydrogenase gene sequence.
XX
SQ Sequence 21 BP; 7 A; 3 C; 6 G; 5 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	28	Length:	21
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.1%	Indels:	0
DB:	10	Gaps:	0

US-10-507-132-4 (1-172) x ADC16597 (1-21)

```
Qy          1 MetGlySerGlnValGlnLys 7
              |||||||||||||||||||||
Db          1 ATGGGTTCGCAAGTTCAAAAG 21
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RESULT 15
ADC16598/c
ID ADC16598 standard; DNA; 23 BP.
XX
AC ADC16598;
XX
DT 18-DEC-2003 (first entry)
XX
DE SCDH related primer #SEQ ID 9.
XX
KW Scytalone dehydrogenase; SCDH; rice blast fungus; enzyme; inhibitor; PCR;
KW primer; ss.
XX
OS Magnaporthe grisea.
XX
PN WO2003076628-A1.
XX
PD 18-SEP-2003.
XX
PF 24-FEB-2003; 2003WO-JP001980.
XX
PR 12-MAR-2002; 2002JP-00066955.
XX
PA (TSUB) KUMIAI CHEM IND CO LTD.
XX
PI Kaku K, Watanabe S, Kawai K, Shimizu T, Nagayama K;
XX

DR WPI; 2003-748394/70.
XX
PT Gene encoding for scytalone dehydrogenase (SCDH), useful for screening
PT for SCDH inhibitors and evaluating sensitivity to them.
XX
PS Example 4; SEQ ID NO 9; 50pp; Japanese.
XX
CC The invention relates to a gene encoding scytalone dehydrogenase (SCDH),
CC that functions in the presence of an inhibitor, comprising an optionally
CC mutated, defined amino acid sequence given in the specification. Also
CC disclosed is a method for evaluating rice blast fungus (Pyricularia
CC oryzae) and Magnaporthe grisea sensitivity to scytalone dehydrogenase
CC inhibitors. The gene is useful for screening for new SCDH inhibitors and
CC evaluating sensitivity to them. The current sequence represents a primer
CC for amplifying the Scytalone dehydrogenase gene sequence.
XX
SQ Sequence 23 BP; 2 A; 8 C; 6 G; 7 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	30.5	Length:	23
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.1%	Indels:	0
DB:	10	Gaps:	0

US-10-507-132-4 (1-172) x ADC16598 (1-23)

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Qy        120 GluValThrMetLysGlyHis 126
              |||||||||||||||||||||
Db         21 GAGGTCACCATGAAGGGCCAC 1
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Search completed: December 4, 2006, 23:59:43
Job time : 591 secs

GenCore version 5.1.9

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2006, 17:22:59 ; Search time 194 Seconds
(without alignments)
2488.382 Million cell updates/sec

Title: US-10-507-132-4
Perfect score: 172
Sequence: 1 MGSQVQKSDEITFSDYLGLM.....WGEFDFDRIFEDGRETFGDK 172

Scoring table: OLIGO
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Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 1403666 seqs, 935554401 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2800955

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=olip2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
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-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

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5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	8	4.7	375	3	US-09-513-999C-23429	Sequence 23429, A
	2	8	4.7	2002	4	US-10-094-749-722	Sequence 722, App
	3	8	4.7	88268	3	US-09-949-016-14178	Sequence 14178, A
	4	8	4.7	152132	3	US-09-949-016-13845	Sequence 13845, A
	5	8	4.7	152145	3	US-09-949-016-12371	Sequence 12371, A
c	6	7	4.1	166	3	US-09-189-060B-23	Sequence 23, Appl
c	7	7	4.1	181	3	US-09-189-060B-25	Sequence 25, Appl
	8	7	4.1	297	3	US-09-711-164-242	Sequence 242, App
	9	7	4.1	303	3	US-09-513-999C-16794	Sequence 16794, A
c	10	7	4.1	377	3	US-09-270-767-9687	Sequence 9687, Ap
c	11	7	4.1	377	3	US-09-270-767-24969	Sequence 24969, A
	12	7	4.1	399	3	US-09-489-039A-1757	Sequence 1757, Ap
c	13	7	4.1	463	3	US-09-513-999C-3332	Sequence 3332, Ap
	14	7	4.1	479	3	US-09-621-976-15423	Sequence 15423, A
c	15	7	4.1	488	3	US-09-513-999C-1132	Sequence 1132, Ap
c	16	7	4.1	601	3	US-09-949-016-26290	Sequence 26290, A
c	17	7	4.1	601	3	US-09-949-016-38776	Sequence 38776, A
c	18	7	4.1	601	3	US-09-949-016-38777	Sequence 38777, A
	19	7	4.1	601	3	US-09-949-016-103519	Sequence 103519,
	20	7	4.1	601	3	US-09-949-016-118088	Sequence 118088,
	21	7	4.1	601	3	US-09-949-016-118089	Sequence 118089,
c	22	7	4.1	601	3	US-09-949-016-143766	Sequence 143766,
c	23	7	4.1	601	3	US-09-949-016-143767	Sequence 143767,
c	24	7	4.1	601	3	US-09-949-016-163784	Sequence 163784,
c	25	7	4.1	601	3	US-09-949-016-169814	Sequence 169814,
c	26	7	4.1	673	3	US-09-280-116-93	Sequence 93, Appl
	27	7	4.1	756	3	US-09-489-039A-1889	Sequence 1889, Ap
	28	7	4.1	861	3	US-09-319-806-3	Sequence 3, Appli
	29	7	4.1	864	3	US-09-902-540-5281	Sequence 5281, Ap
c	30	7	4.1	1083	3	US-09-270-767-10805	Sequence 10805, A
c	31	7	4.1	1197	3	US-09-543-681A-3467	Sequence 3467, Ap
	32	7	4.1	1590	3	US-09-902-540-4236	Sequence 4236, Ap
	33	7	4.1	2089	3	US-09-155-770-6	Sequence 6, Appli
c	34	7	4.1	2236	4	US-09-422-999B-3	Sequence 3, Appli
c	35	7	4.1	2309	3	US-09-949-016-1937	Sequence 1937, Ap
c	36	7	4.1	2349	3	US-09-805-455-1	Sequence 1, Appli
	37	7	4.1	2381	4	US-10-089-057A-3	Sequence 3, Appli
	38	7	4.1	2525	3	US-10-104-047-910	Sequence 910, App
c	39	7	4.1	2604	3	US-09-107-532A-739	Sequence 739, App
	40	7	4.1	2649	3	US-08-400-067-2	Sequence 2, Appli
	41	7	4.1	2741	3	US-09-949-016-2882	Sequence 2882, Ap
	42	7	4.1	2955	2	US-08-687-379-5	Sequence 5, Appli
	43	7	4.1	2955	2	US-08-687-379-7	Sequence 7, Appli
	44	7	4.1	3061	3	US-09-949-016-4055	Sequence 4055, Ap
	45	7	4.1	3407	3	US-08-483-327-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-513-999C-23429
; Sequence 23429, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 23429
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 13
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 14
; OTHER INFORMATION: m=a or c
US-09-513-999C-23429

Alignment Scores:

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Pred. No.:              10.2          Length:         375
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            4.7%          Indels:         0
DB:                     3             Gaps:           0

US-10-507-132-4 (1-172) x US-09-513-999C-23429 (1-375)

Qy         70 ValSerSerLysGlnValLeuGly 77
              |||||||||||||||||||||||
Db        347 GTGAGCTCCAAACAAGTTTTAGGA 370

RESULT 2
US-10-094-749-722
; Sequence 722, Application US/10094749
; Patent No. 6979557
; GENERAL INFORMATION:
;  APPLICANT: ISOGAI, TAKAO
;  APPLICANT:  SUGIYAMA, TOMOYASU
;  APPLICANT:  OTSUKI, TETSUJI
;  APPLICANT:  WAKAMATSU, AI
;  APPLICANT:  SATO, HIROYUKI
;  APPLICANT:  ISHII, SHIZUKO
;  APPLICANT:  YAMAMOTO, JUN-ICHI
;  APPLICANT:  ISONO, YUUKO
;  APPLICANT:  HIO, YURI
;  APPLICANT:  OTSUKA, KAORU
;  APPLICANT:  NAGAI, KEIICHI
;  APPLICANT:  IRIE, RYOTARO
;  APPLICANT:  TAMECHIKA, ICHIRO
;  APPLICANT:  SEKI, NAOHIKO
;  APPLICANT:  YOSHIKAWA, TSUTOMU
;  APPLICANT:  OTSUKA, MOTOYUKI
;  APPLICANT:  NAGAHARI, KENJI
;  APPLICANT:  MASUHO, YASUHIKO
;  TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
;  FILE REFERENCE: 084335/0160
;  CURRENT APPLICATION NUMBER: US/10/094,749
;  CURRENT FILING DATE:  2002-03-12
;  PRIOR APPLICATION NUMBER: 60/350,435
;  PRIOR FILING DATE: 2002-01-24
;  PRIOR APPLICATION NUMBER: JP 2001-328381
;  PRIOR FILING DATE: 2001-09-14
;  NUMBER OF SEQ ID NOS: 3381
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 722
;   LENGTH: 2002
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-094-749-722

Alignment Scores:
Pred. No.:              50.1          Length:         2002
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            4.7%          Indels:         0
DB:                     4             Gaps:           0

US-10-507-132-4 (1-172) x US-10-094-749-722 (1-2002)

Qy         70 ValSerSerLysGlnValLeuGly 77
              |||||||||||||||||||||||
Db        802 GTGAGCTCCAAACAAGTTTTAGGA 825

RESULT 3
US-09-949-016-14178
; Sequence 14178, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14178
;   LENGTH: 88268
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(88268)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14178

Alignment Scores:
Pred. No.:              1.81e+03      Length:         88268
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            4.7%          Indels:         0
DB:                     3             Gaps:           0

US-10-507-132-4 (1-172) x US-09-949-016-14178 (1-88268)

Qy         46 LeuArgIleAspTyrArgSerPhe 53
              |||||||||||||||||||||||
Db      49601 CTTAGAATTGATTACAGATCTTTC 49624

RESULT 4
US-09-949-016-13845
; Sequence 13845, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13845
;   LENGTH: 152132
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-13845

Alignment Scores:
Pred. No.:              3.04e+03      Length:         152132
Score:                  8.00          Matches:        8
Percent Similarity:     100.0%        Conservative:   0
Best Local Similarity:  100.0%        Mismatches:     0
Query Match:            4.7%          Indels:         0
DB:                     3             Gaps:           0

US-10-507-132-4 (1-172) x US-09-949-016-13845 (1-152132)

Qy         95 ValSerGluAspGluValIleGly 102
              |||||||||||||||||||||||
```

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Db     118339 GTATCAGAAGATGAAGTCATCGGG 118362

RESULT 5
US-09-949-016-12371
; Sequence 12371, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12371
;   LENGTH: 152145
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-12371

Alignment Scores:
Pred. No.:              3.04e+03        Length:         152145
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     3               Gaps:           0

US-10-507-132-4 (1-172) x US-09-949-016-12371 (1-152145)

Qy          95 ValSerGluAspGluValIleGly 102
               ||||||||||||||||||||||||
Db     118339 GTATCAGAAGATGAAGTCATCGGG 118362

RESULT 6
US-09-189-060B-23/c
; Sequence 23, Application US/09189060B
; Patent No. 6270968
; GENERAL INFORMATION:
;  APPLICANT: Dalboge, Henrik
;  APPLICANT:  Sandal, Thomas
;  APPLICANT:  Kauppinen, Markus
;  APPLICANT:  Borge, Diderichsen
;  TITLE OF INVENTION: Method Of Providing No. 6270968el DNA Sequences
;  FILE REFERENCE: 4772.204-US
;  CURRENT APPLICATION NUMBER: US/09/189,060B
;  CURRENT FILING DATE:  1998-11-10
;  PRIOR APPLICATION NUMBER: PCT/DK97/00216
;  PRIOR FILING DATE: 1997-05-12
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
;   LENGTH: 166
;   TYPE: DNA
;   ORGANISM: Hybrid
US-09-189-060B-23

Alignment Scores:
Pred. No.:              59              Length:         166
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.1%            Indels:         0
DB:                     3               Gaps:           0

US-10-507-132-4 (1-172) x US-09-189-060B-23 (1-166)

Qy         106 LeuArgValProHisGlnArg 112
               |||||||||||||||||||
Db          34 CTGAGAGTGCCACACCAGCGT 14

RESULT 7
US-09-189-060B-25/c
; Sequence 25, Application US/09189060B
; Patent No. 6270968
; GENERAL INFORMATION:
;  APPLICANT: Dalboge, Henrik
;  APPLICANT:  Sandal, Thomas
;  APPLICANT:  Kauppinen, Markus
;  APPLICANT:  Borge, Diderichsen
;  TITLE OF INVENTION: Method Of Providing No. 6270968el DNA Sequences
;  FILE REFERENCE: 4772.204-US
;  CURRENT APPLICATION NUMBER: US/09/189,060B
;  CURRENT FILING DATE:  1998-11-10
;  PRIOR APPLICATION NUMBER: PCT/DK97/00216
;  PRIOR FILING DATE: 1997-05-12
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 181
;   TYPE: DNA
;   ORGANISM: Hybrid
US-09-189-060B-25

Alignment Scores:
Pred. No.:              64              Length:         181
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.1%            Indels:         0
DB:                     3               Gaps:           0

US-10-507-132-4 (1-172) x US-09-189-060B-25 (1-181)

Qy         106 LeuArgValProHisGlnArg 112
               |||||||||||||||||||
Db          34 CTGCGAGTGCCACACCAGCGT 14

RESULT 8
US-09-711-164-242
; Sequence 242, Application US/09711164
; Patent No. 6589738
; GENERAL INFORMATION:
;  APPLICANT:  Forsyth, R. Allyn
;  APPLICANT:  Ohlsen, Kari
;  APPLICANT:  Zyskind, Judith
;  TITLE OF INVENTION:  GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETO
;  FILE REFERENCE:  ELITRA.008A
;  CURRENT APPLICATION NUMBER: US/09/711,164
;  CURRENT FILING DATE:  2000-11-09
;  PRIOR APPLICATION NUMBER:   US 60/164415
;  PRIOR FILING DATE:   1999-11-9
;  NUMBER OF SEQ ID NOS:  469
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 242
;   LENGTH: 297
;   TYPE: DNA
;   ORGANISM: Escherichia coli
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(297)
US-09-711-164-242

Alignment Scores:
Pred. No.:              102             Length:         297
Score:                  7.00            Matches:        7
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.1%            Indels:         0
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```
DB:                     3              Gaps:          0

US-10-507-132-4 (1-172) x US-09-711-164-242 (1-297)

Qy         46 LeuArgIleAspTyrArgSer 52
              |||||||||||||||||||
Db        175 TTACGTATTGACTATCGCAGT 195

RESULT 9
US-09-513-999C-16794
; Sequence 16794, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 16794
;   LENGTH: 303
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-513-999C-16794

Alignment Scores:
Pred. No.:              104            Length:        303
Score:                  7.00           Matches:       7
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            4.1%           Indels:        0
DB:                     3              Gaps:          0

US-10-507-132-4 (1-172) x US-09-513-999C-16794 (1-303)

Qy         82 ArgThrGlnHisPheIleGly 88
              ||||||||||||||||||||
Db         11 AGGACACAGCATTTTATTGGC 31

RESULT 10
US-09-270-767-9687/c
; Sequence 9687, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9687
;   LENGTH: 377
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
US-09-270-767-9687

Alignment Scores:
Pred. No.:              128            Length:        377
Score:                  7.00           Matches:       7
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            4.1%           Indels:        0
DB:                     3              Gaps:          0

US-10-507-132-4 (1-172) x US-09-270-767-9687 (1-377)

Qy         50 TyrArgSerPheLeuAspLys 56
              ||||||||||||||||||||
Db        140 TATCGTTCGTTCCTCGACAAA 120

RESULT 11
US-09-270-767-24969/c
; Sequence 24969, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24969
;   LENGTH: 377
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
US-09-270-767-24969

Alignment Scores:
Pred. No.:              128            Length:        377
Score:                  7.00           Matches:       7
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            4.1%           Indels:        0
DB:                     3              Gaps:          0

US-10-507-132-4 (1-172) x US-09-270-767-24969 (1-377)

Qy         50 TyrArgSerPheLeuAspLys 56
              ||||||||||||||||||||
Db        140 TATCGTTCGTTCCTCGACAAA 120

RESULT 12
US-09-489-039A-1757
; Sequence 1757, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 1757
;   LENGTH: 399
;   TYPE: DNA
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-1757

Alignment Scores:
Pred. No.:              135            Length:        399
Score:                  7.00           Matches:       7
Percent Similarity:     100.0%         Conservative:  0
Best Local Similarity:  100.0%         Mismatches:    0
Query Match:            4.1%           Indels:        0
DB:                     3              Gaps:          0

US-10-507-132-4 (1-172) x US-09-489-039A-1757 (1-399)

Qy        140 GlyValTrpLysPheAlaGly 146
              ||||||||||||||||||||
Db          3 GGCGTGTGGAAGTTCGCCGGC 23

RESULT 13
US-09-513-999C-3332/c
; Sequence 3332, Application US/09513999C
```

; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3332
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 230..463
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 150
; OTHER INFORMATION: b=c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 450
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 74
; OTHER INFORMATION: Xaa=Asp or Gly
US-09-513-999C-3332

Alignment Scores:

Pred. No.:	156	Length:	463
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.1%	Indels:	0
DB:	3	Gaps:	0

US-10-507-132-4 (1-172) x US-09-513-999C-3332 (1-463)

```
Qy         69 MetValSerSerLysGlnVal 75
              |||||||||||||||||||||
Db        343 ATGGTGTCCTCCAAACAAGTA 323
```

RESULT 14
US-09-621-976-15423
; Sequence 15423, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15423
; LENGTH: 479
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-15423

Alignment Scores:

Pred. No.:	161	Length:	479
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.1%	Indels:	0
DB:	3	Gaps:	0

US-10-507-132-4 (1-172) x US-09-621-976-15423 (1-479)

```
Qy         36 AspArgLeuArgLysValIle 42
              ||||||||||||||||||||
Db        252 GACCGCCTCCGCAAAGTCATC 272
```

RESULT 15
US-09-513-999C-1132/c
; Sequence 1132, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 1132
; LENGTH: 488
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 331..486
US-09-513-999C-1132

Alignment Scores:

Pred. No.:	164	Length:	488
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.1%	Indels:	0
DB:	3	Gaps:	0

US-10-507-132-4 (1-172) x US-09-513-999C-1132 (1-488)

```
Qy         94 LysValSerGluAspGluVal 100
              ||||||||||||||||||||
Db        401 AAGGTGTCGGAAGATGAAGTT 381
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Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

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13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	8	4.7	405	3	US-09-867-701-3030	Sequence 3030, Ap
	2	8	4.7	512	3	US-09-918-995-32405	Sequence 32405, A
c	3	8	4.7	600	10	US-10-972-079-49239	Sequence 49239, A
c	4	8	4.7	1521	6	US-10-106-698-221	Sequence 221, App
	5	8	4.7	1690	13	US-11-097-143-11207	Sequence 11207, A
	6	8	4.7	1877	12	US-10-301-480-36243	Sequence 36243, A
	7	8	4.7	1877	12	US-10-301-480-36244	Sequence 36244, A
	8	8	4.7	1877	12	US-10-301-480-649652	Sequence 649652,
	9	8	4.7	1877	12	US-10-301-480-649653	Sequence 649653,
	10	8	4.7	2002	7	US-10-094-749-722	Sequence 722, App
c	11	8	4.7	4182	13	US-11-097-143-11206	Sequence 11206, A
	12	8	4.7	12822	3	US-09-764-847-1579	Sequence 1579, Ap
	13	8	4.7	12822	6	US-10-092-154-1579	Sequence 1579, Ap
c	14	8	4.7	715517	6	US-10-027-632-53712	Sequence 53712, A
c	15	8	4.7	715517	7	US-10-027-632-53712	Sequence 53712, A
c	16	7	4.1	25	8	US-10-719-956-117872	Sequence 117872,
	17	7	4.1	25	13	US-11-036-317-670216	Sequence 670216,
c	18	7	4.1	25	13	US-11-060-756-118545	Sequence 118545,
c	19	7	4.1	25	13	US-11-060-756-136499	Sequence 136499,
c	20	7	4.1	25	13	US-11-060-756-172179	Sequence 172179,
c	21	7	4.1	25	13	US-11-060-756-206628	Sequence 206628,
c	22	7	4.1	25	13	US-11-060-756-223123	Sequence 223123,
c	23	7	4.1	41	8	US-10-035-833A-6065	Sequence 6065, Ap
	24	7	4.1	50	16	US-11-175-859-11216	Sequence 11216, A
	25	7	4.1	50	16	US-11-175-859-28918	Sequence 28918, A
	26	7	4.1	70	11	US-10-310-914A-10937	Sequence 10937, A
	27	7	4.1	123	8	US-10-424-599-94403	Sequence 94403, A
	28	7	4.1	201	8	US-10-741-601-6346	Sequence 6346, Ap
	29	7	4.1	201	9	US-10-719-993-11191	Sequence 11191, A
c	30	7	4.1	201	9	US-10-719-993-28020	Sequence 28020, A
c	31	7	4.1	201	9	US-10-741-600-34524	Sequence 34524, A
	32	7	4.1	201	9	US-10-741-600-48603	Sequence 48603, A
	33	7	4.1	201	9	US-10-741-600-48622	Sequence 48622, A
	34	7	4.1	201	9	US-10-741-600-48625	Sequence 48625, A
	35	7	4.1	201	9	US-10-741-600-48655	Sequence 48655, A
	36	7	4.1	201	9	US-10-741-600-48818	Sequence 48818, A
	37	7	4.1	201	9	US-10-741-600-48819	Sequence 48819, A
c	38	7	4.1	201	10	US-10-995-561-32837	Sequence 32837, A
	39	7	4.1	201	16	US-11-124-367A-14520	Sequence 14520, A
	40	7	4.1	211	8	US-10-424-599-110025	Sequence 110025,
	41	7	4.1	279	8	US-10-398-221-141	Sequence 141, App
c	42	7	4.1	294	10	US-10-831-070-215	Sequence 215, App
	43	7	4.1	297	7	US-10-287-274-242	Sequence 242, App
	44	7	4.1	305	8	US-10-242-535A-23467	Sequence 23467, A
	45	7	4.1	305	8	US-10-085-783A-23467	Sequence 23467, A

ALIGNMENTS

RESULT 1
US-09-867-701-3030
; Sequence 3030, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3030
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-3030

Alignment Scores:
Pred. No.: 115 Length: 405
Score: 8.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.7% Indels: 0
DB: 3 Gaps: 0

US-10-507-132-4 (1-172) x US-09-867-701-3030 (1-405)

Qy 70 ValSerSerLysGlnValLeuGly 77
||||||||||||||||||||||||
Db 111 GTGAGCTCCAAACAAGTTTTAGGA 134

RESULT 2
US-09-918-995-32405
; Sequence 32405, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32405
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(512)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-32405

Alignment Scores:
Pred. No.: 142 Length: 512
Score: 8.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.7% Indels: 0
DB: 3 Gaps: 0

US-10-507-132-4 (1-172) x US-09-918-995-32405 (1-512)

Qy 70 ValSerSerLysGlnValLeuGly 77
||||||||||||||||||||||||
Db 440 GTGAGCTCCAAACAAGTTTTAGGA 463

RESULT 3
US-10-972-079-49239/c
; Sequence 49239, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF
; TITLE OF INVENTION: LIVESTOCK
; FILE REFERENCE: MMI1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 49239
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Chicken 19866894295080_1
US-10-972-079-49239

Alignment Scores:
Pred. No.: 164 Length: 600
Score: 8.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.7% Indels: 0
DB: 10 Gaps: 0

US-10-507-132-4 (1-172) x US-10-972-079-49239 (1-600)

Qy 38 LeuArgLysValIleAlaProThr 45
||||||||||||||||||||||
Db 560 CTTAGAAAGGTCATTGCTCCCACA 537

RESULT 4
US-10-106-698-221/c
; Sequence 221, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 221
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-106-698-221

Alignment Scores:
Pred. No.: 382 Length: 1521
Score: 8.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 4.7% Indels: 0
DB: 6 Gaps: 0

US-10-507-132-4 (1-172) x US-10-106-698-221 (1-1521)

Qy 70 ValSerSerLysGlnValLeuGly 77
||||||||||||||||||||||||
Db 1212 GTGAGCTCCAAACAAGTTTTAGGA 1189

RESULT 5
US-11-097-143-11207
; Sequence 11207, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28

; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11207
; LENGTH: 1690
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-11207

Alignment Scores:

Pred. No.:	420	Length:	1690
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	13	Gaps:	0

US-10-507-132-4 (1-172) x US-11-097-143-11207 (1-1690)

```
Qy         40 LysValIleAlaProThrLeuArg 47
              ||||||||||||||||||||||||
Db       1040 AAAGTTATAGCTCCGACTCTGAGA 1063
```

RESULT 6
US-10-301-480-36243
; Sequence 36243, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36243
; LENGTH: 1877
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-36243

Alignment Scores:

Pred. No.:	462	Length:	1877
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	12	Gaps:	0

US-10-507-132-4 (1-172) x US-10-301-480-36243 (1-1877)

```
Qy         46 LeuArgIleAspTyrArgSerPhe 53
              |||||||||||||||||||||||
Db        542 CTTAGAATTGATTACAGATCTTTC 565
```

RESULT 7
US-10-301-480-36244
; Sequence 36244, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36244
; LENGTH: 1877
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-36244

Alignment Scores:

Pred. No.:	462	Length:	1877
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	12	Gaps:	0

US-10-507-132-4 (1-172) x US-10-301-480-36244 (1-1877)

```
Qy         46 LeuArgIleAspTyrArgSerPhe 53
              |||||||||||||||||||||||
Db        542 CTTAGAATTGATTACAGATCTTTC 565
```

RESULT 8
US-10-301-480-649652
; Sequence 649652, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 649652
; LENGTH: 1877
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-649652

Alignment Scores:

Pred. No.:	462	Length:	1877
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	12	Gaps:	0

US-10-507-132-4 (1-172) x US-10-301-480-649652 (1-1877)

```
Qy         46 LeuArgIleAspTyrArgSerPhe 53
              |||||||||||||||||||||||
Db        542 CTTAGAATTGATTACAGATCTTTC 565
```

RESULT 9
US-10-301-480-649653
; Sequence 649653, Application US/10301480

; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 649653
; LENGTH: 1877
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-649653

Alignment Scores:

Pred. No.:	462	Length:	1877
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	12	Gaps:	0

US-10-507-132-4 (1-172) x US-10-301-480-649653 (1-1877)

```
Qy         46 LeuArgIleAspTyrArgSerPhe 53
              |||||||||||||||||||||||
Db        542 CTTAGAATTGATTACAGATCTTTC 565
```

RESULT 10
US-10-094-749-722
; Sequence 722, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 722
; LENGTH: 2002
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-094-749-722

Alignment Scores:

Pred. No.:	490	Length:	2002
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	7	Gaps:	0

US-10-507-132-4 (1-172) x US-10-094-749-722 (1-2002)

```
Qy         70 ValSerSerLysGlnValLeuGly 77
              |||||||||||||||||||||||
Db        802 GTGAGCTCCAAACAAGTTTTAGGA 825
```

RESULT 11
US-11-097-143-11206/c
; Sequence 11206, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11206
; LENGTH: 4182
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-11206

Alignment Scores:

Pred. No.:	957	Length:	4182
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	13	Gaps:	0

US-10-507-132-4 (1-172) x US-11-097-143-11206 (1-4182)

```
Qy         40 LysValIleAlaProThrLeuArg 47
              |||||||||||||||||||||||
Db       1714 AAAGTTATAGCTCCGACTCTGAGA 1691
```

RESULT 12
US-09-764-847-1579
; Sequence 1579, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009

; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1579
; LENGTH: 12822
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1579

Alignment Scores:

Pred. No.:	2.65e+03	Length:	12822
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	3	Gaps:	0

US-10-507-132-4 (1-172) x US-09-764-847-1579 (1-12822)

```
Qy         70 ValSerSerLysGlnValLeuGly 77
              ||||||||||||||||||||||||
Db      11559 GTGAGCTCCAAACAAGTTTTAGGA 11582
```

RESULT 13
US-10-092-154-1579
; Sequence 1579, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1579
; LENGTH: 12822
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-154-1579

Alignment Scores:

Pred. No.:	2.65e+03	Length:	12822
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	6	Gaps:	0

US-10-507-132-4 (1-172) x US-10-092-154-1579 (1-12822)

```
Qy         70 ValSerSerLysGlnValLeuGly 77
              ||||||||||||||||||||||||
Db      11559 GTGAGCTCCAAACAAGTTTTAGGA 11582
```

RESULT 14
US-10-027-632-53712/c
; Sequence 53712, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53712
; LENGTH: 715517
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(715517)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-53712

Alignment Scores:

Pred. No.:	1.03e+05	Length:	715517
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	6	Gaps:	0

US-10-507-132-4 (1-172) x US-10-027-632-53712 (1-715517)

```
Qy         37 ArgLeuArgLysValIleAlaPro 44
              ||||||||||||||||||||||||
Db     315054 AGACTCAGAAAAGTGATAGCACCT 315031
```

RESULT 15
US-10-027-632-53712/c
; Sequence 53712, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53712
; LENGTH: 715517
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(715517)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-53712

Alignment Scores:

Pred. No.:	1.03e+05	Length:	715517
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	7	Gaps:	0

US-10-507-132-4 (1-172) x US-10-027-632-53712 (1-715517)

```
Qy         37 ArgLeuArgLysValIleAlaPro 44
              ||||||||||||||||||||||||
Db     315054 AGACTCAGAAAAGTGATAGCACCT 315031
```

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Job time : 1056 secs

GenCore version 5.1.9

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2006, 17:43:39 ; Search time 170 Seconds
(without alignments)
3112.203 Million cell updates/sec

Title: US-10-507-132-4
Perfect score: 172
Sequence: 1 MGSQVQKSDEITFSDYLGLM.....WGEFDFDRIFEDGRETFGDK 172

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 2931743 seqs, 1025338116 residues

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Post-processing: Listing first 45 summaries

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-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=olip2n.rnpbn
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-MAXLEN=2000000000 -HOST=abss06h
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

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3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
11: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	172	100.0	516	6	US-10-507-132-3	Sequence 3, Appli
2	172	100.0	600	6	US-10-507-132-13	Sequence 13, Appl
3	172	100.0	610	6	US-10-507-132-16	Sequence 16, Appl
4	169	98.3	538	6	US-10-507-132-15	Sequence 15, Appl
5	169	98.3	545	6	US-10-507-132-14	Sequence 14, Appl
6	125	72.7	729	6	US-10-507-132-18	Sequence 18, Appl
7	125	72.7	732	6	US-10-507-132-17	Sequence 17, Appl
8	97	56.4	516	6	US-10-507-132-1	Sequence 1, Appli
9	8	4.7	497	8	US-11-266-748A-184560	Sequence 184560,
10	8	4.7	926	8	US-11-266-748A-71004	Sequence 71004, A
c 11	8	4.7	926	8	US-11-266-748A-123815	Sequence 123815,
c 12	8	4.7	1586	9	US-11-218-305-4533	Sequence 4533, Ap
13	8	4.7	3304	8	US-11-266-748A-32509	Sequence 32509, A
14	8	4.7	4322	9	US-11-218-305-16760	Sequence 16760, A
15	7	4.1	21	6	US-10-507-132-8	Sequence 8, Appli
c 16	7	4.1	23	6	US-10-507-132-9	Sequence 9, Appli
17	7	4.1	27	6	US-10-507-132-12	Sequence 12, Appl
18	7	4.1	201	6	US-10-284-444-4992	Sequence 4992, Ap
19	7	4.1	201	6	US-10-284-444-4993	Sequence 4993, Ap
20	7	4.1	201	6	US-10-284-444-11652	Sequence 11652, A
21	7	4.1	201	6	US-10-284-444-11653	Sequence 11653, A
22	7	4.1	201	6	US-10-284-444-11654	Sequence 11654, A
23	7	4.1	201	6	US-10-284-444-11655	Sequence 11655, A
24	7	4.1	235	8	US-11-266-748A-169345	Sequence 169345,
c 25	7	4.1	372	8	US-11-266-748A-377254	Sequence 377254,
26	7	4.1	372	8	US-11-266-748A-460633	Sequence 460633,
c 27	7	4.1	393	10	US-11-314-834-2587	Sequence 2587, Ap
28	7	4.1	420	8	US-11-266-748A-303484	Sequence 303484,
c 29	7	4.1	441	6	US-10-513-369-1608	Sequence 1608, Ap
30	7	4.1	450	8	US-11-266-748A-94729	Sequence 94729, A
c 31	7	4.1	450	8	US-11-266-748A-147540	Sequence 147540,
32	7	4.1	496	8	US-11-266-748A-303304	Sequence 303304,
c 33	7	4.1	550	10	US-11-292-078-13846	Sequence 13846, A
c 34	7	4.1	629	8	US-11-266-748A-53897	Sequence 53897, A
c 35	7	4.1	629	8	US-11-266-748A-211466	Sequence 211466,
36	7	4.1	629	8	US-11-266-748A-235129	Sequence 235129,
37	7	4.1	638	8	US-11-266-748A-412196	Sequence 412196,
c 38	7	4.1	650	10	US-11-292-078-112	Sequence 112, App
c 39	7	4.1	650	10	US-11-292-078-118	Sequence 118, App
c 40	7	4.1	710	8	US-11-266-748A-253499	Sequence 253499,
41	7	4.1	710	8	US-11-266-748A-314016	Sequence 314016,
42	7	4.1	762	8	US-11-217-529-2570	Sequence 2570, Ap
43	7	4.1	764	8	US-11-266-748A-273078	Sequence 273078,
c 44	7	4.1	764	8	US-11-266-748A-333595	Sequence 333595,
45	7	4.1	777	8	US-11-179-064B-75	Sequence 75, Appl

ALIGNMENTS

RESULT 1
US-10-507-132-3
; Sequence 3, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
; APPLICANT: Koichiro KAKU et al.
; TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
; TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
; FILE REFERENCE: 1254-0258PUS1
; CURRENT APPLICATION NUMBER: US/10/507,132
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: JP 2002-66955
; PRIOR FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Pyricularia oryzae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(516)
US-10-507-132-3

Alignment Scores:

Pred. No.:	5.56e-180	Length:	516
Score:	172.00	Matches:	172
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0

```
DB:                    6              Gaps:          0

US-10-507-132-4 (1-172) x US-10-507-132-3 (1-516)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 60

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 120

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 180

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 240

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 300

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 360

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 420

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 480

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
              ||||||||||||||||||||||||||||||||||||
Db        481 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516

RESULT 2
US-10-507-132-13
; Sequence 13, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU et al.
;  TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
;  TITLE OF INVENTION:  AGRICULTURAL FUNGICIDAL AGENT
;  FILE REFERENCE: 1254-0258PUS1
;  CURRENT APPLICATION NUMBER: US/10/507,132
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: JP 2002-66955
;  PRIOR FILING DATE: 2002-03-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 600
;   TYPE: DNA
;   ORGANISM: Pyricularia oryzae
US-10-507-132-13

Alignment Scores:
Pred. No.:              6.4e-180      Length:          600
Score:                  172.00        Matches:         172
Percent Similarity:     100.0%        Conservative:    0
Best Local Similarity:  100.0%        Mismatches:      0
Query Match:            100.0%        Indels:          0
DB:                     6             Gaps:            0

US-10-507-132-4 (1-172) x US-10-507-132-13 (1-600)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         81 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 140

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 200

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 260

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 320

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 380

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 440

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 500

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 560

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
              ||||||||||||||||||||||||||||||||||||
Db        561 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 596

RESULT 3
US-10-507-132-16
; Sequence 16, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU et al.
;  TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
;  TITLE OF INVENTION:  AGRICULTURAL FUNGICIDAL AGENT
;  FILE REFERENCE: 1254-0258PUS1
;  CURRENT APPLICATION NUMBER: US/10/507,132
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: JP 2002-66955
;  PRIOR FILING DATE: 2002-03-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 610
;   TYPE: DNA
;   ORGANISM: Pyricularia oryzae
US-10-507-132-16

Alignment Scores:
Pred. No.:              6.5e-180      Length:          610
Score:                  172.00        Matches:         172
Percent Similarity:     100.0%        Conservative:    0
Best Local Similarity:  100.0%        Mismatches:      0
Query Match:            100.0%        Indels:          0
DB:                     6             Gaps:            0

US-10-507-132-4 (1-172) x US-10-507-132-16 (1-610)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 140

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 200
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Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 260

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 320

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 380

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 440

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 500

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 GTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAGTTCGACTTTGACAGG 560

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
              ||||||||||||||||||||||||||||||||||||
Db        561 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 596

RESULT 4
US-10-507-132-15
; Sequence 15, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU et al.
;  TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
;  TITLE OF INVENTION:  AGRICULTURAL FUNGICIDAL AGENT
;  FILE REFERENCE: 1254-0258PUS1
;  CURRENT APPLICATION NUMBER: US/10/507,132
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: JP 2002-66955
;  PRIOR FILING DATE: 2002-03-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 538
;   TYPE: DNA
;   ORGANISM: Pyricularia oryzae
US-10-507-132-15

Alignment Scores:
Pred. No.:              1.17e-176      Length:         538
Score:                  169.00         Matches:        169
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            98.3%          Indels:         0
DB:                     6              Gaps:           0

US-10-507-132-4 (1-172) x US-10-507-132-15 (1-538)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 90

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 150

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 210

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 270

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 330

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 390

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 450

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GTCTGGAAGTTCGCCGGCCTCAAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGG 510

Qy        161 IlePheGluAspGlyArgGluThrPhe 169
              ||||||||||||||||||||||||||
Db        511 ATCTTTGAGGACGGACGGGAGACCTTT 537

RESULT 5
US-10-507-132-14
; Sequence 14, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU et al.
;  TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
;  TITLE OF INVENTION:  AGRICULTURAL FUNGICIDAL AGENT
;  FILE REFERENCE: 1254-0258PUS1
;  CURRENT APPLICATION NUMBER: US/10/507,132
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: JP 2002-66955
;  PRIOR FILING DATE: 2002-03-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 545
;   TYPE: DNA
;   ORGANISM: Pyricularia oryzae
US-10-507-132-14

Alignment Scores:
Pred. No.:              1.18e-176      Length:         545
Score:                  169.00         Matches:        169
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            98.3%          Indels:         0
DB:                     6              Gaps:           0

US-10-507-132-4 (1-172) x US-10-507-132-14 (1-545)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         38 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 97

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 157

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 217

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 277

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 337
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Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 397

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 457

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 GTCTGGAAGTTCGCCGGCCTCAAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGG 517

Qy        161 IlePheGluAspGlyArgGluThrPhe 169
              |||||||||||||||||||||||||||
Db        518 ATCTTTGAGGACGGACGGGAGACCTTT 544

RESULT 6
US-10-507-132-18
; Sequence 18, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU et al.
;  TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
;  TITLE OF INVENTION:  AGRICULTURAL FUNGICIDAL AGENT
;  FILE REFERENCE: 1254-0258PUS1
;  CURRENT APPLICATION NUMBER: US/10/507,132
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: JP 2002-66955
;  PRIOR FILING DATE: 2002-03-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 729
;   TYPE: DNA
;   ORGANISM: Pyricularia oryzae
US-10-507-132-18

Alignment Scores:
Pred. No.:              4.61e-128      Length:          729
Score:                  125.00         Matches:         125
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            72.7%          Indels:          0
DB:                     6              Gaps:            0

US-10-507-132-4 (1-172) x US-10-507-132-18 (1-729)

Qy         48 IleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetProAlaGluGluPheVal 67
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 ATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTC 414

Qy         68 GlyMetValSerSerLysGlnValLeuGlyAspProThrLeuArgThrGlnHisPheIle 87
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 GGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATC 474

Qy         88 GlyGlyThrArgTrpGluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArg 107
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGC 534

Qy        108 ValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlyHisAla 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 GTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCC 594

Qy        128 HisSerAlaAsnLeuHisTrpTyrLysLysIleAspGlyValTrpLysPheAlaGlyLeu 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 CACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTC 654

Qy        148 LysProAspIleArgTrpGlyGluPheAspPheAspArgIlePheGluAspGlyArgGlu 167
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 AAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGGATCTTTGAGGACGGACGGGAG 714

Qy        168 ThrPheGlyAspLys 172
              ||||||||||||||||
Db        715 ACCTTTGGCGACAAA 729

RESULT 7
US-10-507-132-17
; Sequence 17, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU et al.
;  TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
;  TITLE OF INVENTION:  AGRICULTURAL FUNGICIDAL AGENT
;  FILE REFERENCE: 1254-0258PUS1
;  CURRENT APPLICATION NUMBER: US/10/507,132
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: JP 2002-66955
;  PRIOR FILING DATE: 2002-03-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
;   LENGTH: 732
;   TYPE: DNA
;   ORGANISM: Pyricularia oryzae
US-10-507-132-17

Alignment Scores:
Pred. No.:              4.63e-128      Length:          732
Score:                  125.00         Matches:         125
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            72.7%          Indels:          0
DB:                     6              Gaps:            0

US-10-507-132-4 (1-172) x US-10-507-132-17 (1-732)

Qy         48 IleAspTyrArgSerPheLeuAspLysLeuTrpGluAlaMetProAlaGluGluPheVal 67
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 ATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTC 417

Qy         68 GlyMetValSerSerLysGlnValLeuGlyAspProThrLeuArgThrGlnHisPheIle 87
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 GGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATC 477

Qy         88 GlyGlyThrArgTrpGluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArg 107
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 GGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGC 537

Qy        108 ValProHisGlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlyHisAla 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 GTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCC 597

Qy        128 HisSerAlaAsnLeuHisTrpTyrLysLysIleAspGlyValTrpLysPheAlaGlyLeu 147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 CACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTC 657

Qy        148 LysProAspIleArgTrpGlyGluPheAspPheAspArgIlePheGluAspGlyArgGlu 167
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 AAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGGATCTTTGAGGACGGACGGGAG 717

Qy        168 ThrPheGlyAspLys 172
              ||||||||||||||||
Db        718 ACCTTTGGCGACAAA 732

RESULT 8
US-10-507-132-1
; Sequence 1, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
;  APPLICANT: Koichiro KAKU et al.
;  TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
;  TITLE OF INVENTION:  AGRICULTURAL FUNGICIDAL AGENT
;  FILE REFERENCE: 1254-0258PUS1
;  CURRENT APPLICATION NUMBER: US/10/507,132
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: JP 2002-66955
```

```
;  PRIOR FILING DATE: 2002-03-12
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;    LENGTH: 516
;    TYPE: DNA
;    ORGANISM: Pyricularia oryzae
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (1)..(516)
US-10-507-132-1

Alignment Scores:
Pred. No.:              2.35e-97        Length:         516
Score:                  97.00           Matches:        97
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            56.4%           Indels:         0
DB:                     6               Gaps:           0

US-10-507-132-4 (1-172) x US-10-507-132-1 (1-516)

Qy          76 LeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysVal 95
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         226 CTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTG 285

Qy          96 SerGluAspGluValIleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAsp 115
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         286 TCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGAC 345

Qy         116 ThrThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyr 135
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         346 ACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTAC 405

Qy         136 LysLysIleAspGlyValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGlu 155
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         406 AAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGATATCCGCTGGGGCGAG 465

Qy         156 PheAspPheAspArgIlePheGluAspGlyArgGluThrPheGlyAspLys 172
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         466 TTCGACTTTGACAGGATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 516

RESULT 9
US-11-266-748A-184560
; Sequence 184560, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 184560
;    LENGTH: 497
;    TYPE: DNA
;    ORGANISM: Homo Sapiens
US-11-266-748A-184560

Alignment Scores:
Pred. No.:              25.4            Length:         497
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     8               Gaps:           0

US-10-507-132-4 (1-172) x US-11-266-748A-184560 (1-497)

Qy          70 ValSerSerLysGlnValLeuGly 77
               |||||||||||||||||||||||
Db         308 GTGAGCTCCAAACAAGTTTTAGGG 331

RESULT 10
US-11-266-748A-71004
; Sequence 71004, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 71004
;    LENGTH: 926
;    TYPE: DNA
;    ORGANISM: Homo Sapiens
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (144)..(446)
;    OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-71004

Alignment Scores:
Pred. No.:              45.4            Length:         926
Score:                  8.00            Matches:        8
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            4.7%            Indels:         0
DB:                     8               Gaps:           0

US-10-507-132-4 (1-172) x US-11-266-748A-71004 (1-926)

Qy          70 ValSerSerLysGlnValLeuGly 77
               |||||||||||||||||||||||
```

```
Db        752 GTGAGCTCCAAACAAGTTTTAGGA 775

RESULT 11
US-11-266-748A-123815/c
; Sequence 123815, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 123815
;   LENGTH: 926
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (481)..(783)
;   OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-123815

Alignment Scores:
Pred. No.:                45.4          Length:          926
Score:                    8.00          Matches:         8
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              4.7%          Indels:          0
DB:                       8             Gaps:            0

US-10-507-132-4 (1-172) x US-11-266-748A-123815 (1-926)

Qy          70 ValSerSerLysGlnValLeuGly 77
               |||||||||||||||||||||||
Db         175 GTGAGCTCCAAACAAGTTTTAGGA 152

RESULT 12
US-11-218-305-4533/c
; Sequence 4533, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
;  APPLICANT: MONSANTO TECHNOLOGY, LLC
;  APPLICANT:  McLaird, Paul L.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Wu, Kunsheng
;  TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
;  TITLE OF INVENTION:  Corn.
;  FILE REFERENCE: 38-21 (53660)B
;  CURRENT APPLICATION NUMBER: US/11/218,305
;  CURRENT FILING DATE:  2005-09-01
;  PRIOR APPLICATION NUMBER: US 60/606,880
;  PRIOR FILING DATE: 2004-09-01
;  NUMBER OF SEQ ID NOS: 25043
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4533
;   LENGTH: 1586
;   TYPE: DNA
;   ORGANISM: Zea mays
US-11-218-305-4533

Alignment Scores:
Pred. No.:                75.1          Length:          1586
Score:                    8.00          Matches:         8
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              4.7%          Indels:          0
DB:                       9             Gaps:            0

US-10-507-132-4 (1-172) x US-11-218-305-4533 (1-1586)

Qy          69 MetValSerSerLysGlnValLeu 76
               |||||||||||||||||||||||
Db        1217 ATGGTGAGCTCAAAACAGGTTCTG 1194

RESULT 13
US-11-266-748A-32509
; Sequence 32509, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
;  APPLICANT: Harkin, Paul
;  APPLICANT:  Johnston, Patrick
;  APPLICANT:  Mulligan, Karl
;  TITLE OF INVENTION: Transcriptome Microarray Technology and
;  TITLE OF INVENTION:  Methods of Using the Same
;  FILE REFERENCE: 55815-0102 (319189)
;  CURRENT APPLICATION NUMBER: US/11/266,748A
;  CURRENT FILING DATE:  2005-11-03
;  PRIOR APPLICATION NUMBER: EP 04105479.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105482.6
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105483.4
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105507.0
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105485.9
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: EP 04105484.2
;  PRIOR FILING DATE: 2004-11-03
;  PRIOR APPLICATION NUMBER: US 60/662,276
;  PRIOR FILING DATE: 2005-03-14
;  PRIOR APPLICATION NUMBER: US 60/700,293
;  PRIOR FILING DATE: 2005-07-18
;  NUMBER OF SEQ ID NOS: 483996
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32509
;   LENGTH: 3304
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-11-266-748A-32509

Alignment Scores:
Pred. No.:                149           Length:          3304
Score:                    8.00          Matches:         8
Percent Similarity:       100.0%        Conservative:    0
Best Local Similarity:    100.0%        Mismatches:      0
Query Match:              4.7%          Indels:          0
DB:                       8             Gaps:            0

US-10-507-132-4 (1-172) x US-11-266-748A-32509 (1-3304)

Qy          70 ValSerSerLysGlnValLeuGly 77
               |||||||||||||||||||||||
Db         812 GTGAGCTCCAAACAAGTTTTAGGA 835
```

RESULT 14
US-11-218-305-16760
; Sequence 16760, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO TECHNOLOGY, LLC
; APPLICANT: McLaird, Paul L.
; APPLICANT: Tao, Nengbing
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
; TITLE OF INVENTION: Corn.
; FILE REFERENCE: 38-21 (53660)B
; CURRENT APPLICATION NUMBER: US/11/218,305
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: US 60/606,880
; PRIOR FILING DATE: 2004-09-01
; NUMBER OF SEQ ID NOS: 25043
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16760
; LENGTH: 4322
; TYPE: DNA
; ORGANISM: Zea mays
US-11-218-305-16760

Alignment Scores:

Pred. No.:	192	Length:	4322
Score:	8.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.7%	Indels:	0
DB:	9	Gaps:	0

US-10-507-132-4 (1-172) x US-11-218-305-16760 (1-4322)

```
Qy         94 LysValSerGluAspGluValIle 101
              ||||||||||||||||||||||||
Db         70 AAGGTTTCTGAAGATGAAGTCATT 93
```

RESULT 15
US-10-507-132-8
; Sequence 8, Application US/10507132
; Publication No. US20060223136A1
; GENERAL INFORMATION:
; APPLICANT: Koichiro KAKU et al.
; TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE TO
; TITLE OF INVENTION: AGRICULTURAL FUNGICIDAL AGENT
; FILE REFERENCE: 1254-0258PUS1
; CURRENT APPLICATION NUMBER: US/10/507,132
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: JP 2002-66955
; PRIOR FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: chemically synthesized primer
US-10-507-132-8

Alignment Scores:

Pred. No.:	16.6	Length:	21
Score:	7.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	4.1%	Indels:	0
DB:	6	Gaps:	0

US-10-507-132-4 (1-172) x US-10-507-132-8 (1-21)

```
Qy          1 MetGlySerGlnValGlnLys 7
              |||||||||||||||||||||
Db          1 ATGGGTTCGCAAGTTCAAAAG 21
```

Search completed: December 4, 2006, 17:46:42
Job time : 173 secs

GenCore version 5.1.9

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2006, 17:18:36 ; Search time 4365 Seconds
(without alignments)
3305.198 Million cell updates/sec

Title: US-10-507-132-4
Perfect score: 172
Sequence: 1 MGSQVQKSDEITFSDYLGLM.....WGEFDFDRIFEDGRETFGDK 172

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 48236798 seqs, 27959665780 residues

Word size: 1

Total number of hits satisfying chosen parameters: 96471816

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
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-Q=/abss/ABSSWEB_spool/US10507132/runat_04122006_143531_9655/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=olip2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss07
-USER=US10507132_@CGN_1_1_6323_@runat_04122006_143531_9655 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	172	100.0	619	3	BM863356	BM863356 mgcm006xO
2	171	99.4	657	3	BM864194	BM864194 mgcm008xJ
3	168	97.7	664	3	BM863315	BM863315 mgcm006xE
4	141	82.0	599	3	BM864156	BM864156 mgcm008xD
5	132	76.7	510	3	BM863374	BM863374 mgcm006xC
6	132	76.7	530	3	BM863357	BM863357 mgcm006xO
7	132	76.7	643	3	BM864467	BM864467 mgcm010xH
8	129	75.0	571	3	BM863710	BM863710 mgcm007xE
9	125	72.7	486	3	BM863639	BM863639 mgcm007xG
10	115	66.9	473	3	BM864018	BM864018 mgcm008xG
11	106	61.6	600	3	BM864472	BM864472 mgcm010xJ
12	104	60.5	504	3	BM863499	BM863499 mgcm006xL
13	102	59.3	366	3	BM864053	BM864053 mgcm008xM
14	101	58.7	649	3	BM863340	BM863340 mgcm006xK
15	96	55.8	398	3	BM861952	BM861952 mgcm001xL
c 16	96	55.8	781	3	BM864820	BM864820 mgap007xA
17	91	52.9	593	3	BM863546	BM863546 mgcm006xF
18	91	52.9	602	3	BM863558	BM863558 mgcm006xH
19	85	49.4	515	3	BM861796	BM861796 mgcm001xI
20	85	49.4	523	3	BM863209	BM863209 mgcm005xD
c 21	74	43.0	541	4	CD036729	CD036729 mgsu011xC
c 22	74	43.0	570	4	CD034317	CD034317 mgmt015xP
23	71	41.3	441	3	BM871833	BM871833 mgns015xB
c 24	55	32.0	486	4	CD035120	CD035120 mgmt018xL
c 25	55	32.0	489	3	BM863213	BM863213 mgcm005xD
c 26	55	32.0	491	4	CD035038	CD035038 mgmt018xH
27	35	20.3	430	4	CD028671	CD028671 mgcm007xH
28	17	9.9	377	5	CD276416	CD276416 T143B0271
29	17	9.9	429	5	CD274144	CD274144 T143B0403
30	17	9.9	499	5	CD273332	CD273332 T143B0196
31	17	9.9	507	5	CD275678	CD275678 T143B0071
32	17	9.9	530	5	CD275940	CD275940 T143B0156
33	17	9.9	552	5	CD275566	CD275566 T143B0121
34	17	9.9	588	5	CD275905	CD275905 T143B0122
35	14	8.1	573	3	BQ109916	BQ109916 VD0100E09
36	11	6.4	476	2	BG280255	BG280255 c2b06np.r
37	9	5.2	363	3	BP100008	BP100008 BP100008
38	9	5.2	458	8	CO095673	CO095673 GR__Ea18G
c 39	9	5.2	517	4	BY471348	BY471348 BY471348
40	9	5.2	571	13	CZ697015	CZ697015 OC__Ba001
41	9	5.2	634	10	DV027321	DV027321 ZM_BFb014
42	9	5.2	752	13	CZ781295	CZ781295 OC__Ba014
c 43	9	5.2	881	9	DN476575	DN476575 altr207xo
44	8	4.7	181	3	BP686247	BP686247 BP686247
c 45	8	4.7	213	12	CG904247	CG904247 ZMMBBb051

ALIGNMENTS

RESULT 1
BM863356
LOCUS BM863356 619 bp mRNA linear EST 06-MAY-2003
DEFINITION mgcm006xO03f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm006xO03 5', mRNA sequence.
ACCESSION BM863356
VERSION BM863356.2 GI:30391591
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE 1 (bases 1 to 619)
AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.
TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe grisea
JOURNAL Unpublished (2002)
COMMENT On Mar 7, 2002 this sequence version replaced gi:19231038.
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone

dehydratase >gi|1127197|pdb|1STD|. . . 367 e-101
PCR PRimers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgcm006 row: O column: 03
Seq primer: T3.

FEATURES Location/Qualifiers
source 1. .619
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="Guy11"
/db_xref="taxon:148305"
/clone="mgcm006xO03"
/sex="Mat1-2 hermaphrodite"
/cell_type="mycelium"
/clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2: XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

ORIGIN

Alignment Scores:

Pred. No.:	1.08e-181	Length:	619
Score:	172.00	Matches:	172
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-507-132-4 (1-172) x BM863356 (1-619)

```
Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
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Db         53 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 112

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
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Db        113 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 172

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        173 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 232

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 292

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 352

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
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Db        353 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 412

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 472

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 GTCTGGAAGTTCGCCGGCCTCAAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGG 532

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAspLys 172
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Db        533 ATCTTTGAGGACGGACGGGAGACCTTTGGCGACAAA 568
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RESULT 2
BM864194
LOCUS BM864194 657 bp mRNA linear EST 06-MAY-2003
DEFINITION mgcm008xJ12f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm008xJ12 5', mRNA sequence.
ACCESSION BM864194
VERSION BM864194.2 GI:30390885
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE 1 (bases 1 to 657)
AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.
TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe grisea
JOURNAL Unpublished (2002)
COMMENT On Mar 7, 2002 this sequence version replaced gi:19231876.
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone dehydratase >gi|1127197|pdb|1STD|. . . 365 e-100
PCR PRimers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgcm008 row: J column: 12
Seq primer: T3.

FEATURES Location/Qualifiers
source 1. .657
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="Guy11"
/db_xref="taxon:148305"
/clone="mgcm008xJ12"
/sex="Mat1-2 hermaphrodite"
/cell_type="mycelium"
/clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2: XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."

ORIGIN

Alignment Scores:

Pred. No.:	1.49e-180	Length:	657
Score:	171.00	Matches:	171
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	99.4%	Indels:	0
DB:	3	Gaps:	0

US-10-507-132-4 (1-172) x BM864194 (1-657)

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Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
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```

```
Db         91 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 150

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
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Db        151 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 210

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 270

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 330

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 390

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 450

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
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Db        451 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 510

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
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Db        511 GTCTGGAAGTTCGCCGGCCTCAAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGG 570

Qy        161 IlePheGluAspGlyArgGluThrPheGlyAsp 171
              |||||||||||||||||||||||||||||||||
Db        571 ATCTTTGAGGACGGACGGGAGACCTTTGGCGAC 603

RESULT 3
BM863315
LOCUS       BM863315                664 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm006xE21f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm006xE21 5', mRNA sequence.
ACCESSION   BM863315
VERSION     BM863315.2  GI:30391622
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 664)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19230997.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 364 e-100
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm006  row: E  column: 21
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .664
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm006xE21"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

Alignment Scores:
Pred. No.:              3.44e-177      Length:          664
Score:                  168.00         Matches:         168
Percent Similarity:     100.0%         Conservative:    0
Best Local Similarity:  100.0%         Mismatches:      0
Query Match:            97.7%          Indels:          0
DB:                     3              Gaps:            0

US-10-507-132-4 (1-172) x BM863315 (1-664)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 140

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 200

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 260

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 320

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 380

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 440

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 500

Qy        141 ValTrpLysPheAlaGlyLeuLysProAspIleArgTrpGlyGluPheAspPheAspArg 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 GTCTGGAAGTTCGCCGGCCTCAAGCCCGACATCCGCTGGGGCGAGTTCGACTTTGACAGG 560

Qy        161 IlePheGluAspGlyArgGluThr 168
              |||||||||||||||||||||||
Db        561 ATCTTTGAGGACGGACGGGAGACC 584

RESULT 4
BM864156
LOCUS       BM864156                599 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm008xD02f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm008xD02 5', mRNA sequence.
ACCESSION   BM864156
VERSION     BM864156.2  GI:30390915
KEYWORDS    EST.
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SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 599)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19231838.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 302 3e-87
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm008  row: D  column: 02
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .599
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm008xD02"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

Alignment Scores:
Pred. No.:               5.33e-147      Length:          599
Score:                   141.00         Matches:         141
Percent Similarity:      100.0%         Conservative:    0
Best Local Similarity:   100.0%         Mismatches:      0
Query Match:             82.0%          Indels:          0
DB:                      3              Gaps:            0

US-10-507-132-4 (1-172) x BM864156 (1-599)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
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Db         79 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 138

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 198

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 258

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 318

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
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Db        319 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 378

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 ATCGGCTACCACCAGCTGCGCGTTCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 438

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeuHisTrpTyrLysLysIleAspGly 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTTCACTGGTACAAGAAGATCGACGGC 498

Qy        141 Val 141
              |||
Db        499 GTT 501

RESULT 5
BM863374
LOCUS       BM863374                510 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm006xC10f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm006xC10 5', mRNA sequence.
ACCESSION   BM863374
VERSION     BM863374.2  GI:30391576
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 510)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19231056.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 276 1e-73
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm006  row: C  column: 10
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .510
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm006xC10"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
```

assessed using phredPhrap version 991019 and trimmed
according to phd files (0.05) and for vector seqs."

ORIGIN

Alignment Scores:

Pred. No.:	5.58e-137	Length:	510
Score:	132.00	Matches:	132
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	76.7%	Indels:	0
DB:	3	Gaps:	0

US-10-507-132-4 (1-172) x BM863374 (1-510)

```
Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 142

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 202

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 262

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 322

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 382

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 442

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeu 132
              |||||||||||||||||||||||||||||||||||
Db        443 GTCACCATGAAGGGCCACGCTCACTCGGCAAACCTT 478
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RESULT 6
BM863357
LOCUS BM863357 530 bp mRNA linear EST 06-MAY-2003
DEFINITION mgcm006xO05f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm006xO05 5', mRNA sequence.
ACCESSION BM863357
VERSION BM863357.1 GI:19231039
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE 1 (bases 1 to 530)
AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.
TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe grisea
JOURNAL Unpublished (2002)
COMMENT Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone dehydratase >gi|1127197|pdb|1STD|. . . 276 1e-73
PCR PRimers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgcm006 row: O column: 05
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .530
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="Guy11"
/db_xref="taxon:148305"
/clone="mgcm006xO05"
/sex="Mat1-2 hermaphrodite"
/cell_type="mycelium"
/clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2: XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
ORIGIN

Alignment Scores:

Pred. No.:	5.75e-137	Length:	530
Score:	132.00	Matches:	132
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	76.7%	Indels:	0
DB:	3	Gaps:	0

US-10-507-132-4 (1-172) x BM863357 (1-530)

```
Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 142

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 202

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 262

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 322

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 382

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 442

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeu 132
              |||||||||||||||||||||||||||||||||||
Db        443 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTT 478
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RESULT 7
BM864467
LOCUS BM864467 643 bp mRNA linear EST 06-MAY-2003
DEFINITION mgcm010xH12f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm010xH12 5', mRNA sequence.
ACCESSION BM864467
VERSION BM864467.2 GI:30390655
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)

```
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 643)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19232149.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 320 8e-87
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm010  row: H  column: 12
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .643
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm010xH12"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

Alignment Scores:
Pred. No.:              6.71e-137      Length:         643
Score:                  132.00         Matches:        132
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            76.7%          Indels:         0
DB:                     3              Gaps:           0

US-10-507-132-4 (1-172) x BM864467 (1-643)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 204

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 264

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 324

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 384

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 444

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 504

Qy        121 ValThrMetLysGlyHisAlaHisSerAlaAsnLeu 132
              |||||||||||||||||||||||||||||||||||
Db        505 GTCACCATGAAGGGCCACGCCCACTCGGCAAACCTT 540

RESULT 8
BM863710
LOCUS       BM863710                571 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm007xE24f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm007xE24 5', mRNA sequence.
ACCESSION   BM863710
VERSION     BM863710.2  GI:30391295
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 571)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19231392.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 336 1e-91
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm007  row: E  column: 24
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .571
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm007xE24"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

Alignment Scores:
```

```
Pred. No.:              1.39e-133       Length:         571
Score:                  129.00          Matches:        129
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            75.0%           Indels:         0
DB:                     3               Gaps:           0

US-10-507-132-4 (1-172) x BM863710 (1-571)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 151

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 211

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 271

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 331

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 391

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 ATCGGCTACCACCAGCTGCGCGTCCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 451

Qy        121 ValThrMetLysGlyHisAlaHisSer 129
              |||||||||||||||||||||||||||
Db        452 GTCACCATGAAGGGCCACGCCCACTCG 478

RESULT 9
BM863639
LOCUS       BM863639                486 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm007xG13f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm007xG13 5', mRNA sequence.
ACCESSION   BM863639
VERSION     BM863639.2  GI:30391353
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 486)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19231321.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 293 5e-79
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm007  row: G  column: 13
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .486
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm007xG13"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

Alignment Scores:
Pred. No.:              3.68e-129       Length:         486
Score:                  125.00          Matches:        125
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            72.7%           Indels:         0
DB:                     3               Gaps:           0

US-10-507-132-4 (1-172) x BM863639 (1-486)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         55 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 114

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        115 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 174

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        175 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 234

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        235 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 294

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        295 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 354

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAspThrThrMetLysGlu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        355 ATCGGCTACCACCAGCTGCGCGTTCCGCACCAGAGGTACAAGGACACCACCATGAAGGAG 414

Qy        121 ValThrMetLysGly 125
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Db        415 GTCACCATGAAGGGC 429

RESULT 10
BM864018
LOCUS       BM864018                473 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm008xG12f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm008xG12 5', mRNA sequence.
ACCESSION   BM864018
VERSION     BM864018.2  GI:30391030
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 473)
```

```
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19231700.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 255 2e-67
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm008  row: G  column: 12
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .473
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm008xG12"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

Alignment Scores:
Pred. No.:              5.65e-118      Length:         473
Score:                  115.00         Matches:        115
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            66.9%          Indels:         0
DB:                     3              Gaps:           0

US-10-507-132-4 (1-172) x BM864018 (1-473)

Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 128

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 188

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 248

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 308

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 CTCCGCACGCAGCACTTTATCGGCGGCACGCGCTGGGAGAAAGTGTCCGAGGACGAGGTC 368

Qy        101 IleGlyTyrHisGlnLeuArgValProHisGlnArgTyrLysAsp 115
              |||||||||||||||||||||||||||||||||||||||||||
Db        369 ATCGGTTACCACCAGCTGCGCGTCCCGCACCAAAGGTACAAGGAC 413

RESULT 11
BM864472
LOCUS       BM864472                600 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm010xJ04f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm010xJ04 5', mRNA sequence.
ACCESSION   BM864472
VERSION     BM864472.2  GI:30390651
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 600)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19232154.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 268 5e-71
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm010  row: J  column: 04
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .600
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm010xJ04"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

Alignment Scores:
Pred. No.:              8.12e-108      Length:         600
Score:                  106.00         Matches:        106
Percent Similarity:     100.0%         Conservative:   0
Best Local Similarity:  100.0%         Mismatches:     0
Query Match:            61.6%          Indels:         0
DB:                     3              Gaps:           0

US-10-507-132-4 (1-172) x BM864472 (1-600)
```

```
Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 204

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 264

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 324

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 384

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 CTCCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCCGAGGACGAGGTC 444

Qy        101 IleGlyTyrHisGlnLeu 106
              ||||||||||||||||||
Db        445 ATCGGCTACCACCAGCTG 462
```

RESULT 12
BM863499
LOCUS BM863499 504 bp mRNA linear EST 06-MAY-2003
DEFINITION mgcm006xL19f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm006xL19 5', mRNA sequence.
ACCESSION BM863499
VERSION BM863499.2 GI:30391475
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE 1 (bases 1 to 504)
AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.
TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe grisea
JOURNAL Unpublished (2002)
COMMENT On Mar 7, 2002 this sequence version replaced gi:19231181.
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone dehydratase >gi|1127197|pdb|1STD|. . . 260 7e-69
PCR PRimers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgcm006 row: L column: 19
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .504
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="Guy11"
/db_xref="taxon:148305"
/clone="mgcm006xL19"
/sex="Mat1-2 hermaphrodite"
/cell_type="mycelium"
/clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
/note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2: XhoI; Unidirectional cloning. EcoRI side has T3 primer and predominantly 5' reads. T7 primer on XhoI side of insert. Strain inoculated into complete medium grown for two days at room temperature, 150 rpm, harvested, blended, reinoculated into complete medium 24 h, room temperature, 150 rpm. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 991019 and trimmed according to phd files (0.05) and for vector seqs."
ORIGIN

Alignment Scores:

Pred. No.:	1.22e-105	Length:	504
Score:	104.00	Matches:	104
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	60.5%	Indels:	0
DB:	3	Gaps:	0

US-10-507-132-4 (1-172) x BM863499 (1-504)

```
Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 145

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 205

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 265

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 325

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSerGluAspGluVal 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 CTCCGCACGCAGCACTTCATCGGGGGCACGCGCTGGGAGAAGGTGTCCGAAGACGAGGTC 385

Qy        101 IleGlyTyrHis 104
              ||||||||||||
Db        386 ATCGGCTACCAC 397
```

RESULT 13
BM864053
LOCUS BM864053 366 bp mRNA linear EST 06-MAY-2003
DEFINITION mgcm008xM18f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe grisea cDNA clone mgcm008xM18 5', mRNA sequence.
ACCESSION BM864053
VERSION BM864053.1 GI:19231735
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE 1 (bases 1 to 366)
AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai,K. and Dean,R.A.
TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe grisea
JOURNAL Unpublished (2002)
COMMENT Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact person;Best nr hit (April. 22, 2003) pdb|4STD|A Chain A, High Resolution Structures Of Scytalone Dehy. . . 223 6e-58
PCR PRimers

```
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm008  row: M  column: 18
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .366
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm008xM18"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

Alignment Scores:
Pred. No.:                1.65e-103      Length:          366
Score:                    102.00         Matches:         102
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              59.3%          Indels:          0
DB:                       3              Gaps:            0

US-10-507-132-4 (1-172) x BM864053 (1-366)

Qy          71 SerSerLysGlnValLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThr 90
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           3 TCGAGCAAGCAGGTGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACG 62

Qy          91 ArgTrpGluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgValProHis 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          63 CGCTGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCAC 122

Qy         111 GlnArgTyrLysAspThrThrMetLysGluValThrMetLysGlyHisAlaHisSerAla 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         123 CAGAGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCA 182

Qy         131 AsnLeuHisTrpTyrLysLysIleAspGlyValTrpLysPheAlaGlyLeuLysProAsp 150
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         183 AACCTTCACTGGTACAAGAAGATCGACGGCGTCTGGAAGTTCGCCGGCCTCAAGCCCGAC 242

Qy         151 IleArgTrpGlyGluPheAspPheAspArgIlePheGluAspGlyArgGluThrPheGly 170
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         243 ATCCGCTGGGGCGAGTTCGACTTTGACAGGATCTTTGAGGACGGACGGGAGACCTTTGGC 302

Qy         171 AspLys 172
               ||||||
Db         303 GACAAA 308

RESULT 14
BM863340
LOCUS       BM863340                649 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm006xK09f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm006xK09 5', mRNA sequence.
ACCESSION   BM863340
VERSION     BM863340.2  GI:30391603
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 649)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19231022.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 361 5e-99
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm006  row: K  column: 09
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .649
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm006xK09"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN

Alignment Scores:
Pred. No.:                3.42e-102      Length:          649
Score:                    101.00         Matches:         101
Percent Similarity:       100.0%         Conservative:    0
Best Local Similarity:    100.0%         Mismatches:      0
Query Match:              58.7%          Indels:          0
DB:                       3              Gaps:            0

US-10-507-132-4 (1-172) x BM863340 (1-649)

Qy          32 SerLysAspTrpAspArgLeuArgLysValIleAlaProThrLeuArgIleAspTyrArg 51
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         177 TCCAAGGACTGGGATAGGCTGCGAAAGGTCATTGCGCCTACTCTGCGCATTGACTACCGC 236

Qy          52 SerPheLeuAspLysLeuTrpGluAlaMetProAlaGluGluPheValGlyMetValSer 71
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         237 TCCTTCCTCGACAAGCTCTGGGAGGCAATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCG 296

Qy          72 SerLysGlnValLeuGlyAspProThrLeuArgThrGlnHisPheIleGlyGlyThrArg 91
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         297 AGCAAGCAGGTGCTGGGCGACCCCACCCTCCGCACGCAGCACTTCATCGGCGGCACGCGC 356

Qy          92 TrpGluLysValSerGluAspGluValIleGlyTyrHisGlnLeuArgValProHisGln 111
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         357 TGGGAGAAGGTGTCCGAGGACGAGGTCATCGGCTACCACCAGCTGCGCGTCCCGCACCAG 416
```

```
Qy        112 ArgTyrLysAspThrThrMetLysGluValThrMetLysGlyHisAlaHisSerAlaAsn 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 AGGTACAAGGACACCACCATGAAGGAGGTCACCATGAAGGGCCACGCCCACTCGGCAAAC 476

Qy        132 Leu 132
              |||
Db        477 CTT 479
```

```
RESULT 15
BM861952
LOCUS       BM861952                398 bp    mRNA    linear   EST 06-MAY-2003
DEFINITION  mgcm001xL17f.b Magnaporthe grisea CM Uni-Zap XR Library Magnaporthe
            grisea cDNA clone mgcm001xL17 5', mRNA sequence.
ACCESSION   BM861952
VERSION     BM861952.2  GI:30392735
KEYWORDS    EST.
SOURCE      Magnaporthe grisea (anamorph: Pyricularia grisea)
  ORGANISM  Magnaporthe grisea
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE   1  (bases 1 to 398)
  AUTHORS   Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
            Bhatterai,K. and Dean,R.A.
  TITLE     Expressed sequence tags from the rice blast fungus, Magnaporthe
            grisea
  JOURNAL   Unpublished (2002)
COMMENT     On Mar 7, 2002 this sequence version replaced gi:19229634.
            Contact: Ebbole DJ
            Department of Plant Pathology & Microbiology
            Texas A&M University
            Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
            Tel: 979 845 4831
            Fax: 979 845 6483
            Email: d-ebbole@tamu.edu
            Chromatogram file of this sequence is available, see contact
            person;Best nr hit (April. 22, 2003) sp|P56221|SCYD_MAGGR Scytalone
            dehydratase >gi|1127197|pdb|1STD|. . . 209 7e-54
            PCR PRimers
            FORWARD: T3 primer
            BACKWARD: T7 primer
            Plate: mgcm001  row: L  column: 17
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .398
                     /organism="Magnaporthe grisea"
                     /mol_type="mRNA"
                     /strain="Guy11"
                     /db_xref="taxon:148305"
                     /clone="mgcm001xL17"
                     /sex="Mat1-2 hermaphrodite"
                     /cell_type="mycelium"
                     /clone_lib="Magnaporthe grisea CM Uni-Zap XR Library"
                     /note="Vector: pBluescriptSK-; Site_1: EcoRI; Site_2:
                     XhoI; Unidirectional cloning. EcoRI side has T3 primer and
                     predominantly 5' reads. T7 primer on XhoI side of insert.
                     Strain inoculated into complete medium grown for two days
                     at room temperature, 150 rpm, harvested, blended,
                     reinoculated into complete medium 24 h, room temperature,
                     150 rpm. Sequences were processed by one of two methods.
                     Where a full-length alignment to the M. grisea genome
                     sequence was available, the EST sequence was trimed
                     according to the alignment, otherwise sequence quality was
                     assessed using phredPhrap version 991019 and trimmed
                     according to phd files (0.05) and for vector seqs."
ORIGIN
```

```
Alignment Scores:
Pred. No.:              9.17e-97        Length:         398
Score:                  96.00           Matches:        96
Percent Similarity:     100.0%          Conservative:   0
Best Local Similarity:  100.0%          Mismatches:     0
Query Match:            55.8%           Indels:         0
DB:                     3               Gaps:           0
```

US-10-507-132-4 (1-172) x BM861952 (1-398)

```
Qy          1 MetGlySerGlnValGlnLysSerAspGluIleThrPheSerAspTyrLeuGlyLeuMet 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         88 ATGGGTTCGCAAGTTCAAAAGAGCGATGAGATAACCTTCTCAGACTACCTGGGCCTCATG 147

Qy         21 ThrCysValTyrGluTrpAlaAspSerTyrAspSerLysAspTrpAspArgLeuArgLys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        148 ACTTGCGTCTATGAGTGGGCAGACAGCTACGACTCCAAGGACTGGGATAGGCTGCGAAAG 207

Qy         41 ValIleAlaProThrLeuArgIleAspTyrArgSerPheLeuAspLysLeuTrpGluAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 GTCATTGCGCCTACTCTGCGCATTGACTACCGCTCCTTCCTCGACAAGCTCTGGGAGGCA 267

Qy         61 MetProAlaGluGluPheValGlyMetValSerSerLysGlnValLeuGlyAspProThr 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 ATGCCGGCCGAGGAGTTCGTCGGCATGGTCTCGAGCAAGCAGGTGCTGGGCGACCCCACC 327

Qy         81 LeuArgThrGlnHisPheIleGlyGlyThrArgTrpGluLysValSer 96
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 CTTCGCACGCAGCACTTCATCGGCGGCACGCGCTGGGAGAAGGTGTCC 375
```

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Search completed: December  4, 2006, 18:35:44
Job time : 4369 secs
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